

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 22:03:04 ; Search time 4463.92 Seconds
(without alignments)
12876.070 Million cell updates/sec

Title: US-09-750-240-5

Perfect score: 3549

Sequence: 1 atgtatggttttagtgccct.....aagggaaccaagtggtggcact 3549

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_esti:*

9: gb_esti:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pin:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	808.8	22.8	1039	14	BM811640
2	772	21.8	1016	14	BQ881496
3	718.8	20.3	775	12	BF792125
4	593.4	16.7	676	12	BE840188
5	573.6	16.2	1225	13	BI691747
6	565.8	15.9	1043	12	BG297229

7	559.8	15.8	743	13	BI685206
8	549.6	15.5	796	12	BG287169
9	540.2	15.2	581	13	BG993320
10	532.4	15.0	790	13	BI255147
11	512.4	14.4	905	14	BQ231940
12	494.8	13.9	607	14	BM943080
13	485.4	13.7	487	9	AL119686
14	473.2	13.3	652	9	AA207907
15	463.4	13.1	565	12	BG872335
16	457.6	12.9	737	10	BE377119
17	449.6	12.7	685	14	BM964004
18	442.4	12.5	525	13	BM090325
19	437.8	12.3	809	9	AU169950
20	418.6	11.8	682	14	BQ180663
21	407.4	11.5	420	12	BF935972
22	400.8	11.3	447	10	BE487801
23	393.2	11.1	442	9	AI905602
24	393.2	11.1	466	9	AI905641
25	393.2	11.1	592	13	BI680978
26	392.8	11.1	453	12	BE838164
27	390.2	11.0	618	10	BB866520
28	390.2	11.0	3369	11	BC020148
29	388.2	10.9	456	12	BF553668
30	387.8	10.9	417	12	BE840138
31	381.8	10.8	548	10	AV604444
32	377	10.6	939	13	BI873142
33	370.2	10.4	584	14	BQ355201
34	363.8	10.3	425	10	AW481229
35	361.8	10.2	625	12	BF369868
36	347.2	9.8	611	12	BG004182
37	345.8	9.7	673	14	BQ370134
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39	333.2	9.4	566	9	AI784441
40	326.4	9.2	331	14	F13214
41	325.6	9.2	504	13	BI817175
42	320.4	9.0	821	13	BI257844
43	320.2	9.0	2661	11	BC028085
44	311	8.8	567	13	BI739363
45	305.8	8.6	824	13	BI257519

ALIGNMENTS

RESULT 1	BM811640	1039 bp	mRNA	linear	EST 05-MAR-2002
LOCUS	BM811640	AGENCOURT_6489534	NIH_MGC_125	Homo sapiens	cdna clone IMAGE:5724057
DEFINITION	5', mRNA sequence.				
ACCESSION	BM811640				
VERSION	BM811640.1	GI:19128463			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1039)				
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Invitrogen CDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Agencourt Bioscience Corporation Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov High quality sequence stop: 644. Location/Qualifiers 1..1039				

Db	162	GTCTGTCGGCAGCATTTCCGCTACGGGCACATAGCCGCTAGTTGGCATCTTTTCCG	221					
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Db	222	TCCTGCTGTGTTTACTTCTGCCATTGCCAACATGTTTCACTGTAAACACACACCCCATAC	281					
Qy	2306	GGAGCTGTGCAGCCCGGATGCTGAATTTAAACACTGCTGACATCACTGCCACCTGC	2365					
Db	282	GGAGCTGTGCAGCCCGGATGCTGAATTTAAACACTGCTGACATCACTGCCACCTGC	341					
Qy	2366	AGCAGCTCAATTACTCTCTGGGCGCTGATGCTCCCTGTTGTGAGGGCACCATGCCACCT	2425					
Db	342	AGCAGCTCAATTACTCTCTGGGCGCTGATGCTCCCTGTTGTGAGGGCACCATGCCACCT	401					
Qy	2426	GCAGCTTTCCTGAGGTTGCCATCGGGAAACATGCTGCTGAGTCTCTTGGCCAGCTCTGTCT	2485					
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Qy	2486	TCCTGTCACATCAGCAGCATCGGGAAGTTGGGCATGATCTTTGTGCTTGGGGCTCATCTATT	2545					
Db	462	TCCTGTCACATCAGCAGCATCGGGAAGTTGGGCATGATCTTTGTGCTTGGGGCTCATCTATT	521					
Qy	2546	TGSGTGTGCTCTCTCTGGGTCCCGCCAGCCCATCTTTGACAACTATGACCTACTGCTTG	2605					
Db	522	TGSGTGTGCTCTCTCTGGGTCCCGCCAGCCCATCTTTGACAACTATGACCTACTGCTTG	581					
Qy	2606	CGCTCCCATGGCTTGGCTTCTTCCAAATGAGACCTTTGATGGCTGCTGCAGCTGCAG	2665					
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Qy	2666	GGAGGGT-GGCGCTCAAAATATATGACCCCTGTGATTTCTGCTGTTTGGCGTGGCGCTG	2724					
Db	641	GGAGGGTGGGCGCTCAAAATATATGACCCCTGTGATTTCTGCTGTTTGGCGTGGCGCTG	700					
Qy	2725	TATCTGCATGCTCAGCAGGTGGAATCGACTG-CCCGCCTAAACTTCTCTGGAAACTACA	2783					
Db	701	TATCTGCATGCTCAGCAGGTGGAATCGACTGCGCCCGCTAGACTTCTCTGGAAACTACA	760					
Qy	2784	GGCAACAGGGGAAAAGAGGAGATGG-AGGAGCTACAGGCATACAACCGGAGGCTGCTGC	2842					
Db	761	GGCAACAGGGGAAAAGAGGAGATGGAGGAGCTACAGGCATACAACCGGAGGCTGCTGC	820					
Qy	2843	ATAACATCTTGCCCAAGGACGTGGCGGCCACTTCCCTGG--CCCGGAGGCGCCCAATGA	2900					
Db	821	ATAACATCTTGCCCAAGGACGTGGCGGCCCTTCTTGGCGCGGGAACGCGGCCAATGA	880					
Qy	2901	TGAATCTACTATCAGTC---GTGTGAGTGTGGCTGTGTTATGTTTGCCTCCATT-GCCA	2956					
Db	881	TGAATCTACTATCAGTCTGTGAATGGGTGGGCTGTATGTTTGGCTTCCATTGGCCCA	940					
Qy	2957	ACTTCTCTGAGTTCTTAT-GTGGAGCTGGAGGCAACAATGAGGGTG	3001					
Db	941	CCTTCTCTGAGTTCCATGGGGAGCTGGGAGAAACAATGAAGGG	986					
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LOCUS	602252571F1 NIH_MGC_84	Homo sapiens	cDNA	clone IMAGE:4345144 5'				
DEFINITION	mRNA sequence.							
ACCESSION	BF792125							
VERSION	BF792125.1	GI:12097179						
KEYWORDS	EST.							
SOURCE	human.							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
AUTHORS	1 (bases 1 to 775)							
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .							
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)							
COMMENT	Unpublished (1999)							
	Contact: Robert Strausberg, Ph.D.							

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QY 3403 CTAGCTCCCAAGGCTACCAAGCTGAGTGTGAGGGGTGCTCAAGGTGAAGGGCAAGGG 3462
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Db 671 CTAGCTCCCAAGGCTACCAAGCTGAGTGTGAGGGGTGCTCCACGTGAAGGGCAAGGG 730
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QY 3463 GAGATGACCACTTACTTCTCAATGGGGGCC 3494
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Db 731 GAGATGACACTAA--TTCTCAATGGGGGCC 760
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LOCUS BE840188 676 bp mRNA linear EST 22-SEP-2000
DEFINITION QV0-FN0181-100800-335-d08 FN0181 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE840188
VERSION BE840188.1 GI:10272566
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 676)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL PROC. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel.: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-QV0-FN0181-100
800-335-d08&t3=2000-08-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 625.
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/db_xref="taxon:9606"
/clone_lib="FN0181"
/dev_stage="Adult"
/notes="Organ: prostate-normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT 125 a 203 c 193 g 155 t
ORIGIN
Query Match 16.7%; Score 593.4; DB 12; Length 676;
Best Local Similarity 95.9%; Pred. No. 2.1e-124;
Matches 609; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
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Db 2 GACCAGCAGGGTGGCGTGTGGCGAGCTGCAAGCGTACCTCAAGGAGCAGCATTGAG 61
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QY 1642 ACTTCTCTATCTTGGCGCGCAGCCAGCAAAACGGAAGAGGAGGATGCTGGCCAG 1701
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Db 542 CTAAATCACTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 601
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QY 2182 CAAGTCTGTCGCGCAGCATTTGCTCGCTCAAGGCG 2216
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Db 602 CAAGTCTGTCGCGCAGCATTTGCTCGCTCAAGGCG 636
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RESULT 5
BI691747
LOCUS BI691747 1225 bp mRNA linear EST 18-SEP-2001
DEFINITION BI691747.1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5343565 5',
mRNA sequence.
ACCESSION BI691747
VERSION BI691747.1 GI:15654376
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1225)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11872 row: n column: 14
High quality sequence start: 2
High quality sequence stop: 693.
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/strain="FVB/N"
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QY 3251 TTGGGCTGAACATGGGCCCCAGTCTGTCGAGGTGTCATCGGGGCTCGGAAGCCACAGATG 3310

Db 490 TCGGGTTGAACATGGTCCGGTTCTAGCAGCGCTCATCGGGGCCGGAAGCCACAGATG 549

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Db 550 ACATCTGGGGAATACCGTGAATGCTCTAGTCTATGATGGACAGCAGCGGGTCCCCGACC 609

QY 3371 GAATCCAGGTGACACAGCACTGTACCAAGTCTTAGCTGCCAAGGGTACCAAGTGGAGT 3430

Db 610 GAATACAGGTGACTACCGAGCTATACCAAGTCTTAGCTGCCAAGGGTACCAAGTGGAGG 669

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Db 728 GGCACAGCAGGTAGCAAG 746

RESULT 7

BI685206 743 bp mRNA linear EST 18-SEP-2001

LOCUS 603310213F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5346147 5',

DEFINITION mRNA sequence.

ACCESSION BI685206

VERSION BI685206.1 GI:15647834

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

AUTHORS NIH-MGC http://mgi.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: Jeffrey Green M.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLAMI1879 row: j column: 04

High quality sequence stop: 741.

Location/Qualifiers

1. 743

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/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: Salt; Site:2: NotI; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 149 a 208 c 213 g 173 t

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Query Match 15.88; Score 559.8; DB 13; Length 743;

Best Local Similarity 87.7%; Pred. No. 9.8e-117;

Matches 634; Conservative 0; Mismatches 87; Indels 2; Gaps 2;

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Db 23 CTGAGGTTCCCTTGAGTACTTCTGTCGGAACAGTGTCTGCTGAGTCTTCTAGCCAGCTCTGT 82

QY 2484 CTTCTCTACATCAGCAGCATCGGAAAGTTGGCCATGATCTTTGTCTTGGGGTTCATCTA 2543

Db 83 CTTCTCTACATCAGCAGCATCGGAAAGTTGGCCATGATCTTTGTCTTGGGGTTCACCTA 142

QY 2544 TTTGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2603

Db 143 CTTGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 202

QY 2604 TGGCGTCCATGGCTTGGCTTCTTCCATGAGACCTTTGATGGGCTGGACGTGTCAGCTGC 2663

Db 203 TGGCGTCCATGGCTTGGCTTCTTCCATGAGACCTTTGATGGGCTGGACGTGTCAGCTGC 262

QY 2664 AGGAGGCTGGCCCTCAATATATATGACCCCTGTGATTTCTGCTGGTGTGCTGGTGGCGCT 2723

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QY 2724 GTATCTGATGCTCAGCAGGTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2783

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QY 2784 GGCAACAGGGGAAAGAGGAGATGGAGGACTACAGGCATACAAACCGGAGGCTGCTGCA 2843

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Db 623 TGAGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 681

QY 3084 GATCAACAGCATTTGGTAGCACCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3143

Db 682 GATCAACAGCATTTGGTAGCACCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 740

QY 3144 TCA 3146

Db 741 CCA 743

RESULT 8

BI685206 796 bp mRNA linear EST 21-FEB-2001

LOCUS 602381888F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4499589 5',

DEFINITION mRNA sequence.

ACCESSION BI685206

VERSION BI685206.1 GI:13040741

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS NIH-MGC http://mgi.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM10363 row: p column: 22
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High quality sequence stop: 680.

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/clone_lib="NIH_MGC_93"
/clone_type="translational cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

BASE COUNT 207 a 193 c 245 g 151 t

Query Match 15.5%; Score 549.6; DB 12; Length 796;
Best Local Similarity 97.0%; Pred. No. 2.1e-114; Indels 5; Gaps 5;
Matches 613; Conservative 0; Mismatches 14;

Qy 2920 TGTGAGTGTGGCTGTATGTTGGCTCCCATGTCACACTTCTCTGAGTCTTATGTGGAG 2979
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Db 1 TGAAGGTGTGGCTGTATG-TTGGCTCCATGGCACTTCTGAGTCTTATGTGGAG 59
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Qy 2980 CTGAGGCAACAATGAGGGTGCAGTGCCTGCGGCTGCTCAACGAGATCATCGTGAC 3039
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Qy 3040 TTTGATGAGATTATCAGCGAGGAGCGGTTCCGGCAGCTGGAAGATCAAGACGATTGCT 3099
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Qy 3100 AGCACCTACATGGCTGCTCAGGCGTGAACGCCAGCACTACGATCAGTGGCGCGTCC 3159
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Qy 3220 GAGCACTCTTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGGCCCACTGCTGGCA 3279
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Db 298 GAGCACTCTTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGGCCCACTGCTGGCA 357
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Qy 3280 GGTGTCACTGGGGCTCGGAAGCCACAGPATGACATCTCGGGGGAACACAGTAATGTCTCT 3339
|||
Db 358 GGTGTCACTGGGGCTCGGAAGCCACAGPATGACATCTCGGGGGAACACAGTAATGTCTCT 417
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Qy 3340 ACTGATATGACAGACAGGGGGTCCCGACCGAATCCAGGTGACACAGGACCTGTACACAG 3399
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Db 418 AGTCGATATGACAGACAGGGGGTCCCGACCGAATCCAGGTGACACAGGACCTGTACACAG 477
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Qy 3400 GTTCTAGCTGCCAAGGGCTACACGTGAGTGTGAGGGGTGGTCAAGGTGAAGGGCAAG 3459
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Db 478 GTTCTAGCTGCCAAGGGCTACACGTGAGTGTGAGGGGTGGTCAAGGTGAAGGGCAAG 537
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Qy 3460 GGGAGATGACACCTACTTCTCT-CAATGGGGGGCCCCAGCAGTAAACAGGGCCCCAGCCAC 3518
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Db 538 GGGAGATGACACCTACTTCTCTCAATGGGGGGCCCCAGCAGTAAACAGGGCCCCAGCCAC 597
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Qy 3519 AAATTCAGCTG-AAGGGACCAAGGTGGGCACT 3549
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Db 598 AATTCAAGCTTGAAAGGGGACCAAGGTGGGCATT 629

RESULT 9
BG993320

LOCUS 581 bp mRNA linear EST 13-JUN-2001

DEFINITION MR3-HT0999-070201-003-h04 HT0999 Homo sapiens cDNA, mRNA sequence.

ACCESSION BG993320

VERSION BG993320.1 GI:14397390

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 581)

REFERENCE
AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663

TITLE

JOURNAL
MEDLINE
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=Hr3&t2=MR3-HT0999-070201-003-h04&t3=2001-02-07&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 581.

FEATURES
source
1..581
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0999"
/dev_stage="Adult"
/note="Organ: head neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 118 a 157 c 199 g 106 t 1 others

ORIGIN

Query Match 15.2%; Score 540.2; DB 13; Length 581;
Best Local Similarity 98.2%; Pred. No. 2.6e-112;
Matches 556; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Qy 1256 GCCTGAGGATCAAGATCTTTGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGGAGGCC 1315
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Db 17 GCCTGAGGATCAAGATCTTTGGGGAC-GTTACTACTGTGTGTCAGGGCTGCCGGAGGCC 75
|||||
Qy 1316 GGGCCGACCATGCCACCTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGC 1375
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Db 76 GGGCCGACCATGCCACCTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGC 135
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Qy 1376 TGGTACGTGAGTGACAGGTGTGAATGTGAACATCGCGTGGGCATCCACACGCGGCGCG 1435
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Db 136 TGGTACGTGAGTGACAGGTGTGAATGTGAACATCGCGTGGGCATCCACACGCGGCGCG 195
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Qy 1436 TGCATCGGGCGTCCCTTGGCTTGGCGAAATGCACTTCGATGTGTGTTCCATGATGTGA 1495
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Db 196 TGCACTCGGGGTCCTTTGGCTTGGCGAAATGGCAGTTTCGATGTGTGTCCTCAATGATGTA 255
QY 1496 CCCTGGCAACACATGAAGCAGGAAGCGGGGTGGCCGCATCCACATCACTCGGGCAA 1555
Db 256 CCCTGGCAACACATGAAGCAGGAGCGGGGTGGCCGCATCCACATCACTCGGGCAA 315
QY 1556 CACTGCAAGTACCTGAACGGGGACTACGAAGTGGAGCGAGCGCGGTGGGAAGCGCAACG 1615
Db 316 CACTGCAAGTACCTGAACGGGGACTACGAAGTGGAGCGAGCGCGGTGGGAAGCGCAACG 375
QY 1616 CGTACCTCAAGGAGCAGCACAATGAGACTTTCCTCATCTTGGCGCCGAGCAGCAAAACGGA 1675
Db 376 CGTACCTCAAGGAGCAGCACAATGAGACTTTCCTCATCTTGGCGCCGAGCAGCAAAACGGA 435
QY 1676 AAGAGGAGAAGGATGCTGGCCAAAGTGCAGCGGACTCGGGCCAACTCCATGGAAGGGC 1735
Db 436 AAGAGGAGAAGGATGCTGGCCAAAGTGCAGCGGACTCGGGCCAACTCCATGGAAGGGC 495
QY 1736 TGATCGCGGATGGGTTCCCTGATGCTGCTCTTCCCGGACCAAGGACTCCAAGGCCCTTCC 1795
Db 496 TGATCGCGGATGGGTTCCCTGATGCTGCTCTTCCCGGACCAAGGACTCCAAGGCCCTTCC 555
QY 1796 GCCAGATGGCATGATGATTCACG 1821
Db 556 GNCAGATGGGCATGATGATTCACG 581

RESULT 10
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LOCUS 602977410F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5122130 5',
DEFINITION mRNA sequence.
ACCESSION BI255147
VERSION BI255147.1 GI:14808265
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-femail.nih.gov
Tissue Procurement: ATCC
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11298 row: d column: 03
High quality sequence stop: 634.
FEATURES
    Location/Qualifiers
    1..790
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:5122130"
    /clone_lib="NIH_MGC_12"
    /tissue_type="cervical carcinoma cell line"
    /lab_host="DH10B"
    /note="Organ: cervix; Vector: pCMV-Sport6; Site:1: NotI;
    Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.
    Average insert size 1.4 kb. Library prepared by Life
    Technologies."
BASE COUNT 168 a 202 c 231 g 189 t
ORIGIN
Query Match 15.0%; Score 532.4; DB 13; Length 790;
Best Local Similarity 89.9%; Pred. No. 1.7e-110;
Matches 707; Conservative 0; Mismatches 61; Indels 18; Gaps 12;

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QY 2542 TATTTGGTGTGCTTCTGTGCTGGTCCCGAGCCGCCACTTTTGACAACTATGACCTACTG 2601
Db 10 TATTTGGTGTGCTG-TTCTGTGCTGGTCCCGAGCCGCCACTTTTGACAACTATGACCTACTG 68
QY 2602 CTTGGCGCTCATGGCTTGGCTTCTTCCAAATGAGACCTTTTGTATGGGCTGGAGCTGTCCAGCT 2661
Db 69 CTTGGCGCTC--ATGGCTTGGTCTTCCAAATGAGACCTTTTGTATGGGCTGGAGCTGTCCAGCT 126
QY 2662 GCAGGGAGGGTGGCCCTCAAAATATATGACCCCTGTGATTTCTGTGCTGTTTGGCTGGCG 2721
Db 127 GCAGGGAGGGTGGCCCTCAAAATATATGACCCCTGTGATTTCTGTGCTGTTG-TTGGCTGGCG 185
QY 2722 CTGTATCTGCATGCTCAGCAGGTGGAATCGACTGCCCGCTTAAACTTCTCTGGAACATA 2781
Db 186 CTGTATCTGCATGCTCAGCAGGTGGAATCGACTGCCCGCTTAAACTTCTCTGGAACATA 245
QY 2782 CAGGCAACAGGGGAAAAGAGGAGATGGAGAGCTACAGGCATACACCCGAGGCTGCTG 2841
Db 246 CAGGCAACAGGGGAAAAGAGGAGATGGAGAGCTACAGGCATACACCCGAGGCTGCTG 305
QY 2842 CATAAATCTTGCCTCAAGGACGTGGCGGCCACTTCTGCGCGGGAGCGCCGCAATGAT 2901
Db 306 CATAAATCTTGCCTCAAGGACGTGGCGG-CACTTCTGCGCGGGAGCGCCGCAATGAT 364
QY 2902 GAACTCTACTATCAGTCGTGTGAGTGTGTGCTGTTATGTTTGCCTCATTGTC-AACTT 2960
Db 365 GAACTCTACTATCAGTCGTGTGAGTGTGTGCTGTTATGTTTGCCTCATTGTCAAACTT 424
QY 2961 CTCTGAGTTCTATGTGGAGCTGGAGCAACAATGAGGGTGGCGAGTGCCTTGGCGCTGCT 3020
Db 425 CTCTGAGTTCTATGTGGAGCTGGAGCAACAATGAGGGTGTGCGAGTGCCTTGGCGTTGTC 484
QY 3021 CAACGAGATCATCGTGACTTTT-GATGAGATTATCAGCAGGAGCGGTTCCCGCAGC--T 3077
Db 485 AACCGAGATCATCGTGACTTTTCGATGAGATTATCAGGAGGAGCGGTTCCCGCAGCGTG 544
QY 3078 GGAAGAATCAAGACGATGGTACGACCTACATGCTCAGGCTCAGGGCTGAACGCCAGCA- 3136
Db 545 GAACACGATCAAGACGATGGTATGACACCTACATGGCTGCCTCAGGCTTGAACGCCAGCAA 604
QY 3137 -CCTACGATC--AGTGGCGCGCTCCACATCACTGCCCTGGCTGCTAGCTAC-GCATCGCG 3192
Db 605 CCTTACGATCCAGGTGGCGCGCTCCACATATGTCCTCTGTGCTAGCGGCTATCGCG 664
QY 3193 CTCATGGAGCAGATGAAGCACATCAATGA---GCATCTCTTCAACAATTTCCAGATGAAG 3249
Db 665 TCATTGGAGCAGATGAAGCACATCAATGACGCACTTCTTCAACAATTTCCAGATTAAG 724
QY 3250 ATTGGGCTGAACA-TGGGCGGAGTGTGGCAGGTGTGTCATCGGGCTCGGAAGCCACAGTA 3308
Db 725 ATGGGCTTGAACATTTGGGCGGAGTGTGTCATCGGGCTCGGAAGCCACAGTAT 784
QY 3309 TGACAT 3314
Db 785 TGACAT 790

RESULT 11
BI231940
LOCUS BQ231940
DEFINITION BQ231940 905 bp mRNA linear EST 02-MAY-2002
ACCESSION BQ231940
VERSION BQ231940.1 GI:20413340
KEYWORDS 5', mRNA sequence.
SOURCE EST.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

```

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM13345 row: p column: 01
High quality sequence stop: 609.

FEATURES

source

1. .905
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6067056"
/clone_lib="NIH_MGC_92"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

BASE COUNT 208 a 242 c 270 g 184 t 1 others

ORIGIN

Query Match 14.4%; Score 512.4; DB 14; Length 905;
Best Local Similarity 99.8%; Pred. No. 6.6e-106;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3036 TGACTTTGATGAGATTATCAGCAGGAGCGGTTCGGCAGCTGGAAGATCAAGACGAT 3095
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Qy 3096 TGGTAGACCTACATGGCTGCCTCAGGCTGGAAGCCAGCACCTACGATCAGTGGGCGG 3155
Db 61 TGGTAGACCTACATGGCTGCCTCAGGCTGGAAGCCAGCACCTACGATCAGTGGGCGG 120

Qy 3156 CTCCACATCATCTCCCTGGCTGACTACGCATCGCTCATGCGAGCAGATGAAGCACAT 3215
Db 121 CTCCACATCATCTCCCTGGCTGACTACGCATCGCTCATGCGAGCAGATGAAGCACAT 180

Qy 3216 CAATGAGCAGCTCTTCAACATTTCCAGATGAAGATTGGGCTGAACATGGGCCAGTCGT 3275
Db 181 CAATGAGCAGCTCTTCAACATTTCCAGATGAAGATTGGGCTGAACATGGGCCAGTCGT 240

Qy 3276 GCGAGGTGTATCGGGCTCGGAAGCCACAGATGACATCTGGGGGACACAGTGAATGT 3335
Db 241 GCGAGGTGTATCGGGCTCGGAAGCCACAGATGACATCTGGGGGACACAGTGAATGT 300

Qy 3336 CTCTAGTCGTATGACAGCAGCGGGTCCCGACCGAATCCAGGTGACCGGACCTGTA 3395
Db 301 CTCTAGTCGTATGACAGCAGCGGGTCCCGACCGAATCCAGGTGACCGGACCTGTA 360

Qy 3396 CCAGGTTCTAGCTGCCAAGGGCTACCAAGCTGAGTGTGAGGGGTGGTCAAGGTTGAAGG 3455
Db 361 CCAGGTTCTAGCTGCCAAGGGCTACCAAGCTGAGTGTGAGGGGTGGTCAAGGTTGAAGG 420

Qy 3456 CAAGGGGAGATGACCACTACTTCCATGAGTGGGGGCCCCAGCAGTTAAACAGGCCCCAGC 3515
Db 421 CAAGGGGAGATGACCACTACTTCCATGAGTGGGGGCCCCAGCAGTTAAACAGGCCCCAGC 480

Qy 3516 CACAAATTCAGCTGAAGGGACCAAGGTGGGCAT 3549
Db 481 CACAAATTCAGCTGAAGGGACCAAGGTGGGCAT 514

RESULT 12

BM943080/c

LOCUS

DEFINITION BM943080 607 bp mRNA linear EST 29-APR-2002
UI-M-CG0p-beo-d-02-0-UI.r1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone
UI-M-CG0p-beo-d-02-0-UI 5', mRNA sequence.

ACCESSION

BM943080.1 GI:19402943

VERSION

EST.

KEYWORDS

house mouse.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 607)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

Contact: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: mEST@mail.nih.gov

Tissue Procurement: Dr. Xin-Yuan Fu, Yale University School of

Medicine

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).

Seq primer: M13 REVERSE.

Location/Qualifiers

1. .607

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UI-M-CG0p-beo-d-02-0-UI"

/clone_lib="NIH_BMAP_Ret4_S2"

/lab_host="DH10B (Life Technologies)"

/note="Vector: pRT3D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; The

NIH_BMAP_Ret4_S2 library is a subtracted library,

ultimately derived from mouse retina tissue libraries at

various stages of development. For a detailed description

of the library from which this clone was derived, please

visit our web site at brainest.eng.uiowa.edu. The tissue

for this library was contributed by Dr. Xin-Yuan Fu, Yale

University School of Medicine"

BASE COUNT 136 a 180 c 162 g 126 t 3 others

ORIGIN

Query Match 13.9%; Score 494.8; DB 14; Length 607;

Best Local Similarity 88.9%; Pred. No. 5.9e-102;

Matches 547; Conservative 0; Mismatches 60; Indels 8; Gaps 1;

Qy 2542 TATTTGGTGTCTTCTGCTGGTCCCGCCAGCGCCATCTTTGACAACTATGACTACTG 2601

Db 607 TACTTGGTGTCTTNTGCTGGTCCCGCCGCGCCATCTTGTGACAACTATGACTACTG 548

Qy 2602 CTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACCTTTGATGGCTGGACTGTCCAGCT 2661

Db 547 CTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACCTTTGATGGCTGGACTGTCCAGCT 488

Qy 2662 GCAGGGAGGGTGGCCCTCAAAATATATGACCCCTGTGATTCGTGCGTGTGCGTGGCG 2721

Db 487 GTGGGAGGGTGGCGCTCAAAATATATGACCCCGCTGATTCGTGCGTGTGCGTGGCG 428

Qy 2722 CTGTATCTGCATCTCAGCAGTGAATCGACTGCCCGCTAAACTCTCTGGAACTA 2781

Db 427 CTGTATCTGCATGCACACAGAGTGAATCGACTGCCCGCTGGACTTCTGTGGAAGTTA 368

Qy 2782 CAGGCACAGGGGAAAAAGAGAGATGGAGGAGTACAGGCATACACCGGAGGCTGCTG 2841

Db 367 CAGGCACAGGGGAGAGAGATGGAGGAGTACAGGCATACACCGGAGGCTGCTG 308

Qy 2842 CATAACATCTGCCCAAGAGAGTGGCGGCCACCTCTCTGGCCCCGGGAGCGCCGAATGAT 2901

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Db 307 CATAAATCTTCCCAAGGACGTGGCGCCACATTCCTGCGCGGAGACGCCGCAACGAT 248
QY 2902 GAACCTCTACTATCAGTGTGAGTGAGTGCTGTTATGTTGCTCTCATTTGCCAATTC 2961
Db 247 GAGCTGTACTACCAAGTCTGTGAATGTGTGGCTGTCTATGTTGCTCTCATCGCCAAATTC 188
QY 2962 TCTGAGTCTTATGTGGAGCTGGAGGCAACAATGAGGCTGCCAGTGCCTCGCGCTGCTC 3021
Db 187 TCGAGTCTTACGTGGAGCTCGAGGCAACAACAGAGGCGTGGAGTCCCTGCGCTGCTC 128
QY 3022 AACGAGATCATCGCTGACTTTTGATGAGATTATCATCAGCAGGAGCGGTTCCGCGACCTGGAA 3081
Db 127 AATGAGATCATCGCAGACTTTTGAGC-----AGTGAGGAGAGATTCCGCGCAGTTGGAG 76
QY 3082 AAGATCAAGACGATTGTGATGACCACTTACATGCTGCTGCCCTCAGGCGTGAACGCCAGCACCTAC 3141
Db 75 AAGATCAAGACCAATCGGTAGCACCTTACATGCGCGCCTCTGGGCTAAATGCGAGCACCTAT 16
QY 3142 GATCAGGTGGGCCGC 3156
Db 15 GACCAGTGGGCCG 1

RESULT 13
AL119686
LOCUS
DEFINITION
AL119686 487 bp mRNA linear EST 25-FEB-2000
DEFINITION DKFZp761N2323_r1 761 (synonym: hamy2) Homo sapiens cDNA clone
AL119686 DKFZp761N2323 5', mRNA sequence.
ACCESSION
VERSION AL119686.1 GI:5925585
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 487)
AUTHORS Bloeker,H., Boecher,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
TITLE EST (Bloeker, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Bloeker H
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GbF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZp761N2323) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
Location/Qualifiers
source
1..487
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/db_xref="taxon:9606"
/clone="DKFZp761N2323"
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/lab_post="DH108"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

BASE COUNT 114 a 129 c 142 g 102 t
ORIGIN
Query Match 13.7%; Score 485.4; DB 9; Length 487;
Best Local Similarity 99.88; Pred. No. 7.7e-100;
Matches 486; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2935 GTTATGTTTCCCTCCATTCGCAACTTCTGTAGTTCTATGTGGAGCTGGAGGCAACAAT 2994
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Db 1 GTTATGTTTCCCTCCATTCGCAACTTCTGTAGTTCTATGTGGAGCTGGAGGCAACAAT 60
QY 2995 GAGGGTCCCGAGTGCCTGCGGCTGCTCAACGAGATCATCTGACTTTGATGAGATTATC 3054
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Db 61 GAGGGTGTGAGTGCCTGCGGCTGCTCAACGAGATCATCTGACTTTGATGAGATTATC 120
QY 3055 AGCGAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCCTACATGGCT 3114
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Db 121 AGCGAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCCTACATGGCT 180
QY 3115 GCCTCAGGGCTGAACGCCAGCACCTAGCATCAGTGGGGCGCTCCACATCAGTGCCTG 3174
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Db 181 GCCTCAGGGCTGAACGCCAGCACCTAGCATCAGTGGGGCGCTCCACATCAGTGCCTG 240
QY 3175 GCTGACTACGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCTCTCAAC 3234
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Db 241 GCTGACTACGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCTCTCAAC 300
QY 3235 AATTTCCAGATGAAGATTGGGCTGAACATGGGCCAGTGGCAGGTGTCTATGGCGGCT 3294
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Db 301 AATTTCCAGATGAAGATTGGGCTGAACATGGGCCAGTGGCAGGTGTCTATGGCGGCT 360
QY 3295 CGGAAGCCACAGTATGACATCTGGGGGAACACAGTGAATCTCTAGTCTATGGACAGC 3354
|||||
Db 361 CGGAAGCCACAGTATGACATCTGGGGGAACACAGTGAATCTCTAGTCTATGGACAGC 420
QY 3355 ACGGGGTCCCGACCAATCCAGGTGACCAAGCTGTACAGGTTCTAGTGTGCCAAG 3414
|||||
Db 421 ACGGGGTCCCGACCAATCCAGGTGACCAAGCTGTACAGGTTCTAGTGTGCCAAG 480
QY 3415 GGCTACC 3421
|||||
Db 481 GGCTACC 487

RESULT 14
AA207907
LOCUS
DEFINITION
AA207907 652 bp mRNA linear EST 12-MAR-1997
DEFINITION mv84h06.r1 GuayWoodford Beier mouse kidney day 7 Mus musculus cDNA
clone IMAGE:661787 5', similar to gb:M93422 Mouse adenylyl cyclase
type VI mRNA, complete cds (MOUSE);, mRNA sequence.
ACCESSION AA207907
VERSION AA207907.1 GI:1804964
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 652)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:407635
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 417.
FEATURES
Location/Qualifiers
source
1..652
/organism="Mus musculus"
/db_xref="C57BL/6J"
/db_xref="taxon:10090"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 565)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: coapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

```

found through the I.M.A.G.E. Consortium/LEML at:
http://image.lini.gov
Plate: L1AM10845 row: p column: 03
High quality sequence start: 11
High quality sequence stop: 565.
Location/Qualifiers
1..565
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4923890"
/clone_lib="NCI_CGAP_SC2"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: salivary gland; Vector: pCMV-SPORT6; Site:1:
NotI; Site:2: SalI; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
133 a 174 g 117 t
BASE COUNT

```

Db	361	ACAGCGACGTGTGCACTTGGCGGCTCTTGGCTTACGGAATGCGAGTTTGATGTCTGGT	420
QY	1484	CCATGATGTGACCTTGGCCAAACACATGGAAGCAGGAAGCCGGGCTGGCCGCATCCACA	1543
Db	421	CAACGATGTGACCTTGGCTTAACACATGAGAGCCGGGGCCGGCCGCATCCACA	480
QY	1544	TCACTCGGGCAACACTGCAGTACCTGTGAACGGGACTACGA-AGTGGAGCCAGGCCCTGGT	1602
Db	481	TCACTCGGGCTACACTGCAGTACTTGAACGGGACTATGACGGTGGAGCCAGGCCGTGGT	540

QY 1603 GGCAAGCGCAACCGGTACCTCAAGG 1627
|| | |||| ||||| |||||
Db 541 GGTGAACGCAATCGGTACCTCAAGG 565

Search completed: February 23, 2003, 04:21:47
Job time : 4501.92 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 22:03:04 ; Search time 394.948 Seconds
(without alignments)
12876.070 Million cell updates/sec

Title: US-09-750-240-1

Perfect score: 314

Sequence: 1 atgtcatgttttagtgacct.....acacggcgggaccgctgaa 314

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_nam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	ID	Description
1	199.2	63.4	618	10	BB866520
2	180	57.3	631	10	BB866451
3	60.2	19.2	1011	17	CNS02STX
4	58.8	18.7	941	13	BG916212
5	51.4	16.4	925	17	CNS0091P
6	50.4	16.1	1009	17	CNS010EW

7	43.4	13.8	846	17	CNS010RJ	AL099337 Drosophil
8	43	13.7	932	17	CNS0072Q	AL066742 Drosophil
9	43	13.7	950	14	BQ948546	BQ948546 AGENCOURT
10	42.4	13.5	778	14	BQ892531	BQ892531 AGENCOURT
11	42.4	13.5	925	17	CNS0091P	AL053013 Drosophil
12	42.4	13.5	1085	17	CNS0108S	AL098662 Drosophil
13	41.8	13.3	935	17	CNS006XK	AL066051 Drosophil
14	41.8	13.3	968	17	AG030603	AG030603 Pan trogl
15	41.4	13.2	1075	17	AG073983	AG073983 Pan trogl
16	41.2	13.1	1010	14	BQ064125	BQ064125 AGENCOURT
17	41.2	13.1	1203	17	CNS015Y4	AL106054 Drosophil
18	40.6	12.9	884	17	CNS018NP	AL109567 Drosophil
19	40.6	12.9	948	14	BQ646304	BQ646304 AGENCOURT
20	40.4	12.9	486	10	BE233788	BE233788 140263 MA
21	40.4	12.9	894	17	CNS0159I	AL105168 Drosophil
22	40.4	12.9	1612	13	BM455541	BM455541 AGENCOURT
23	40.2	12.8	1101	17	CNS0150D	AL104839 Drosophil
24	40	12.7	844	17	CNS0052P	AL056652 Drosophil
25	40	12.7	844	17	CNS0052P	AL056652 Drosophil
26	40	12.7	932	17	CNS0072Q	AL066742 Drosophil
27	40	12.7	935	17	CNS006XK	AL066051 Drosophil
28	40	12.7	1125	17	AG073746	AG073746 Pan trogl
29	39.8	12.7	906	17	AG081338	AG081338 Pan trogl
30	39.6	12.6	731	17	AG061169	AG061169 Pan trogl
31	39.6	12.6	935	17	AG073949	AG073949 Pan trogl
32	39.6	12.6	1538	17	AG030607	AG030607 Pan trogl
33	39.4	12.5	717	17	CNS0111L	AL100311 Drosophil
34	39.2	12.5	858	12	BG481980	BG481980 602527810
35	39.2	12.5	877	17	CNS0285S	AL211694 Tetradon
36	39.2	12.5	1003	14	BQ886908	BQ886908 AGENCOURT
37	39	12.4	635	10	BB656840	BB656840 MI-P-CP1-
38	38.8	12.4	447	13	BI403012	BI403012 MI-P-CP1-
39	38.8	12.4	481	10	BE233791	BE233791 140269 MA
40	38.8	12.4	587	13	BI399585	BI399585 MI-P-AV1-
41	38.8	12.4	588	13	BI402027	BI402027 MI-P-CP0-
42	38.8	12.4	687	13	BI182737	BI182737 UNL-P-FN-
43	38.8	12.4	725	13	BI181902	BI181902 UNL-P-FN-
44	38.8	12.4	839	17	CNS004NB	AL054280 Drosophil
45	38.6	12.3	504	13	BI669206	BI669206 603295447

ALIGNMENTS

RESULT 1	BB866520	618 bp	linear	EST 27-NOV-2001
LOCUS	BB866520	RIKEN full-length enriched, colon RCB-0549	Cle-H3 cdna Mus	
DEFINITION	musculus cdna clone G431005N18 5', mRNA sequence.			
ACCESSION	BB866520			
VERSION	BB866520.1	GI:17112730		
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 618)			
	Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Numasaka, K., Okazaki, R., Okazaki, Y., Okada, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., et al.			
TITLE	RIKEN Encyclopedia of Mouse Full-length cDNAs (AKIMURA, T., et al. 2001)			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan			

Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura
S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
Y., and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

FEATURES

source

Location/Qualifiers
1. 618
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="G431005N18"
/clone_lib="RIKEN full-length enriched, colon RCB-0549
Cle-H3 cDNA"

/tissue_type="colon"
/cell_line="RCB-0549 Cle-H3"
/note="pooled cell lines : (cell_line=CRL-1751 WEHI 164),
(cell_line=CRL-2116 JC), (cell_line=RCB-0035 WEHI-3),
(cell_line=RCB-0464 Meth-A), (cell_line=RCB-0545 ORTA),
(cell_line=RCB-0559 K-1 Fl), (cell_line=RCB-1283 B16
melanoma), (cell_type=B cells, cell_line=CRL-1702 WEHI 231
) , (cell_type=Leidyid cells, cell_line=CRL-2065 MLTC-1),
(cell_type=Nullipotent stem cell, cell_line=CRL-2070 NE),
(tissue_type=bladder, cell_line=RCB-0544 MBT-2),
(tissue_type=bone marrow, cell_type=stroma cell,
cell_line=RCB-2028 SR-498), (tissue_type=colon,
cell_line=RCB-0549 Cle-H3), (tissue_type=kidney,
cell_line=CCL-142 RAG), (tissue_type=submandibular gland,
cell_line=CRL-1734 SCA-9 clone 15), (strain=BALB/C,
cell_type=B cells, cell_line=CRL-1669 BC11 Clone 13 20-3B3
) , (strain=C3H, tissue_type=brain, cell_line=CRL-1443
BC3H1)"

BASE COUNT 105 a 189 c 196 g 127 t 1 others

ORIGIN

Query Match 63.4%; Score 199.2; DB 10; Length 618;
Best Local Similarity 82.3%; Pred. No. 3.4e-39;
Matches 241; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

QY 1 ATGTCATGTTTGTAGTGGCTCTCTGTCCTTAAAGTGATGACGGAACACAGCTGGGGT 60
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Db 37 ATGTCATGTTTGTAGTGGCTCTCTGTCCTTAAAGTGATGACGGAACACAGCTGGGGT 96
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QY 61 GAACCAATGGCAGACGGTTCGGGGCGCGTGCATCGGGCAGGTGGCTTCGACAG 120
|||||
Db 97 GAACCAATGGCAGACGGTTCGGGGCGCGTGCATCGGGCAGGTGGCTTCGACAG 153
|||||
QY 121 CCCCGCTATATGAGTGTCTCGGGATGCAGACCCAGCCAGCCCGCTCGGGCGCCC 180
|||||
Db 154 CCTGCTACATGAGTGTCTCAAGATGCGGAGCCAGCCAGCCCGCTCGCTGACCTCAC 213
|||||
QY 181 CCTCGGTGCCCTGGCAGGATGACCCCTTCATCCGAGGGGGCGGCCANGCAGGCAAG 240
|||||
Db 214 ACTCGGTGCCCTGGCAGGATGACCCCTTCATCAGGAGGGGGCGGCCANGGAGGTGTG 273
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QY 241 GAATGGGGTGGGGGAGTGGCCCTCGGGCTTCGAAGATACCGAAGTACACAC 293

Db 274 GAGCTGGGGCTCGGCTCAGTGGCTTTGGGCTTTGACGACACTGAGGTGACCC 326
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RESULT 2

BB866451

LOCUS

DEFINITION

BB866451 RIKEN full-length enriched, colon RCB-0549 Cle-H3 cDNA Mus

musculus cDNA clone G431005J18 5', mRNA sequence.

ACCESSION

BB866451

VERSION

BB866451.1 GI:17112661

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 631)

AUTHORS

Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,

Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii

Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,

Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,

Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,

Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa

A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toyai, T.,

Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.

2001)

TITLE

Unpublished (2001)

JOURNAL

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@sc.riken.go.jp,

URL: http://genome.gsc.riken.go.jp/

M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,

Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura

S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and

Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara

Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for

further details.

e mouse tissues.

Location/Qualifiers

1. 631

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="G431005J18"

/clone_lib="RIKEN full-length enriched, colon RCB-0549

Cle-H3 cDNA"

/tissue_type="colon"

/cell_line="RCB-0549 Cle-H3"

/note="pooled cell lines : (cell_line=CRL-1751 WEHI 164),

(cell_line=CRL-2116 JC), (cell_line=RCB-0035 WEHI-3),

(cell_line=RCB-0464 Meth-A), (cell_line=RCB-0545 ORTA),

(cell_line=RCB-0559 K-1 Fl), (cell_line=RCB-1283 B16

melanoma), (cell_type=B cells, cell_line=CRL-1702 WEHI 231

), (cell_type=Leidyid cells, cell_line=CRL-2065 MLTC-1),

(cell_type=Nullipotent stem cell, cell_line=CRL-2070 NE),

(tissue_type=bladder, cell_line=RCB-0544 MBT-2),
(tissue_type=bone marrow, cell_type=stroma cell,
cell_line=RCB-2028 SR-4987), (tissue_type=colon,
cell_line=RCB-0549 C1e-H3), (tissue_type=kidney,
cell_line=CCL-142 RAG), (tissue_type=submandibular gland,
cell_line=CRL-1734 SCA-9 clone 15), (strain=BALB/C,
cell_type=B cells, cell_line=CRL-1669 BCL1 Clone 13.20-3B3
) (strain=C3H, tissue_type=brain, cell_line=CRL-1443
BC3H1)"

BASE COUNT 90 a 217 c 174 g 150 t

ORIGIN

Query Match 57.3%; Score 180; DB 10; Length 631;

Best Local Similarity 78.2%; Pred. No. 1.9e-34;

Matches 229; Conservative 0; Mismatches 61; Indels 3; Gaps 1;

QY 1 ATGTCATGTTTGTAGTGGCCCTCTGTCCTTAAGTGGATGAACGGAAACAGCCTGGGT 60
|||||
Db 37 ATGTCATGTTTGTAGTGGCCCTCTGTCCTCAAGTGGATGAACGGAAACAGCCTGGGG 96
|||||
QY 61 GAACGCAATGGGAGAGAGCGTTTCGGCGGCCGCTGGCACTCGGCGAGGTCTTCTGCACG 120
|||||
Db 97 GAACGCAATGGGAGAGAGCGTTTCGGCGGCCGCTGGCACTCGGCGAGGTCTTCTGCACG 153
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QY 121 CCCCCTATATAGTCCCTCCGCGGATGAGAGCCACCCAGCCCTCGCGGCC 180
|||||
Db 154 CTTGCTACTTGTAGTCCCTCCGCGGATGAGAGCCACCCAGCCCTCGCGGCC 213
|||||
QY 181 CCTCGTGGCCCTGGCAGATGAGCGCTTCATCCGAGGGGGGCCAGCAGGGGCAAG 240
|||||
Db 214 ACTTGTGGCCCTGGCAGATGAGCGCTTCATCAAGAGGGGGGCCAGCAGGGGCGTG 273
|||||
QY 241 GAATGGGGCTGGCGGCGAGTGGCCCTGGGCTTCAAGATACCGAAGTGCACAC 293
|||||
Db 274 GATCGGGGCTGGCGGCGAGTGGCCCTGGGCTTCAAGATACCGAAGTGCACAC 326
|||||

RESULT 3
CNS02STX/C

LOCUS

DEFINITION

Tetraodon nigroviridis genome survey sequence PUC-ori end of clone
162F16 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION

AL212334.1 GI:7871153

VERSION

GSS: genome survey sequence.

KEYWORDS

Tetraodon nigroviridis.

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

REFERENCE

1 (bases 1 to 1011)

Roest-Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.

TITLE

Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 1011)

Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.

TITLE

Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

JOURNAL

Unpublished

REFERENCE

3 (bases 1 to 1011)

Genoscope.

TITLE

Direct Submission

JOURNAL

Submitted (12-APR-2000)

COMMENT

This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at

http://www.genoscope.cns.fr/Tetraodon.

FEATURES

Source

Location/Qualifiers
1..1011
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="162F16"
/clone_lib="G"
/note="Genoscope sequence ID : COAG162DC08SP1-end ;
PUC-ori"

BASE COUNT 191 a 297 c 324 g 175 t 24 others

ORIGIN

Query Match 19.2%; Score 60.2; DB 17; Length 1011;

Best Local Similarity 63.1%; Pred. No. 9.1e-05;

Matches 128; Conservative 1; Mismatches 64; Indels 10; Gaps 2;

QY 1 ATGTCATGTTTGTAGTGGCCCTCTGTCCTTAAGTGGATGAACGGAAACAGCCTGGGT 60
|||||

Db 283 ATGTCATGTTTGTAGTGGCCCTCTGTCCTTAAGTGGATGAACGGAAACAGCCTGGGG 224
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QY 61 GAACGCAATGGGAGAGAGCGTTTCGGCGGCCGCTGGCACTCGGCGAGGTCTTCTGCACG 120
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Db 223 GACGCAATGGGAGAGAGCGTTTCGGCGGCCGCTGGCACTCGGCGAGGTCTTCTGCACG 173
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QY 121 CCCCCTATATAGTCCCTCCGCGGATGAGAGCCACCCAGCCCTCGCGGCC 179
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Db 172 CCCCCTATATAGTCCCTCCGCGGATGAGAGCCACCCAGCCCTCGCGGCC 113
|||||

QY 180 CCTCGTGGCCCTGGCAGGATG 202
|||||

Db 112 CTCCATCAGCAGCAGCAGGAGG 90
|||||

RESULT 4

LOCUS

DEFINITION

mus musculus

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

Journal

Comment

NIH-MGC http://mgc.nhl.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth

Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10870 row: f column: 08

High quality sequence stop: 151.

Location/Qualifiers

1..941

/organism="Mus musculus"

/strain="NMRI"

/db_xref="taxon:10090"

/clone="IMAGE:4937095"

/clone_lib="NCI_CGAP_Mam4"

/tissue_type="tumor, gross tissue"

/dev_stage="5 months"

/lab_host="DH10B"

Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furch, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."

BASE COUNT	206 a	234 c	311 g	189 t	1 others
ORIGIN					
Query Match	18.7%	Score 58.8;	DB 13;	Length 941;	
Best Local Similarity	84.8%;	Pred. No. 0.0002;			
Matches	78;	Conservative	0;	Mismatches 12;	Gaps 1;
QY	1	ATGTCATGGTTAGTGGCTCCTGG--TCCTTAAGTGGATGAACGAAACACACCTGGG	58		
Db	12	ATGTCATGGTTGAGAGGCTCCTGGATCCCAACAGTGGATGAACGAAACACACCTGGG	71		
QY	59	GTGAACGCAATGGCGAAGAAAGGTTTCGGGGCGC	90		
Db	72	GGGAACGCAATGGCGACAGAGGCCACGCCAC	103		
RESULT 5					
CNS0091P/c					
LOCUS	CNS0091P	925 bp	DNA	linear	GSS 03-JUN-1999
DEFINITION	Drosophila melanogaster genome survey sequence fET3 end of BAC # BACR19D16 of RPC1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL053013				
VERSION	AL053013.1	GI:4934461			
KEYWORDS	GSS.				
SOURCE	Drosophila melanogaster.				
ORGANISM	Drosophila melanogaster.				
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
AUTHORS	1 (bases 1 to 925)				
TITLE	Genoscope.				
JOURNAL	Direct Submission				
COMMENT	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)				
	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org/TheBDGP				
	melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammossier in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm .				
FEATURES	Location/Qualifiers				
source	1..925				
	/organism="Drosophila melanogaster"				
	/db_xref="taxon:7227"				
	/clone="BACR19D16"				
	/clone_lib="RPC1-98"				
	/notes="end : fET3"				
BASE COUNT	120 a	61 c	61 g	172 t	511 others
ORIGIN					
Query Match	16.4%;	Score 51.4;	DB 17;	Length 925;	
Best Local Similarity	15.8%;	Pred. No. 0.013;			
Matches	44;	Conservative	126;	Mismatches 108;	Gaps 0;
QY	34	GTGATGAACGGAACAGCCTGGGGTGAACGCAATGGCGAAGACGCTTCGGCGCGGT	93		
Db	807	GSGASASHSSSSACBSSSSSSCASCSWSSSSASSSRRSGGCGAGGSGASSRRSSSS	748		

Db 784 GCNSGGSGGCGCGCGSSSSGSGSGCGSCGRCGCGCGGCS 737

RESULT 7

CNS010RJ

LOCUS

DEFINITION

CNS010RJ 846 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN04N13 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AL099337.1 GI:5610948
GSS.
Drosophila melanogaster.
Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 846)

REFERENCE

AUTHORS

TITLE

JOURNAL

Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT

Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES

source

Location/Qualifiers

1..846

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone="BACN04N13"

/clone_lib="DrosBAC"

/plasmid="pBelobAC11"

/note="end : T7"

BASE COUNT 300 a 47 c 40 g 175 t 284 others

ORIGIN

Query Match

Best Local Similarity 13.8%; Score 43.4; DB 17; Length 846;

Matches 40; Conservative 127; Mismatches 111; Indels 0; Gaps 0;

QY 29 CTAAGTGGATGACCGAAGAACACCTGGGTGAACGCATGGCGAGAACCGTTCGCGGC 88

Db 564 CGATTGARADKAGCGGRARSSAAGAGGGGGGCGAGGSSSSSSGSAVGSSSSV 623

QY 89 GCGGTGGCACTCGGCGAGGTGGCTTCTGCACGCCCGCTATATGAGTGCCTCCGGGATG 148

Db 624 SSSASSSSSSSSSSSSAASAGASVSSASAVSSSSSSAASASSASVSSSSSVS 683

QY 149 CAGAGCACACCCACCCACCCCTCGCGGCCCTCGGTCCCTCGGAGGATGACGCCT 208

Db 684 AVASASSSSSVSVSSSSAASAVVSSASASVSSSVSSGCAASSASASTSTSSS 743

QY 209 TCATCGGAGGGGCGCCGANGCAAGGCAAGAACTGGGCTGCGGGGAGTGCCTGG 268

Db 744 SAASSSSSSGSSAGSSSSAASSSAASAVSSAVSSASASSSSASASSSSAS 803

QY 269 GCTTCAAGATCCGAGTGCACACGACACCGCGGGA 306

Db 804 SSSSSTSSASSASAAAASAVSSSSGSSASASSAGA 841

RESULT 8

CNS0072Q

LOCUS

DEFINITION

CNS0072Q 932 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit

fly), genomic survey sequence.

AL066742

AL066742.1 GI:4945205

GSS.

Drosophila melanogaster.

Drosophila melanogaster.

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 932)

Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see http://www.fruitfly.org The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and

Aaron Mamoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

EcoRI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain y2; cn bw sp, the same strain used for the BDGP's

PI and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Qualifiers

1..932

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone="BACR14B09"

/clone_lib="RPCI-98"

/note="end : T7"

BASE COUNT 155 a 202 c 241 g 91 t 243 others

ORIGIN

Query Match

Best Local Similarity 13.7%; Score 43; DB 17; Length 932;

Matches 70; Conservative 49; Mismatches 95; Indels 0; Gaps 0;

QY 52 GCTTGGGTGAACCAATGGCGAGGCTTCGCGGCCCGCTGGCACTCGGGCAGGTGGC 111

Db 627 GCGCGGSSSSCGSCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 686

QY 112 TTCTGACGCCCCGCTATATGAGTCTCGGCGATGACAGCCACCCAGCCACCCCT 171

Db 687 SGCCCCSSGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCCGCCS 746

QY 172 GCGGGCCCCCTCGTCCCTTCGAGATGACGCTTCATCCGAGGGGGCGCCANGC 231

Db 747 SCGSSSSSSGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGSG 806

QY 232 AAGGCAAGGAACCTGGGCTGCGGCGAGTGGGCC 265

Db 807 SSSGSSCGGSGCGSSGCGSSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 840

RESULT 9

BQ948546

LOCUS

DEFINITION

BQ948546 950 bp mRNA linear EST 21-AUG-2002
AGENCOURT_8841400 Lupski_sciatic_nerve Homo sapiens cDNA clone
IMAGE:6199251 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


```

Query Match      13.3%; Score 41.8; DB 17; Length 935;
Best Local Similarity 36.7%; Pred. No. 3.2;
Matches 69; Conservative 45; Mismatches 73; Indels 1; Gaps 1;

Qy 83 GCGGCGCGGCGGACTCGGCGAGTGTCTGTGCACCGCCCGCTATATGAGCTGCTCC 142
||||: || || || || || || || || || || || || || || || || || || ||
682 GCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 741
||||: || || || || || || || || || || || || || || || || || ||
Qy 143 GGGATGCAGACCCACCGACCCCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 202
||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
Db 742 GCGSCGSSGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 800
||||: || || || || || || || || || || || || || || || || || ||
Qy 203 ACGCTTATCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 262
||||: || || || || || || || || || || || || || || || || || ||
Db 801 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 860
||||: || || || || || || || || || || || || || || || || || ||
Qy 263 CCCTGGGC 270
||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
Db 861 CGSGGCGS 868

RESULT 14
AG030603      968 bp DNA linear GSS 01-NOV-2001
LOCUS      Pan troglodytes DNA, clone: PTB-003A16.F, genomic survey sequence.
DEFINITION
ACCESSION  AG030603
VERSION    AG030603.1 GI:16557476
KEYWORDS  GSS.
SOURCE    Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
          BAC Library clone:PTB-003A16.F.
ORGANISM  Pan troglodytes
REFERENCE  1
AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
          Tokoki,Y., Watanabe,H. and Sakaki,Y.
TITLE     BAC end sequences of Library PTB
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 968)
AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
          Tokoki,Y., Watanabe,H. and Sakaki,Y.
TITLE     Direct Submission
JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
          and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
          1-7-22 Suehiro-chou,Tsuri-ku, Yokohama, Kanagawa 230-0045, Japan
          (E-mail:chimbos@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
          Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT   Clones are derived from the chimpanzee BAC library PTB This BAC end
          was generated during the R&D process and may have higher chance of
          clone tracking errors.
PRIMERS
LIBRARY    Sequencing: -21M13
Vector     : pKS145
R.Site 1  : SacI
R.Site 2  : SacI.
FEATURES   Location/Qualifiers
source     1..968
           /organism="Pan troglodytes"
           /db_xref="taxon:9598"
           /clone="PTB-003A16.F"
           /sex="male"
           /cell_type="lymphoblast"
           /clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT 40 a 361 c 474 g 16 t 77 others
ORIGIN
Query Match      13.3%; Score 41.8; DB 17; Length 968;
Best Local Similarity 48.8%; Pred. No. 3.2;
Matches 106; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

Qy 83 GCGGCGCGGCGGACTCGGCGAGTGTCTGTGCACCGCCCGCTATATGAGCTGCTCC 142
||||: || || || || || || || || || || || || || || || || || || ||

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Db 736 GCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 795
||||: || || || || || || || || || || || || || || || || || ||
Qy 143 GGGATGCAGACCCACCGACCCCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 202
||||: || || || || || || || || || || || || || || || || || ||
Db 796 GCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 855
||||: || || || || || || || || || || || || || || || || || ||
Qy 203 ACGCTTATCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 262
||||: || || || || || || || || || || || || || || || || || ||
Db 856 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 915
||||: || || || || || || || || || || || || || || || || || ||
Qy 263 CCCTGGGTTCGAAGATACCGAAGTGACAACGACACC 299
||||: || || || || || || || || || || || || || || || || || ||
Db 916 GCGGCGCGGCGGAGCGCGGAGACGACGACAAAC 952
||||: || || || || || || || || || || || || || || || || || ||
RESULT 15
AG073983      1075 bp DNA linear GSS 03-NOV-2001
LOCUS      Pan troglodytes DNA, clone: PTB-065P04.F, genomic survey sequence.
DEFINITION
ACCESSION  AG073983
VERSION    AG073983.1 GI:16625785
KEYWORDS  GSS.
SOURCE    Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
          BAC Library clone:PTB-065P04.F.
ORGANISM  Pan troglodytes
REFERENCE  1
AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
          Tokoki,Y., Watanabe,H. and Sakaki,Y.
TITLE     BAC end sequences of Library PTB
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 1075)
AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
          Tokoki,Y., Watanabe,H. and Sakaki,Y.
TITLE     Direct Submission
JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
          and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
          1-7-22 Suehiro-chou,Tsuri-ku, Yokohama, Kanagawa 230-0045, Japan
          (E-mail:chimbos@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
          Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT   Clones are derived from the chimpanzee BAC library PTB This BAC end
          was generated during the R&D process and may have higher chance of
          clone tracking errors.
PRIMERS
LIBRARY    Sequencing: -21M13
Vector     : pKS145
R.Site 1  : SacI
R.Site 2  : SacI.
FEATURES   Location/Qualifiers
source     1..1075
           /organism="Pan troglodytes"
           /db_xref="taxon:9598"
           /clone="PTB-065P04.F"
           /sex="male"
           /cell_type="lymphoblast"
           /clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT 55 a 388 c 553 g 18 t 61 others
ORIGIN
Query Match      13.2%; Score 41.4; DB 17; Length 1075;
Best Local Similarity 47.6%; Pred. No. 4.1;
Matches 111; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

Qy 78 GCGTTTCGGGCGCGGTGGCACTCGGCGAGTGTCTTCACAGCCCGCTATATGAGCTG 137
||||: || || || || || || || || || || || || || || || || || ||
Db 589 GCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 648
||||: || || || || || || || || || || || || || || || || || ||
Qy 138 CCTCGGGATGACAGACCCAGCCAGCCCTCGGCGGCGGCGGCGGCGGCGGCGGCG 197
||||: || || || || || || || || || || || || || || || || || ||
Db 649 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 708
||||: || || || || || || || || || || || || || || || || || ||

```


GenCore version 5.1.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 22:29:24 ; Search time 53.5045 Seconds
(without alignments)
9128.329 Million cell updates/sec

Title: US-09-750-240-1
Perfect score: 314
Sequence: 1 atgtcatgttttagtgccct.....acacggcgaggaccgtgaa 314

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2850587 seqs, 77717511 residues
Total number of hits satisfying chosen parameters: 5701174

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New.*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	295.2	94.0	1386	1	PCT-US02-36759-83
2	199.2	63.4	5826	6	US-10-144-771-5921
3	39.8	12.7	36303	6	US-10-152-724-24
4	39.8	12.7	36303	6	US-10-152-724A-24
5	38.2	12.2	1878	5	US-09-724-676-33617
6	38.2	12.2	1878	5	US-09-724-676A-33617
7	38.2	12.2	3174	6	US-10-218-140-5849
8	38.2	12.2	3182	5	US-09-724-676-33618
9	38.2	12.2	3182	5	US-09-724-676A-33618
10	36.6	11.7	1542	1	PCT-US02-38526-349
11	36.6	11.7	2216	1	PCT-US02-38526-347
12	36.4	11.6	485	5	US-09-585-645A-59
13	36	11.5	22118	6	US-10-287-313-16
14	35.8	11.4	1824	5	US-09-724-676-45770
15	35.8	11.4	1824	5	US-09-724-676A-45770
16	35.2	11.2	2893	6	US-10-125-923A-157
17	35.2	11.2	2893	6	US-10-205-892-157
18	35.2	11.2	2893	6	US-10-174-575-157
19	35.2	11.2	2893	6	US-10-174-575A-157
20	35.2	11.2	2893	6	US-10-015-610A-23
21	35.2	11.2	2893	6	US-10-226-254A-23
22	35.2	11.2	2893	6	US-10-187-755-157
23	35.2	11.2	2893	6	US-10-187-749-157
24	35.2	11.2	2893	6	US-10-017-253A-23
25	35.2	11.2	2893	6	US-10-199-672-157
26	35.2	11.2	2893	6	US-10-194-486-157

C 27	35.2	11.2	4303	1	PCT-US02-32117-3
C 28	35.2	11.2	4303	6	US-10-271-697-3
C 29	35	11.1	1194	1	PCT-US02-38445-65
C 30	34.8	11.1	344	5	US-09-513-999C-21648
C 31	34.6	11.0	4536	1	PCT-US02-32117-1
C 32	34.6	11.0	4536	6	US-10-271-697-1
C 33	34.6	11.0	9104	5	US-09-949-002-652
C 34	34.4	11.0	2220	6	US-10-144-771-23402
C 35	34.4	11.0	5583	6	US-10-072-012-319
C 36	34.4	11.0	6797	6	US-10-094-886-179
C 37	33.8	10.8	1295	6	US-10-240-851-66
C 38	33.8	10.8	3237	6	US-10-144-771-17257
C 39	33.6	10.7	930	6	US-10-144-771-26872
C 40	33.6	10.7	1025	5	US-10-262-839-143
C 41	33.4	10.6	1392	5	US-09-724-676-14604
C 42	33.4	10.6	1392	5	US-09-724-676A-14604
C 43	33.4	10.6	2988	5	US-09-724-676-14611
C 44	33.4	10.6	2988	5	US-09-724-676A-14611
C 45	33.4	10.6	3060	5	US-09-724-676-14602

ALIGNMENTS

RESULT 1
PCT-US02-36759-83
; Sequence 83, Application PC/TUS0236759
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DUGGAN, Brendan M.
; APPLICANT: YANG, Junming
; APPLICANT: GIETZEN, Kimberly J.
; APPLICANT: LEE, Soo Yeun
; APPLICANT: TANG, Y. Tom
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: WALIA, Narinder K.
; APPLICANT: WARREN, Bridget A.
; APPLICANT: BARROSO, Ines
; APPLICANT: BECHA, Shanya D.
; APPLICANT: YUE, Henry
; APPLICANT: LEHR-MASON, Patricia M.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: LEE, Sally
; APPLICANT: EMERLING, Brooke M.
; APPLICANT: KABLE, Amy E.
; APPLICANT: KHARE, Reena
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: TRAN, Uyen K.
; APPLICANT: RICHARDSON, Thomas W.
; APPLICANT: MARQUIS, Joseph P.
; APPLICANT: LAL, Preeti G.
; APPLICANT: FORSYTHE, Ian J.
; APPLICANT: LEE, Ernestine A.
; APPLICANT: SWARNAKAR, Anita.
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: GORVAD, Ann E.
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: ISON, Craig H.
; APPLICANT: JIN, Pei
; APPLICANT: JIANG, Xin
; APPLICANT: JACKSON, Alan
; APPLICANT: BHATIA, Umesh
; APPLICANT: BURRILL, John D.
; APPLICANT: BLAKE, Julie J.
; APPLICANT: HO, Ann
; APPLICANT: ZHENG, Wenjin
; APPLICANT: GAO, Jing

TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS
FILE REFERENCE: PF-1279 PCT
CURRENT APPLICATION NUMBER: PCT/US02/36759

```

; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 60/333,097
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,274
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/340,542
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/342,166
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/347,580
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/348,687
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PERL Program
; SEQ ID NO 83
; LENGTH: 1386
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7506194CB1
; PCT-US02-36759-83

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Query Match	94.0%	Score 295.2;	DB 1;	Length 1386;
Best Local Similarity	97.1%	Pred. No. 1.5e-65;		
Matches 300;	Conservative	0;	Mismatches 9;	Indels 0;
Gaps	0;			
Qy	1	ATGTCATGGTTT	AGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT	60
Db	25	ATGTCATGGTTT	AGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT	84
Qy	61	GAACGCAATGGGCA	AGAGCGTTTCGCGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG	120
Db	85	GAACGCAATGGGCA	AGAGCGTTTCGCGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG	144
Qy	121	CCCCGCTATATGAGCT	GCCTCCGGGATGCAGAGCACCCAGCCGCCACCCCTGCGGGGCCCC	180
Db	145	CCCCGCTATATGAGCT	GCCTCCGGGATGCAGAGCACCCAGCCGCCACCCCTGCGGGGCCCC	204
Qy	181	CCTCGGTGCCCTGGC	AGGATGACGCTTCATCCGGAGGGCGGCCCCANGCAAGGCGAAG	240
Db	205	CCTCGGTGCCCTGGC	AGGATGACGCTTCATCCGGAGGGCGGCCCCAGGCAAGGCGAAG	264
Qy	241	GAACATGGGGGTGCG	GGGCAGTGGCCCTCGGGCTTCGAAGATACCGAAGTGACAAACGACACCG	300
Db	265	GAGCTGGGGGTGCG	GGGCAGTGGCCCTCGGGCTTCGAGGATACCGAAGTGACAAACGACACCG	324
Qy	301	CGCGGGACCG	309	
Db	325	GGCGGGACG	333	

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RESULT 2
US-10-144-771-5921
; Sequence 5921, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 5921
; LENGTH: 5826
; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-5921

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Qy	1	ATGTCATGTTTTAGTGGCCCTCTGGTCCCTTAAGTGGATGAACGGAAAACACGCTGGGGT	60
Db	96	ATGTCATGTTTTAGTGGCCCTCTGGTCCCAAAAGTGGATGAACGGAAAACAGCTTGGGG	155
Qy	61	GAACGCAATGGGCAAGCGCTTCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCCTGCAG	120
Db	156	GAACGCAATGGGCAAGCG---CCACGCCACGCCAATCGAGCCAGTGGCTTCCTGC	212
Qy	121	CCCGCGCTATATGAGCTGCCCTCCGGGATGACAGCCACCCAGGCCCCACCCTCGGGCCCC	180
Db	213	CCTCGCTACATGAGCTGCCCTCAAGAATGCGGAGCCACCCAGGCCCCACTCCTGCAGCTCAC	272
Qy	181	CCTCGGTGCCCTGGCAGGATGAGCCTTCATCCGGAGGGGGCGCCANGCAAGGCGAAG	240
Db	273	ACTCGGTGCCCTGGCAGGATGAGCCTTCATCAGGAGCGGGCGGCCGGCGAGGGGTGTG	332
Qy	241	GAACGGGGGTGGGGCAGTGGCCCCCTGGGCTTCGAAAGATACCGAAGTGAACAAC	293
Db	333	GAGCTGGGGTGGGGTCAGTGGCCTTGGGGTTTGACGACACTGAGGTGACCAC	385

RESULT 3

US-10-152-724-24/c

; Sequence 24, Application US/10152724

; GENERAL INFORMATION:

; APPLICANT: LITTLE, Melissa

; APPLICANT: HOLMES, Gregory

; APPLICANT: KOLLE, Gabriel

; APPLICANT: YAMADA, Toshiya

; APPLICANT: GEORGAS, Kylie

; APPLICANT: WILKINSON, Lorine

; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptide

; FILE REFERENCE: P2378

; CURRENT APPLICATION NUMBER: US/10/152,724

; CURRENT FILING DATE: 2002-05-23

; PRIOR APPLICATION NUMBER: Australian App No PQ 4348

; PRIOR FILING DATE: 1999-11-26

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 24

; LENGTH: 36303

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-152-724-24

RESULT 4
US-10-152-724A-24/c
: Sequence 24, Application US/10152724A
: GENERAL INFORMATION:
: APPLICANT: LITTLE, Melissa
: APPLICANT: HOLMES, Gregory
: APPLICANT: KOLLE, Gabriel
: APPLICANT: YAMADA, Toshiya
: APPLICANT: GEORGAS, Kylie
: APPLICANT: WILKINSON, Lorine
: TITLE OF INVENTION: Novel Nucleic Acid and Polypeptide

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; FILE REFERENCE: P22378
; CURRENT APPLICATION NUMBER: US/10/152,724A
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: Australian App No PQ 4348
; PRIOR FILING DATE: 1999-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 36303
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-152-724A-24

Query Match      12.7%; Score 39.8; DB 6; Length 36303;
Best Local Similarity 55.4%; Pred. No. 1.3;
Matches 77; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 78 GCGTTCGCGGCGCGTGGCACTCGGGCAGGTGGCTTCTGCAGCGCCCGCTATATGAGCTG 137
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 34505 GAGTGGCGGGCCCGCGGGAGTGGGGGAGGCTCCCTACCCCTGCCCGCAGCCGCGAG 34446

Qy 138 CTTCCGGGATGACAGACCCACCCAGCCACCCCTCGGGGCCCCCTCGGTGCCCTGGCA 197
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 34445 CCTACGCGCGAGCTCTCTCTCGGCCCTCTCTCCCGCGGAGCGGAGTCCCCGCC 34386

Qy 198 GGATGACGCCCTTCATCCGG 216
   ||||| ||||| |||||
Db 34385 TCTCGCCTCTCTCTCCGG 34367

RESULT 5
US-09-724-676-33617/c
; Sequence 33617, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724, 676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33617
; LENGTH: 1878
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-33617

Query Match      12.2%; Score 38.2; DB 5; Length 1878;
Best Local Similarity 46.0%; Pred. No. 1.7;
Matches 127; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

Qy 13 AGTGGCCTCTCTGTCCTAAAGTGGATGAACGGAAACAGCCTGGGTGAACGCAATGGG 72
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1319 AGAGCCCCCAGGCCCGGAGAGCCGAGAGCCGCTGGCTGGCAGAGGTGGAGGTGAGGA 1260

Qy 73 CAGAAGCGTTTCGGCGGCCCTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCCGCTATATG 132
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1259 CAGACAGCCCCCAGCAAAATGGCAGGTGGGCGTGGCGTGCAGGCAGACGTGCTGTG 1200

Qy 133 AGCTGCCTTCGGGATGACAGAGCCACCCAGCCACCCCTCGGGGCCCCCTCGGTGCC 192
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1199 TGCTGCCAGGCGGGGCCCCCTGCTGCTCGCCCTCTTGGCAGGCTCCCGGTAGATCGGC 1140

Qy 193 TGGCAGGATGACGCTTTCATCCGAGGCGGGGCCCCANGCAAGGCAAGAACTGGGCTG 252
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1139 AAGCATATGACTGCGCTGGCCCAAGCGCTGCAGCGCGAGTGGCGTGGGGCGGCG 1080

Qy 253 CGGCGAGTGGCCCTGGGCTTTCGAAGATACCGAAGTG 288
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1079 CAGCGGGCGGCTGCACCCAGCGGCGAGGCTG 1044

RESULT 6
US-10-218-140-5849
; Sequence 5849, Application US/10218140
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES
; FILE REFERENCE: 15966-543 CON
; CURRENT APPLICATION NUMBER: US/10/218,140
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/127,728
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/127,636
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/127,607
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 6322
; SOFTWARE: Curanator Version 1.0
; SEQ ID NO 5849
; LENGTH: 3174
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1870)..(2332)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: "n" = "a", "c", "t" or "g"
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US-09-724-676A-33617/c
; Sequence 33617, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724, 676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33617
; LENGTH: 1878
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-33617

Query Match      12.2%; Score 38.2; DB 5; Length 1878;
Best Local Similarity 46.0%; Pred. No. 1.7;
Matches 127; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

Qy 13 AGTGGCCTCTCTGTCCTAAAGTGGATGAACGGAAACAGCCTGGGTGAACGCAATGGG 72
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1319 AGAGCCCCCAGGCCCGGAGAGCCGAGAGCCGCTGGCTGGCAGAGGTGGAGGTGAGGA 1260

Qy 73 CAGAAGCGTTTCGGCGGCCCTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCCGCTATATG 132
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1259 CAGACAGCCCCCAGCAAAATGGCAGGTGGGCGTGGCGTGCAGGCAGACGTGCTGTG 1200

Qy 133 AGCTGCCTTCGGGATGACAGAGCCACCCAGCCACCCCTCGGGGCCCCCTCGGTGCC 192
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1199 TGCTGCCAGGCGGGGCCCCCTGCTGCTCGCCCTCTTGGCAGGCTCCCGGTAGATCGGC 1140

Qy 193 TGGCAGGATGACGCTTTCATCCGAGGCGGGGCCCCANGCAAGGCAAGAACTGGGCTG 252
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1139 AAGCATATGACTGCGCTGGCCCAAGCGCTGCAGCGCGAGTGGCGTGGGGCGGCG 1080

Qy 253 CGGCGAGTGGCCCTGGGCTTTCGAAGATACCGAAGTG 288
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1079 CAGCGGGCGGCTGCACCCAGCGGCGAGGCTG 1044

RESULT 7
US-10-218-140-5849
; Sequence 5849, Application US/10218140
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES
; FILE REFERENCE: 15966-543 CON
; CURRENT APPLICATION NUMBER: US/10/218,140
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/127,728
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/127,636
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/127,607
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 6322
; SOFTWARE: Curanator Version 1.0
; SEQ ID NO 5849
; LENGTH: 3174
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1870)..(2332)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: "n" = "a", "c", "t" or "g"
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (961)...(961)
OTHER INFORMATION: "n" = "a", "c", "t" or "g"
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1191)...(1191)
OTHER INFORMATION: "n" = "a", "c", "t" or "g"
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1193)...(1193)
OTHER INFORMATION: "n" = "a", "c", "t" or "g"
US-10-218-140-5849

Query Match 12.2%; Score 38.2; DB 6; Length 3174;
Best Local Similarity 53.4%; Pred. No. 1.9;
Matches 79; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 137 GCTCGGGATGAGAGCCACCCAGCCCTCGGGCCCCCTCGGTGCCCTGGC 196
DB 2049 GCCCCTCCAGGCTGAGCTTCAACCCACAGCCTCCGGGTGCCACATTGCCCTCAGC 2108
QY 197 AGATGACCCCTTCATCCGGAGGGGGCCCGCCAGGAGGCAAGCACTGGGGCTCGGG 256
DB 2109 AGGGCTTATCCAGTTCTCGGGTGGGGGAGGAGTGCCCTGGCACAGTGCACAGGCT 2168
QY 257 CAGTGGCCCTGGGCTTCGAAGATACCGA 284
DB 2169 CAGGCGCCCTGGCTAGCTGGACATCCA 2196

RESULT 8
US-09-724-676-33618/c
Sequence 33618, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Comugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Comugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 33618
LENGTH: 3182
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-676-33618

Query Match 12.2%; Score 38.2; DB 5; Length 3182;
Best Local Similarity 46.0%; Pred. No. 1.9;
Matches 127; Conservative 0; Mismatches 149; Indels 0; Gaps 0;
QY 13 AGTGGCTCTGCTCCCTAAAGTGGATGAACGAAACAGCCTGGGTGAACGCAATGGG 72
DB 2623 AGAGCCCCCAGCCCGGAGAGCAGGAGCGTGGCTGGCAGAGGTGGAAGGTGAGGA 2564
QY 73 CAGAAGCGTTTCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACGCCCGCTATATG 132
DB 2563 CAGACAGCCCCCAGCAAAATGGCAGGTGGCGTGGCGGTGCAGGCAGACGTGCTGCTG 2504
QY 133 AGCTGCTCCGGGATGCAGAGCCACCCAGCCCTCGGGCCCCCTCGGTGCCGCC 192
DB 2503 TGCTGCCAGGGGGGGCCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2444
QY 193 TGGCAGGATGAGCCTTCATCCGGAGGGGGCGCCCAAGCAAGCAAGCAAGCAAGCAAG 252
DB 2443 AAGCAGATGACTGCGCTTGCAGCCAGCCCTGCGAGCCGAGTGGCCGTGGGGGGGGG 2384
QY 253 CGGGCAGTGGCGGTTCGAAGATACCGAAGTG 288
DB 2383 CAGCGGGGGCGGTGCACCCAGCGGCGAGCGAGCTG 2348

RESULT 9
US-09-724-676A-33618/c
Sequence 33618, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Comugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Comugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 33618
LENGTH: 3182
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-676A-33618

Query Match 12.2%; Score 38.2; DB 5; Length 3182;
Best Local Similarity 46.0%; Pred. No. 1.9;
Matches 127; Conservative 0; Mismatches 149; Indels 0; Gaps 0;
QY 13 AGTGGCTCTGCTCCCTAAAGTGGATGAACGAAACAGCCTGGGTGAACGCAATGGG 72
DB 2623 AGAGCCCCCAGCCCGGAGAGCAGGAGCGTGGCTGGCAGAGGTGGAAGGTGAGGA 2564
QY 73 CAGAAGCGTTTCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACGCCCGCTATATG 132
DB 2563 CAGACAGCCCCCAGCAAAATGGCAGGTGGCGTGGCGGTGCAGGCAGACGTGCTGCTG 2504
QY 133 AGCTGCTCCGGGATGCAGAGCCACCCAGCCCTCGGGCCCCCTCGGTGCCGCC 192
DB 2503 TGCTGCCAGGGGGGGCCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2444
QY 193 TGGCAGGATGAGCCTTCATCCGGAGGGGGCGCCCAAGCAAGCAAGCAAGCAAGCAAG 252
DB 2443 AAGCAGATGACTGCGCTTGCAGCCAGCGCTGCGAGCCGAGTGGCCGTGGGGGGGGG 2384
QY 253 CGGGCAGTGGCGGTTCGAAGATACCGAAGTG 288
DB 2383 CAGCGGGGGCGGTGCACCCAGCGGCGAGCGAGCTG 2348

RESULT 10
PCT-US02-38526-349/c
Sequence 349, Application PC/TUS0238526
GENERAL INFORMATION:
APPLICANT: Ghosh, Malabika
APPLICANT: Tang, Y. Tom
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Zhiwei
APPLICANT: Zhao, Qing
APPLICANT: Xu, Chongjun
APPLICANT: Mulero, Julio J
APPLICANT: Boyle, Bryan J.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL POLYPEPTIDES AND POLY
FILE REFERENCE: HYS-BI/PCT
CURRENT APPLICATION NUMBER: PCT/US02/38526
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: PCT/US00/34263
PRIOR FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: PCT/US01/03800


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; ORGANISM: Homo sapiens
PCT-US02-38526-349

Query Match      11.7%   Score 36.6;   DB 1;   Length 1542;
Best Local Similarity 47.0%;   Pred. No. 4.2;
Matches 111;   Conservative 0;   Mismatches 125;   Indels 0;   Gaps 0

QY  70  GGGCAGAGCGTTCGGCGCCGTGGGCACTCGGGCAGTGGCTTCTGACACGCCCGCGCTAT
      |||||
Db   821  GGGCGCGCTGGCGCTCGCGGGGGGGTCTCGGCTGTCAGCGGCTCTCTCGGGCGCTCTGCGG
      |||||

QY  130  ATGAGCTGCCTCCGGGATGCAGAGCCACACAGCCACACCCCTGCGGGGCCCCCTCGGTGTC
      |||||
Db   761  GCGCGCGGGGGCGAGGGGGCGCTGCTGCTGAACACACACTCTGCGGGGGCCCCACGGGCT
      |||||

QY  190  CCCTGGCAGGATGACGCGCTTCATCCGGAGGGGGGGCCCGCCANGCAAGGGCAAGGAACCTGGGG
      |||||
Db   701  CTCGCCGGGCTGCCGAGGGACCTCTCCCGGGGGGCCCGAGGCTCGCGGAGGGCGCGTGAG
      |||||

QY  250  CTGCGGGCAGTGGCCCTTGGGGTTTCGAAGATACCGAAGTGACAACGACACCGCGGGG 305
      |||||
Db   641  GAGGGCTCAGGCTCCACAGAGGGCGCGGGCCACAGCGCCACCTGTCGACGCGGAAG 586
      |||||

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	Query Match	11.6%	Score 36.4	DB 5	Length 485
	Best Local Similarity	54.7%	Pred. No. 3.7		
	Matches	70	Conservative	0	Mismatches 58
					Indels 0
					Gaps 0
Qy	110	GCTTCTGCAGCCCGCGTATATGAGTGCCTCCGGGATGAGAGCCACCCAdCCCCACC	169		
Db	253	GCTTCTGCAGCGCTCACTCGCGCGCGCCCGCGCGCGCGCGCGCGCGCG	194		
Qy	170	CTGGGGGGCCCCCTCGGTGCCCTTGGCAGGATAGCGCTTCATCGGAGGGCGGGCCCAN	229		
Db	193	CCGCGCGCGCGCGGTCTCCCGGGGTGCTCCGCGGAACGCGNCGCGCGCGCGCGCG	134		

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/ PRIOR APPLICATION NUMBER: US 05/436,914
/ PRIOR FILING DATE: 2000-02-03
/ PRIOR APPLICATION NUMBER: US 09/560,875
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: PCT/US01/03800
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: US 09/598,075
/ PRIOR FILING DATE: 2000-06-20
/ PRIOR APPLICATION NUMBER: PCT/US01/04098
/ PRIOR FILING DATE: 2001-02-05
/ Remaining Prior Application data removed - See File Wrapper or PALM
/ NUMBER OF SEQ ID NOS: 653
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; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45770
; LENGTH: 1824
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1515)..(1516)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1522)..(1522)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1525)..(1525)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1528)..(1528)
; OTHER INFORMATION: n is a,c,g, or t
; US-09-724-676A-45770
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Query Match      11.4%; Score 35.8; DB 5; Length 1824;
Best Local Similarity 47.3%; Pred. No. 6.9;
Matches 97; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

Qy 104 CAGGTGCTTCTGACGCCCGCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCC 163
      ||| || | | |||| | |||| | |||| | |||| | |||| | |||| |
Db 1634 CAGGAGCCCCCCTCACCCCGGGTCTGAGTGGCACACAGGAGGGGCTGGGGCGGCC 1575

Qy 164 CCACCCCTGGGGCCCCCTCGGTGCCCTGGCAGGATGAGCCTTCATCCGGAGGGGCG 223
      || | | | | |||| | |||| | |||| | |||| | |||| | |||| |
Db 1574 AGCACCAGCGGCGTCTGCTCAGCCCTCTGCAGGGAGCGAGCAGNCNGNAAAGNN 1515

Qy 224 GCCCANGCAAGGGCAAGGAAGTGGGGCTGCGGCGAGTGGCCCTGGGCTTCGAGATACCG 283
      ||| || |||| | || | |||| | |||| | |||| | |||| | |||| |
Db 1514 CCCCCAAAAGGCGAGCAAGCCGCTGGGCGGTGGGACGTCACCACCGCAGGAATCGCG 1455

Qy 284 AAGTGACAACGACACCGCGGGGACC 308
      || | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1454 AATGAAGCTCCAGAGCTTGGTGACC 1430
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Search completed: February 23, 2003, 07:47:45
Job time : 73.8378 secs

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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 22:19:04 ; Search time 619.645 Seconds
(without alignments)
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Title: US-09-750-240-1
Perfect score: 314
Sequence: 1 atgtcatgttttagtgccct.....acaccgcgagaccgctgaa 314

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 24791104 seqs, 12571243825 residues
Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
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12: /cgn2_6/ptodata/1/pna/pna/US088_COMB.seq.*
13: /cgn2_6/ptodata/1/pna/pna/US089_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	313	99.7	314	18	US-09-472-667-1	Sequence 1, Appli
2	313	99.7	314	29	US-09-750-240-1	Sequence 1, Appli
3	295.2	94.0	3549	18	US-09-472-667-5	Sequence 5, Appli
4	295.2	94.0	3549	29	US-09-750-240-5	Sequence 5, Appli
5	295.2	94.0	3552	18	US-09-472-667-10	Sequence 10, Appli
6	295.2	94.0	3552	29	US-09-750-240-10	Sequence 10, Appli
7	295.2	94.0	3582	29	US-09-750-240-12	Sequence 12, Appli
8	295.2	94.0	4942	42	US-10-201-000-1	Sequence 1, Appli
c 9	263.2	83.8	18618	68	US-60-245-228-129	Sequence 129, App
c 10	263.2	83.8	36346	68	US-60-248-592-55	Sequence 55, Appl
11	199.2	63.4	5826	80	US-60-360-207-5921	Sequence 5921, Ap
12	198.2	63.1	4131	9	US-08-538-815-11	Sequence 11, Appl
13	163.4	52.0	358	18	US-09-482-933-165	Sequence 165, App
14	163.4	52.0	358	35	US-09-933-797-165	Sequence 165, App
15	148.6	47.3	562	17	US-09-397-022-2574	Sequence 2574, Ap
16	148.6	47.3	562	24	US-09-637-890-6437	Sequence 6437, Ap
17	148.6	47.3	562	25	US-09-649-164-5083	Sequence 5083, Ap
18	148.6	47.3	562	31	US-09-808-383-2574	Sequence 2574, Ap
19	94.6	30.1	220	29	US-09-728-445-487	Sequence 487, App
20	94.6	30.1	220	29	US-09-750-456-487	Sequence 487, App
21	80	25.5	3706	68	US-60-248-592-183	Sequence 183, App


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Db 1 ATGTCATGGTTTACTGGCTCCTGCTCCCTAAAGTGGATGAACGAGAAACAGCCTGGGGT 60

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Db 61 GAACGCAATGGGAGAGAGCGTTCCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120

QY 121 CCCCCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGCGGGCCCC 180
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QY 181 CCTCGTGCCCTGGCAGGATGACGCTTCATCCGAGGGCGGCCCCANGCAAGGCAAG 240
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QY 241 GAACCTGGGGCTGGGGCAGTGGCCCTTCCAAAGATACCGAAGTGACAAACACACCG 300
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RESULT 3

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US-09-472-667-5
; Sequence 5, Application US/09473667
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. Kirk
; APPLICANT: Insel, Paul A.
; APPLICANT: Insel, Peipei
; APPLICANT: Post, Steven R.
; APPLICANT: Gao, Meihua
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056722
; CURRENT APPLICATION NUMBER: US/09/472,667
; CURRENT FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: PCT/US99/02702
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 09/021,773
; PRIOR FILING DATE: 1998-02-11
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: PCT/US97/15610
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/058,209
; PRIOR FILING DATE: 1996-09-05
; PRIOR APPLICATION NUMBER: PCT/US96/02631
; PRIOR FILING DATE: 1996-02-27
; PRIOR APPLICATION NUMBER: US 08/396,207
; PRIOR FILING DATE: 1995-02-28
; PRIOR APPLICATION NUMBER: US 08/485,472
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-472-667-5

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Best Local Similarity 97.1%; Pred. No. 1.4e-56;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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QY 61 GAACGCAATGGGAGAGAGCGTTCCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120
Db 61 GAACGCAATGGGAGAGAGCGTTCCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120

QY 121 CCCCCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGCGGGCCCC 180
Db 121 CCCCCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGCGGGCCCC 180

QY 181 CCTCGTGCCCTGGCAGGATGACGCTTCATCCGAGGGCGGCCCCANGCAAGGCAAG 240
Db 181 CCTCGTGCCCTGGCAGGATGACGCTTCATCCGAGGGCGGCCCCANGCAAGGCAAG 240

QY 241 GAACCTGGGGCTGGGGCAGTGGCCCTTCCAAAGATACCGAAGTGACAAACACACCG 300
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QY 301 GCGGACCG 309
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RESULT 4

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US-09-750-240-5
; Sequence 5, Application US/09750240
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-240-5

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Best Local Similarity 97.1%; Pred. No. 1.4e-56;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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Db 1 ATGTCATGGTTTACTGGCTCCTGCTCCCTAAAGTGGATGAACGAGAAACAGCCTGGGGT 60

QY 61 GAACGCAATGGGAGAGAGCGTTCCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120
Db 61 GAACGCAATGGGAGAGAGCGTTCCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120

QY 121 CCCCCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGCGGGCCCC 180
Db 121 CCCCCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGCGGGCCCC 180
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QY 241 GAACCTGGGGCTCGGGCAGTGGCCCTCGAGAGTACCGAAGTGCACACGACACCG 300
Db 241 GAGCTGGGGCTCGGGCAGTGGCCCTTCGAGGATACCGAGGTGACAACGACACCG 300
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RESULT 5
US-09-472-667-10
; Sequence 10, Application US/09472667
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. Kirk
; APPLICANT: Insel, Paul A.
; APPLICANT: Ping, Peipei
; APPLICANT: Post, Steven R.
; APPLICANT: Gao, Meihua
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056722
; CURRENT APPLICATION NUMBER: US/09/472,667
; CURRENT FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: PCT/US99/02702
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 09/021,773
; PRIOR FILING DATE: 1998-02-11
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: PCT/US97/15610
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; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
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; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: PCT/US96/02631
; PRIOR FILING DATE: 1996-02-27
; PRIOR APPLICATION NUMBER: US 08/396,207
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; PRIOR APPLICATION NUMBER: US 08/485,472
; PRIOR FILING DATE: 1995-06-07
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 3552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-472-667-10

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Best Local Similarity 97.1%; Pred. No. 1.4e-56;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTAGTGGCTCTCGTCCCTAAAGTGGATGAACGGAAAAACAGCCTGGGGT 60
Db 1 ATGTCATGTTTAGTGGCTCTCGTCCCTAAAGTGGATGAACGGAAAAACAGCCTGGGGT 60
QY 61 GAACCAATGGGCAGAAAGCTTCGGGGCCGCTGGCACTCGGGCAGGTGCTTCGACG 120
Db 61 GAACCAATGGGCAGAAAGCTTCGGGGCCGCTGGCACTCGGGCAGGTGCTTCGACG 120
QY 121 CCCCGCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180
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QY 1 ATGTCATGTTTAGTGGCTCTCGTCCCTAAAGTGGATGAACGGAAAAACAGCCTGGGGT 60
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QY 61 GAACCAATGGGCAGAAAGCTTCGGGGCCGCTGGCACTCGGGCAGGTGCTTCGACG 120
Db 61 GAACCAATGGGCAGAAAGCTTCGGGGCCGCTGGCACTCGGGCAGGTGCTTCGACG 120
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QY 301 GCGGGACCG 309
Db 301 GCGGGACG 309
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QY 181 CCTCGTGCCTCGCAGGATGACGCCTTCATCCCGAGGGGGGCCCCANGCAAGGCAAG 240
Db 181 CCTCGTGCCTCGCAGGATGACGCCTTCATCCCGAGGGGGGCCCCAGGCAAGGCAAG 240
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Db 241 GAGCTGGGGCTCGGGCAGTGGCCCTTCGAGGATACCGAGGTGACAACGACACCG 300
QY 301 GCGGGACCG 309
Db 301 GCGGGACG 309

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US-09-750-240-10
; Sequence 10, Application US/09750240
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 3552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-240-10

Query Match 94.0%; Score 295.2; DB 29; Length 3552;
Best Local Similarity 97.1%; Pred. No. 1.4e-56;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTAGTGGCTCTCGTCCCTAAAGTGGATGAACGGAAAAACAGCCTGGGGT 60
Db 1 ATGTCATGTTTAGTGGCTCTCGTCCCTAAAGTGGATGAACGGAAAAACAGCCTGGGGT 60
QY 61 GAACCAATGGGCAGAAAGCTTCGGGGCCGCTGGCACTCGGGCAGGTGCTTCGACG 120
Db 61 GAACCAATGGGCAGAAAGCTTCGGGGCCGCTGGCACTCGGGCAGGTGCTTCGACG 120
QY 121 CCCCGCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180
Db 121 CCCCGCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180
QY 181 CCTCGTGCCTCGCAGGATGACGCCTTCATCCCGAGGGGGGCCCCANGCAAGGCAAG 240
Db 181 CCTCGTGCCTCGCAGGATGACGCCTTCATCCCGAGGGGGGCCCCAGGCAAGGCAAG 240
QY 241 GAACCTGGGGCTCGGGCAGTGGCCCTTCGAGAGTACCGAAGTGCACACGACACCG 300
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Db 301 GCGGGACG 309
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RESULT 7
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; Sequence 12, Application US/09750240
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 22002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 3582
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified AC-VI
US-09-750-240-12

Query Match 94.0%; Score 295.2; DB 29; Length 3582;
Best Local Similarity 97.1%; Pred. No. 1.4e-56;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 ATGTCATGTTTACTGGCTCTCTGCTCCTAAAGTGATGAACGAAACAGCCTGGGGT 60
|||||
Db 22 ATGTCATGTTTACTGGCTCTCTGCTCCTAAAGTGATGAACGAAACAGCCTGGGGT 81
QY 61 GAACGCAATGGGAGAGAGCGTTTCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
|||||
Db 82 GAACGCAATGGGAGAGAGCGTTTCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 141
QY 121 CCCGCTATATGACTCGCTCCGGGATGCAGACCCAGCCACCCCTGCGGGCCCC 180
Db 142 CCCGCTATATGACTCGCTCCGGGATGCAGACCCAGCCACCCCTGCGGGCCCC 201
QY 181 CCTCGGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGCGGCCCAAGCAAGGCAAG 240
Db 202 CCTCGGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGCGGCCCAAGCAAGGCAAG 261
QY 241 GAACGCGGGTGGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTACACACACACCG 300
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Db 262 GAGCTGGGGTGGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACACACACG 321
QY 301 GCGGGACCG 309
Db 322 GCGGGACCG 330

RESULT 8
US-10-201-000-1
; Sequence 1, Application US/10201000
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLIL
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5028-01-US

; CURRENT APPLICATION NUMBER: US/10/201,000
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US/09/474,076
; PRIOR FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-10-201-000-1
Query Match 94.0%; Score 295.2; DB 42; Length 4942;
Best Local Similarity 97.1%; Pred. No. 1.4e-56;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 ATGTCATGTTTACTGGCTCTCTGCTCCTAAAGTGATGAACGAAACAGCCTGGGGT 60
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Db 145 ATGTCATGTTTACTGGCTCTCTGCTCCTAAAGTGATGAACGAAACAGCCTGGGGT 204
QY 61 GAACGCAATGGGAGAGAGCGTTTCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
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Db 205 GAACGCAATGGGAGAGAGCGTTTCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 264
QY 121 CCCGCTATATGACTCGCTCCGGGATGCAGACCCAGCCACCCCTGCGGGCCCC 180
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Db 265 CCCGCTATATGACTCGCTCCGGGATGCAGACCCAGCCACCCCTGCGGGCCCC 324
QY 181 CCTCGGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGCGGCCCAAGCAAGGCAAG 240
Db 325 CCTCGGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGCGGCCCAAGCAAGGCAAG 384
QY 241 GAACGCGGGTGGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTACACACACACCG 300
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Db 385 GAGCTGGGGTGGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACACACACG 444
QY 301 GCGGGACCG 309
Db 445 GCGGGACCG 453

RESULT 9
US-60-245-228-129/c
; Sequence 129, Application US/60245228
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000878
; CURRENT APPLICATION NUMBER: US/60/245,228
; CURRENT FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 630
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 129
; LENGTH: 18618
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(18618)
; OTHER INFORMATION: n = A,T,C or G
US-60-245-228-129

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Query Match      83.8%; Score 263.2; DB 68; Length 18618;
Best Local Similarity 94.5%; Pred. No. 2.4e-49;
Matches 294; Conservative 0; Mismatches 14; Indels 3; Gaps 2;

QY 1 ATGTCATGTTTGTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGT 60
DB 16838 ATGTCATGTTTGTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGT 16779

QY 61 GAACCAATGGCAGAAAGGTTTCGGCGCGCTGGCACTCGGCGAGGTCTTCTGCACG 120
DB 16778 GAACCAATGGCAGAAAGGTTTCGGCGCGCTGGCACTCGGCGAGGTCTTCTGCACG 16719

QY 121 CCCGCTATATGAGTGGCTCCGGATGACAGCACCAGCCACCCCTCGGGCCCC 180
DB 16718 CCCGCTATATGAGTGGCTCCGGATGACAGCACCAGCCACCCCTCG- GCGCCC 16660

QY 181 CCTCGTGGCCCTGGCAGATGACGCTT- -CATCGGAGGGGGGCCCCANGCAAGGGCA 238
DB 16659 CCTCGTGGCCCTGGCAGATGACGCTTTCATCGGAAGGGCGGCCAGGCAAGGGCA 16600

QY 239 AGGAACTGGGCTGGCGAGTGGCCCTGGGCTTCAAGATACCGAAGTGACAAGCAC 298
DB 16599 AGGAACTGGGCTGGCGAGTGGCCCTGGGCTTCAAGATACCGAAGTGACAAGCAC 16540

QY 299 CGGCGGGACCG 309
DB 16539 CGGCGGGACG 16529

RESULT 10
US-60-248-592-55/c
; Sequence 55, Application US/60248592
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES
; TITLE OF INVENTION: THEROF
; FILE REFERENCE: CL000961
; CURRENT APPLICATION NUMBER: US/60/248,592
; CURRENT FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 36346
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(36346)
; OTHER INFORMATION: n = A,T,C or G
US-60-248-592-55

Query Match      83.8%; Score 263.2; DB 68; Length 36346;
Best Local Similarity 94.5%; Pred. No. 2.4e-49;
Matches 294; Conservative 0; Mismatches 14; Indels 3; Gaps 2;

QY 1 ATGTCATGTTTGTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGT 60
DB 16838 ATGTCATGTTTGTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGT 16779

QY 61 GAACCAATGGCAGAAAGGTTTCGGCGCGCTGGCACTCGGCGAGGTCTTCTGCACG 120
DB 16778 GAACCAATGGCAGAAAGGTTTCGGCGCGCTGGCACTCGGCGAGGTCTTCTGCACG 16719

QY 121 CCCGCTATATGAGTGGCTCCGGATGACAGCACCAGCCACCCCTCGGGCCCC 180
DB 16718 CCCGCTATATGAGTGGCTCCGGATGACAGCACCAGCCACCCCTCG- GCGCCC 16660

QY 181 CCTCGTGGCCCTGGCAGATGACGCTT- -CATCGGAGGGGGGCCCCANGCAAGGGCA 238
DB 16659 CCTCGTGGCCCTGGCAGATGACGCTTTCATCGGAAGGGGGGCCAGGCAAGGGCA 16600

QY 239 AGGAACTGGGCTGGCGAGTGGCCCTGGGCTTCAAGATACCGAAGTGACAAGCAC 298
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DB 16599 AGGAGTGGGCTGGCGGAGTGGCCCTGAGTACCGAGGTGACAACGACAG 16540
QY 299 CGGCGGGACCG 309
DB 16539 CGGCGGGACG 16529

RESULT 11
US-60-360-207-5921
; Sequence 5921, Application US/60360207
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/60/360,207
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 5921
; LENGTH: 5826
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
US-60-360-207-5921

Query Match      63.4%; Score 199.2; DB 80; Length 5826;
Best Local Similarity 82.3%; Pred. No. 6e-35;
Matches 241; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

QY 1 ATGTCATGTTTGTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGT 60
DB 96 ATGTCATGTTTGTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGG 155

QY 61 GAACCAATGGCAGAAAGGTTTCGGCGCGCTGGCACTCGGCGAGGTCTTCTGCACG 120
DB 156 GAACCAATGGCAGAAAGGTTTCGGCGCGCTGGCACTCGGCGAGGTCTTCTGCACG 212

QY 121 CCCGCTATATGAGTGGCTCCGGATGACAGCACCAGCCACCCCTCGGGCCCC 180
DB 213 CCTCGTACATGAGTGGCTCAAGAATGGGAGCAGCCAGCCAGCCAGCTCAC 272

QY 181 CCTCGTGGCCCTGGCAGATGACGCTTTCATCGGAGGGGGGCCANGCAAGGCAAG 240
DB 273 ACTCGTGGCCCTGGCAGATGAAGCTTTCATCAGAGGGGGGGGGGGGGGTGTG 332

QY 241 GAACCTGGGCTGGCGAGTGGCCCTGAGTGGCTTCAAGATACCGAAGTGACAAC 293
DB 333 GAGCTGGGCTGGCGTCACTGGCTTGGGTTTGACGACACTGAGGTGACCAC 385

RESULT 12
US-08-538-815-11
; Sequence 11, Application US/08538815
; GENERAL INFORMATION:
; APPLICANT: Tang, Wei-Jen
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYL
; TITLE OF INVENTION: CYCLASE AND USES THEREFOR
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/538,815
; FILING DATE: Concurrently Herewith
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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSD:450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4131 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-538-815-11

Query Match 63.1%; Score 198.2; DB 9; Length 4131;
Best Local Similarity 79.9%; Pred. No. 1e-34;
Matches 246; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 1 ATGTCATGTTTACTGGCTTCTGCTCCCTAAAGTGATGAACGAAACAGCCTGGGT 60
DB 56 ATGTCATGTTTACTGGCTTCTGCTCCCTAAAGTGATGAACGAAACAGCCTGGGT 115
QY 61 GAAGCAATGGCAGAGCGTTCGCGCGCGCTGGCACTGGCGAGTGGCTTCTGCACG 120
DB 116 GAAGCAATGGCAGAGCGTTCGCGCGCGCTGGCACTGGCGAGTGGCTTCTGCACG 172
QY 121 CCCGCTATATAGCTGCCCTCCGGGATGACAGCCACCCAGCCCTCCCTGGCGGCC 180
DB 173 CCCGCTATATAGCTGCCCTCCGGGATGACAGCCACCCAGCCCTCCCTGGCGGCC 232
QY 181 CCTCGTTCATGAGCTGGCAGTGGCTTCCGAAGTACCGAAGTGACAACACACCG 240
DB 233 ACTCGTGGCCCTGGCAGTGGCTTCCGAAGTACCGAAGTGACAACACACCG 292
QY 241 GAACGCAATGGCAGAGCGTTCGCGCGCGCTGGCACTGGCGAGTGGCTTCTGCACG 300
DB 293 GAGCTGGGGTGGCGTTCAGTGGCTTCTGATGACACTGAGGTGACACACCGATG 352
QY 301 GCGGACCG 308
DB 353 GGGACAGC 360

RESULT 13
US-09-482-933-165
; Sequence 165, Application US/09482933
; GENERAL INFORMATION:
; APPLICANT: Robert A. Sikes et al.
; TITLE OF INVENTION: Isolation and Use of Fetal Urogenital
; FILE OF INVENTION: Sinus Expressed Sequences
; FILE REFERENCE: 9901-007-999
; CURRENT APPLICATION NUMBER: US/09/482,933
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: PCT/US99/10746
; PRIOR FILING DATE: 1999-05/14
; PRIOR APPLICATION NUMBER: 60/085,383
; NUMBER OF SEQ ID NOS: 811
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 165
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Murine
US-09-482-933-165

Query Match 52.0%; Score 163.4; DB 18; Length 358;
Best Local Similarity 83.1%; Pred. No. 6.5e-27;
Matches 196; Conservative 2; Mismatches 35; Indels 3; Gaps 1;

QY 1 ATGTCATGTTTACTGGCTTCTGCTCCCTAAAGTGATGAACGAAACAGCCTGGGT 60
DB 123 ATGTCATGTTTACTGGCTTCTGCTCCCTAAAGTGATGAACGAAACAGCCTGGGT 182
QY 61 GAAGCAATGGCAGAGCGTTCGCGCGCGCTGGCACTGGCGAGTGGCTTCTGCACG 120
DB 183 GAAGCAATGGCAGAGCGTTCGCGCGCGCTGGCACTGGCGAGTGGCTTCTGCACG 239
QY 121 CCCGCTATATAGCTGCCCTCCGGGATGACAGCCACCCAGCCCTCCCTGGCGGCC 180
DB 240 CCTCGTTCATGAGCTGGCAGTGGCTTCCGAAGTACCGAAGTGACAACACACCG 299
QY 181 CCTCGTTCATGAGCTGGCAGTGGCTTCCGAAGTACCGAAGTGACAACACACCG 236
DB 300 ACTCGTGGCCCTGGCAGTGGCTTCCGAAGTACCGAAGTGACAACACACCG 355

RESULT 15
US-09-397-022-2574
; Sequence 2574, Application US/09397022
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE OF INVENTION: HUMAN FETAL SKIN LIBRARY
; FILE REFERENCE: MLN98-46pM
; CURRENT APPLICATION NUMBER: US/09/397,022
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QY 1 ATGTCATGTTTACTGGCTTCTGCTCCCTAAAGTGATGAACGAAACAGCCTGGGT 60
DB 123 ATGTCATGTTTACTGGCTTCTGCTCCCTAAAGTGATGAACGAAACAGCCTGGGT 182
QY 61 GAAGCAATGGCAGAGCGTTCGCGCGCGCTGGCACTGGCGAGTGGCTTCTGCACG 120
DB 183 GAAGCAATGGCAGAGCGTTCGCGCGCGCTGGCACTGGCGAGTGGCTTCTGCACG 239
QY 121 CCCGCTATATAGCTGCCCTCCGGGATGACAGCCACCCAGCCCTCCCTGGCGGCC 180
DB 240 CCTCGTTCATGAGCTGGCAGTGGCTTCCGAAGTACCGAAGTGACAACACACCG 299
QY 181 CCTCGTTCATGAGCTGGCAGTGGCTTCCGAAGTACCGAAGTGACAACACACCG 236
DB 300 ACTCGTGGCCCTGGCAGTGGCTTCCGAAGTACCGAAGTGACAACACACCG 355

RESULT 14
US-09-933-797-165
; Sequence 165, Application US/09933797
; GENERAL INFORMATION:
; APPLICANT: Robert A. Sikes et al.
; TITLE OF INVENTION: Isolation and Use of Fetal Urogenital
; FILE OF INVENTION: Sinus Expressed Sequences
; FILE REFERENCE: 9901-007-999
; CURRENT APPLICATION NUMBER: US/09/933,797
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US/09/482,933
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: PCT/US99/10746
; PRIOR FILING DATE: 1999-05/14
; PRIOR APPLICATION NUMBER: 60/085,383
; NUMBER OF SEQ ID NOS: 811
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 165
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Murine
US-09-933-797-165

Query Match 52.0%; Score 163.4; DB 35; Length 358;
Best Local Similarity 83.1%; Pred. No. 6.5e-27;
Matches 196; Conservative 2; Mismatches 35; Indels 3; Gaps 1;

QY 1 ATGTCATGTTTACTGGCTTCTGCTCCCTAAAGTGATGAACGAAACAGCCTGGGT 60
DB 123 ATGTCATGTTTACTGGCTTCTGCTCCCTAAAGTGATGAACGAAACAGCCTGGGT 182
QY 61 GAAGCAATGGCAGAGCGTTCGCGCGCGCTGGCACTGGCGAGTGGCTTCTGCACG 120
DB 183 GAAGCAATGGCAGAGCGTTCGCGCGCGCTGGCACTGGCGAGTGGCTTCTGCACG 239
QY 121 CCCGCTATATAGCTGCCCTCCGGGATGACAGCCACCCAGCCCTCCCTGGCGGCC 180
DB 240 CCTCGTTCATGAGCTGGCAGTGGCTTCCGAAGTACCGAAGTGACAACACACCG 299
QY 181 CCTCGTTCATGAGCTGGCAGTGGCTTCCGAAGTACCGAAGTGACAACACACCG 236
DB 300 ACTCGTGGCCCTGGCAGTGGCTTCCGAAGTACCGAAGTGACAACACACCG 355

RESULT 15
US-09-397-022-2574
; Sequence 2574, Application US/09397022
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE OF INVENTION: HUMAN FETAL SKIN LIBRARY
; FILE REFERENCE: MLN98-46pM
; CURRENT APPLICATION NUMBER: US/09/397,022
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	295.2	94.0	3549	10	US-09-750-240-5
3	295.2	94.0	3552	10	US-09-750-240-10
4	295.2	94.0	3582	10	US-09-750-240-12
5	295.2	94.0	4942	9	US-10-201-000-1
6	163.4	52.0	358	9	US-09-933-797-165
7	94.6	30.1	220	10	US-09-728-445-487
8	38.6	12.3	6503	10	US-09-935-541-12
9	37.2	11.8	1438	9	US-10-081-280-5
10	37.2	11.8	1438	9	US-10-112-793-5
11	37.2	11.8	1438	9	US-10-112-193-5
12	37.2	11.8	1438	10	US-09-884-733-5
13	37.2	11.8	1438	10	US-09-993-234-5
14	36.6	11.7	3243	9	US-09-945-901-44
15	36.6	11.7	3243	9	US-10-007-747-44
16	36.6	11.7	3243	9	US-10-038-937-44
17	36.6	11.7	3698	9	US-09-945-901-43
18	36.6	11.7	3698	9	US-10-007-747-43
19	36.6	11.7	3698	9	US-10-038-937-43

c 20	36.6	11.7	4002	9	US-09-945-901-53	Sequence 53, Appl
c 21	36.6	11.7	4002	9	US-10-007-747-53	Sequence 53, Appl
c 22	36.6	11.7	4002	9	US-10-038-937-53	Sequence 53, Appl
c 23	36.6	11.7	4017	9	US-09-945-901-49	Sequence 49, Appl
c 24	36.6	11.7	4017	9	US-10-007-747-49	Sequence 49, Appl
c 25	36.6	11.7	4017	9	US-10-038-937-49	Sequence 49, Appl
c 26	36.6	11.7	4053	9	US-09-945-901-47	Sequence 47, Appl
c 27	36.6	11.7	4053	9	US-10-007-747-47	Sequence 47, Appl
c 28	36.6	11.7	4053	9	US-10-038-937-47	Sequence 47, Appl
c 29	36.6	11.7	4068	9	US-09-945-901-5	Sequence 5, Appl
c 30	36.6	11.7	4068	9	US-10-007-747-5	Sequence 5, Appl
c 31	36.6	11.7	4068	9	US-10-038-937-5	Sequence 5, Appl
c 32	36.6	11.7	4077	9	US-09-945-901-51	Sequence 51, Appl
c 33	36.6	11.7	4077	9	US-10-007-747-51	Sequence 51, Appl
c 34	36.6	11.7	4077	9	US-10-038-937-51	Sequence 51, Appl
c 35	36.6	11.7	4092	9	US-09-945-901-45	Sequence 45, Appl
c 36	36.6	11.7	4092	9	US-10-007-747-45	Sequence 45, Appl
c 37	36.6	11.7	4092	9	US-10-038-937-45	Sequence 45, Appl
c 38	36.4	11.6	485	9	US-10-004-717-59	Sequence 59, Appl
c 39	36	11.5	22118	9	US-09-799-462A-16	Sequence 16, Appl
c 40	36	11.5	22118	9	US-10-125-767-16	Sequence 16, Appl
c 41	36	11.5	22118	9	US-09-815-981-5	Sequence 5, Appl
c 42	36	11.5	22118	9	US-09-836-911A-16	Sequence 16, Appl
c 43	35.6	11.3	10797	10	US-09-764-847-1577	Sequence 1577, App
c 44	35.2	11.2	2883	9	US-10-174-590-157	Sequence 157, App
c 45	35.2	11.2	2883	9	US-10-176-758-157	Sequence 157, App

ALIGNMENTS

RESULT 1
US-09-750-240-1
; Sequence 1, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART FAILURE
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 314
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(314)
; OTHER INFORMATION: n = A,T,C or G
US-09-750-240-1

Query Match 99.7%; Score 313; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 2.9e-73;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTCATGTTTAGTGGCTTCCTGGTCCCTAAAGTGGATGACGGAACAGCCTGGGT 60

Db 1 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGGAAACAGCCCTGGGGT 60
Qy 61 GAACGCAATGGCAGAACGGTTCGGGGCGCGTGCACCTCGGGCAGGTGGCTTCTGCACG 120
Db 61 GAACGCAATGGCAGAACGGTTCGGGGCGCGTGCACCTCGGGCAGGTGGCTTCTGCACG 120
Qy 121 CCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCCTGCAGGCGCCC 180
Db 121 CCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCCTGCAGGCGCCC 180
Qy 181 CCTCGGTGCCCTGGCAGGATGACGCCCTTCATCCGAGGGCGGCCANGCAAGGCAAG 240
Db 181 CCTCGGTGCCCTGGCAGGATGACGCCCTTCATCCGAGGGCGGCCANGCAAGGCAAG 240
Qy 241 GAACCTGGGGTCCGGGCACTGCCCTGGCTTCGAGATACCGAAGTACACACGACCG 300
Db 241 GAACCTGGGGTCCGGGCACTGCCCTGGCTTCGAGATACCGAAGTACACACGACCG 300
Qy 301 GCGGACCGCTGAA 314
Db 301 GCGGACCGCTGAA 314

RESULT 2

US-09-750-240-5
; Sequence 5, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09750,240
; PRIOR FILING DATE: 2001-10-12
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-240-5

Query Match 94.0%; Score 295.2; DB 10; Length 3549;
Best Local Similarity 97.1%; Pred. No. 2e-68;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGGAAACAGCCCTGGGGT 60
Db 1 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGGAAACAGCCCTGGGGT 60
Qy 61 GAACGCAATGGCAGAACGGTTCGGGGCGCGTGCACCTCGGGCAGGTGGCTTCTGCACG 120
Db 61 GAACGCAATGGCAGAACGGTTCGGGGCGCGTGCACCTCGGGCAGGTGGCTTCTGCACG 120
Qy 121 CCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCCTGCAGGCGCCC 180
Db 121 CCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCCTGCAGGCGCCC 180

Qy 181 CCTCGTCCCTGGCAGGATGACGCCCTTCATCCGAGGGCGGCCANGCAAGGCAAG 240
Db 181 CCTCGTCCCTGGCAGGATGACGCCCTTCATCCGAGGGCGGCCANGCAAGGCAAG 240
Qy 241 GAACCTGGGGTCCGGGCACTGCCCTGGCTTCGAGATACCGAAGTACACACGACCG 300
Db 241 GAGCTGGGGCTCGGGCAGTGGCCCTGGCTTCGAGGATACCGAGGTGACAACGACGCG 300
Qy 301 GCGGACCG 309
Db 301 GCGGACCG 309

RESULT 3

US-09-750-240-10
; Sequence 10, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09750,240
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 3552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-240-10

Query Match 94.0%; Score 295.2; DB 10; Length 3552;
Best Local Similarity 97.1%; Pred. No. 2e-68;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGGAAACAGCCCTGGGGT 60
Db 1 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGGAAACAGCCCTGGGGT 60
Qy 61 GAACGCAATGGCAGAACGGTTCGGGGCGCGTGCACCTCGGGCAGGTGGCTTCTGCACG 120
Db 61 GAACGCAATGGCAGAACGGTTCGGGGCGCGTGCACCTCGGGCAGGTGGCTTCTGCACG 120
Qy 121 CCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCCTGCAGGCGCCC 180
Db 121 CCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCCTGCAGGCGCCC 180
Qy 181 CCTCGTCCCTGGCAGGATGACGCCCTTCATCCGAGGGCGGCCANGCAAGGCAAG 240
Db 181 CCTCGTCCCTGGCAGGATGACGCCCTTCATCCGAGGGCGGCCANGCAAGGCAAG 240
Qy 241 GAACCTGGGGTCCGGGCACTGCCCTGGCTTCGAGATACCGAAGTACACACGACCG 300
Db 241 GAGCTGGGGCTCGGGCAGTGGCCCTGGCTTCGAGGATACCGAGGTGACAACGACGCG 300
Qy 301 GCGGACCG 309
Db 301 GCGGACCG 309

RESULT 4

US-09-750-240-12
; Sequence 12, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 3582
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified AC-VI
US-09-750-240-12

Query Match 94.0%; Score 295.2; DB 10; Length 3582;
Best Local Similarity 97.1%; Pred. No. 2e-68;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGGTTTGTAGTGGCTCCTCGTCCCTAAAGTGGATGACGAGAAACAGCCTGGGGT 60
|||||
DB 22 ATGTCATGGTTTGTAGTGGCTCCTCGTCCCTAAAGTGGATGACGAGAAACAGCCTGGGGT 81
|||||
QY 61 GAACGCAATGGGCAGAGCGTTCCGGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
|||||
DB 82 GAACGCAATGGGCAGAGCGTTCCGGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 141
|||||
QY 121 CCCGCTATATGAGCTGCCCTCCGGGATGACGAGCCACCCAGCCCTCGCGGGCCCC 180
|||||
DB 142 CCCGCTATATGAGCTGCCCTCCGGGATGACGAGCCACCCAGCCCTCGCGGGCCCC 201
|||||
QY 181 CCTCGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGCGGCCGANGCAAGGCAAG 240
|||||
DB 202 CCTCGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGCGGCCGANGGCAAGGCAAG 261
|||||
QY 241 GAACCTGGGGCTGGCGGAGTGCGCCCTGGGCTTCGAAGATACCGAAGTGACACACGACCG 300
|||||
DB 262 GAGCTGGGGCTGGCGGAGTGCGCCCTGGGCTTCGAGGATACCGAAGTGACACACGACCG 321
|||||
QY 301 GCGGGACCG 309
| || ||
DB 322 GCGGGACG 330

RESULT 5

US-10-201-000-1
; Sequence 1, Application US/10201000
; Publication No. US20020187540A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.

; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/10/201,000
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US/09/474,076
; PRIOR FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-10-201-000-1

Query Match 94.0%; Score 295.2; DB 9; Length 4942;
Best Local Similarity 97.1%; Pred. No. 2.2e-68;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGGTTTGTAGTGGCTCCTCGTCCCTAAAGTGGATGACGAGAAACAGCCTGGGGT 60
|||||
DB 145 ATGTCATGGTTTGTAGTGGCTCCTCGTCCCTAAAGTGGATGACGAGAAACAGCCTGGGGT 204
|||||
QY 61 GAACGCAATGGGCAGAGCGTTCCGGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
|||||
DB 205 GAACGCAATGGGCAGAGCGTTCCGGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 264
|||||
QY 121 CCCGCTATATGAGCTGCCCTCCGGGATGACAGACCCAGCCCTCGCGGGCCCC 180
|||||
DB 265 CCCGCTATATGAGCTGCCCTCCGGGATGACAGACCCAGCCCTCGCGGGCCCC 324
|||||
QY 181 CCTCGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGCGGCCGANGCAAGGCAAG 240
|||||
DB 325 CCTCGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGCGGCCGANGGCAAG 384
|||||
QY 241 GAACCTGGGGCTGGCGGAGTGCGCCCTGGGCTTCGAAGATACCGAAGTGACACACGACCG 300
|||||
DB 385 GAGCTGGGGCTGGCGGAGTGCGCCCTGGGCTTCGAGGATACCGAAGTGACACACGACCG 444
|||||
QY 301 GCGGGACCG 309
| || ||
DB 445 GCGGGACG 453

RESULT 6

US-09-933-797-165
; Sequence 165, Application US/09933797
; Patent No. US20020155119A1
; GENERAL INFORMATION:
; APPLICANT: Robert A. Sikes et al.
; TITLE OF INVENTION: Isolation and Use of Fetal Urogenital ;
; FILE REFERENCE: 9901-007-999
; CURRENT APPLICATION NUMBER: US/09/933,797
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US/09/482,933
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: PCT/US99/10746
; PRIOR FILING DATE: 1999-05/14
; PRIOR APPLICATION NUMBER: 60/085,383
; PRIOR FILING DATE: 1998-05-14
; NUMBER OF SEQ ID NOS: 811
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 165

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; LENGTH: 358
; TYPE: DNA
; ORGANISM: Murine
US-09-933-797-165

Query Match      52.0%; Score 163.4; DB 9; Length 358;
Best Local Similarity 83.1%; Pred. No. 4e-34;
Matches 196; Conservative 2; Mismatches 35; Indels 3; Gaps 1;

QY 1 ATGTCATGTTTAGTGGCTCTCGTCCCTAAGTGGATGAACGGAACACAGCTGGGT 60
   |||||
Db 123 ATGTCATGTTTAGTGGCTCTCGTCCCTAAGTGGATGAACGGAACACAGCTGGGT 182
   |||||

QY 61 GAACGCAATGGGAGAGGTTTCGCGCGCCGCTTCACCTCGGCGAGGTGCTTCTGCAG 120
   |||||
Db 183 GAACGCAATGGGAGAGG---CCACGCGCCAGCGGAATCGAGCCAGTGCCTCTGCVCA 239
   |||||

QY 121 CCGCGTATATAGTGCCTCCGGATGAGAGCCACCCAGCCCGCTCGGGGCCCC 180
   |||||
Db 240 CCGCGTATATAGTGCCTCCAGAAATGGGAGCCACCCAGCCCGCTCGGAGTCC 299
   |||||

QY 181 CCGCGTGCCTCGGAGATGACGCTTCATCCGAGGGGGGGCCCGCANGCAAGG 236
   |||||
Db 300 ACTCGTGCCTCGGAGATGAAGCTTCATCAGAGGGGGGGGGCCCGGCGAGGG 355
   |||||

RESULT 7
US-09-728-445-487
; Sequence 487, Application US/09728445
; Patent No. US20020102543A1
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020102543A1el Mutated Mammalian Cells and
; FILE REFERENCE: LEX-0102-USA
; CURRENT APPLICATION NUMBER: US/09/728,445
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168,358
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 891
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 487
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-728-445-487

Query Match      30.1%; Score 94.6; DB 10; Length 220;
Best Local Similarity 84.4%; Pred. No. 3.6e-16;
Matches 119; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY 1 ATGTCATGTTTAGTGGCTCTCGTCCCTAAGTGGATGAACGGAACACAGCTGGGT 60
   |||||
Db 67 ATGTCATGTTTAGTGGCTCTCGTCCCTAAGTGGATGAACGGAACACAGCTGGGT 126
   |||||

QY 61 GAACGCAATGGGAGAGGTTTCGCGCGCCGCTTCACCTCGGCGAGGTGCTTCTGCAG 120
   |||||
Db 127 GAACGCAATGGGAGAGG---CCACGCGCCAGCGGAATCGAGCCAGTGCCTCTGCAG 183
   |||||

QY 121 CCGCGTATATAGTGCCTCC 141
   |||||
Db 184 CCGCGTATATAGTGCCTCC 204
   |||||

RESULT 8
US-09-935-541-12/c
; Sequence 12, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
```

```
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6503
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-935-541-12

Query Match      12.3%; Score 38.6; DB 10; Length 6503;
Best Local Similarity 55.2%; Pred. No. 0.29;
Matches 74; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 141 CGGGGATGACAGACCCACCCAGCCCGCCCTCGGGGCCCCCTCGGTGCCCCCTGGCAGGA 200
   |||||
Db 173 CGGGCTGGAGAGGACCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 114
   |||||

QY 201 TGACGCTTCATCCGAGGGGGGGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 260
   |||||
Db 113 GCGCCCGCGGGGAGGGGAGCGGCATGACAGGGGGGGGGCGGGCGGGGGGGGGGGCCAT 54
   |||||

QY 261 GCGCCCTGGGCTTCG 274
   |||||
Db 53 GCGGGGCGGGTCCG 40
   |||||

RESULT 9
US-10-081-280-5/c
; Sequence 5, Application US/10081280
; Patent No. US20020165157A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/081,280
; FILING DATE: 21-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,270
; FILING DATE: 31-Mar-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
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Db 332 TGCCCGCTCGTTCATCGGCTTCCAGCCCGCGCCGAGGGCCCGCGCGCTCGAGA 273
Qy 198 GGATGACGCTTCATCGGAGGGGGGCGCCANGCAAGGCAAGAACTGGGGCTCGGGGC 257
Db 272 AGGGCCCGCTCGGCGGGGGGAGGGGGCCCGCCGAGGCCCAACGAGTCCGACCG 213
Qy 258 AGTGCCCTCGGCTTCGAAGATACCAAGAGTGACACGACACCGGGG 304
Db 212 GTGCCCCCTCTGCTCGGCTAGACCTGAGCTCATTAGGCGGCGAGCGG 166

RESULT 12

US-09-884-733-5/c
; Sequence 5, Application US/09884733
; Patent No. US20020123116A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 Ligand Inhibitor
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/884,733
; FILING DATE: 19-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/304,003
; FILING DATE: 14-JUNE-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-884-733-5

Query Match 11.8%; Score 37.2; DB 10; Length 1438;
Best Local Similarity 47.6%; Pred. No. 0.51;
Matches 108; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

Qy 78 GCGTTCGGGCGCCCTGCGCACTCGGGCAGGTGGCTTCTGCACGCCCGCCGCTATATGAGCTG 137
Db 392 GCGGCGGTGTCTCCATAGCCCTCCGACGGGCGCCGAGGGCTTCGCGGCTCGCTCTC 333
Qy 138 CCGTCCGGATGACAGCCACCCAGCCCGCTCGGGCGCCCGCTCGTGGCCCTCGCA 197
Db 332 TGCCCGTCTGTTCCGCTTCAGCCCGCGCGCCGAGGGCCCGCCGCGCTCGAGA 273
Qy 198 GGATGACGCTTCATCGGAGGGGGGCGCCANGCAAGGCAAGAACTGGGGCTCGGGGC 257
Db 272 AGGGCCCGCTCGGCGGGGGGAGGGCGGCGCCGAGGCCCAACGAGTCCGACCG 213
Qy 258 AGTGCCCTCGGCTTCGAAGATACCAAGTGACACGACACCGGGG 304

Db 212 GTGCCCCCTCTGCTCGGCTAGACCTGAGCTCATTAGGCGGAGCGG 166

RESULT 13

US-09-993-234-5/c
; Sequence 5, Application US/09993234
; Patent No. US20020146768A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/993,234
; FILING DATE: 19-NO. US20020146768A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,683
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-993-234-5

Query Match 11.8%; Score 37.2; DB 10; Length 1438;
Best Local Similarity 47.6%; Pred. No. 0.51;
Matches 108; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

Qy 78 GCGTTCGGGCGCCCTGCGCACTCGGGCAGGTGGCTTCTGCACGCCCGCCGCTATATGAGCTG 137
Db 392 GCGGCGGTGTCTCCATAGCCCTCCGACGGGCGCCGAGGGCTTCGCGGCTCGCTCTC 333
Qy 138 CCGTCCGGATGACAGCCACCCAGCCCGCTCGGGCGCCCGCTCGTGGCCCGCTGGA 197
Db 332 TGCCCGTCTGTTCCGCTTCAGCCCGCGCGCCGAGGGCCCGCCGCGCTCGAGA 273
Qy 198 GGATGACGCTTCATCGGAGGGGGGCGCCANGCAAGGCAAGAACTGGGGCTCGGGGC 257
Db 272 AGGGCCCGCTCGGCGGGGGGAGGGCGGCGCCGAGGCCCAACGAGTCCGACCG 213
Qy 258 AGTGCCCTCGGCTTCGAAGATACCAAGTGACACGACACCGGGG 304;
Db 212 GTGCCCCCTCTGCTCGGCTAGACCTGAGCTCATTAGGCGGAGCGG 166

RESULT 14

US-09-945-901-44/c
; Sequence 44, Application US/09945901
; Patent No. US20020161215A1

US-09-008-097-1

Query Match 99.7%; Score 313; DB 4; Length 314;
Best Local Similarity 100.0%; Pred. No. 7.1e-71;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTCATGTTAGTGGCTCCTGCTCCTAAAGTGGATGAACGAAACAGCCTGGGT 60
Db 1 ATGTCATGTTAGTGGCTCCTGCTCCTAAAGTGGATGAACGAAACAGCCTGGGT 60

Qy 61 GAACCAATGGCAGAGGTTCCGGGCGCTTAAAGTGGATGAACGAAACAGCCTGGGT 120
Db 61 GAACCAATGGCAGAGGTTCCGGGCGCTTAAAGTGGATGAACGAAACAGCCTGGGT 120

Qy 121 CCCCTATATGAGTGGCTCCTGCGGATGACAGCCACCCAGCCCTCGGGCCCC 180
Db 121 CCCCTATATGAGTGGCTCCTGCGGATGACAGCCACCCAGCCCTCGGGCCCC 180

Qy 181 CCTCGTGCCTTGCAGGATGACGCCCTTCATCCGAGGGGGCCGANGCAAGGCAAG 240
Db 181 CCTCGTGCCTTGCAGGATGACGCCCTTCATCCGAGGGGGCCGANGCAAGGCAAG 240

Qy 241 GAACCTGGGCTCGGGCAGTGGCCCTTGCAGAGTACCGAAGTACCAACGACACCG 300
Db 241 GAACCTGGGCTCGGGCAGTGGCCCTTGCAGAGTACCGAAGTACCAACGACACCG 300

Qy 301 GCGGACCGCTGAA 314
Db 301 GCGGACCGCTGAA 314

RESULT 2

US-09-008-097-5
; Sequence 5, Application US/09080897
; Patent No. 6306830
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. Kirk
; APPLICANT: Insel, Paul A.
; APPLICANT: Ping, Peipei
; APPLICANT: Post, Steven R.
; APPLICANT: Gao, Meihua
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
; TITLE OF INVENTION: HEART FAILURE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,097
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dylan, Tyler M
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 22000-20567.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:

LENGTH: 3549 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...3501
OTHER INFORMATION:
US-09-008-097-5

Query Match 94.0%; Score 295.2; DB 4; Length 3549;
Best Local Similarity 97.1%; Pred. No. 3.4e-66;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ATGTCATGTTAGTGGCTCCTGCTCCTAAAGTGGATGAACGAAACAGCCTGGGT 60
Db 1 ATGTCATGTTAGTGGCTCCTGCTCCTAAAGTGGATGAACGAAACAGCCTGGGT 60

Qy 61 GAACCAATGGCAGAGGTTCCGGGCGCTTAAAGTGGATGAACGAAACAGCCTGGGT 120
Db 61 GAACCAATGGCAGAGGTTCCGGGCGCTTAAAGTGGATGAACGAAACAGCCTGGGT 120

Qy 121 CCCCTATATGAGTGGCTCCTGCGGATGACAGCCACCCAGCCCTCGGGCCCC 180
Db 121 CCCCTATATGAGTGGCTCCTGCGGATGACAGCCACCCAGCCCTCGGGCCCC 180

Qy 181 CCTCGTGCCTTGCAGGATGACGCCCTTCATCCGAGGGGGCCGANGCAAGGCAAG 240
Db 181 CCTCGTGCCTTGCAGGATGACGCCCTTCATCCGAGGGGGCCGANGCAAGGCAAG 240

Qy 241 GAACCTGGGCTCGGGCAGTGGCCCTTGCAGAGTACCGAAGTACCAACGACACCG 300
Db 241 GAACCTGGGCTCGGGCAGTGGCCCTTGCAGAGTACCGAAGTACCAACGACACCG 300

Qy 301 GCGGACCG 309
Db 301 GCGGACCG 309

RESULT 3

US-09-474-076-1
; Sequence 1, Application US/09474076
; Patent No. 6465237
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/09/474,076
; CURRENT FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-09-474-076-1

Query Match 94.0%; Score 295.2; DB 4; Length 4942;
Best Local Similarity 97.1%; Pred. No. 3.5e-66;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ATGTCATGTTAGTGGCTCCTGCTCCTAAAGTGGATGAACGAAACAGCCTGGGT 60

Db 131 ATGTCGTGGTTAGTGGCTCCTGCTCCCAAAAGTGGATGAACGAAGACAGCCCTGGGGT 190
QY 61 GAACCAATGGCAGAACGTTTCGGGGGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120
Db 191 GAACCAATGGCAGAACGTTTCGGGGGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 247
QY 121 CCCGCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCCCCCTGCGGGCCCC 180
Db 248 CCCGCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGTCCCAACCCCTGCGGCTCCC 307
QY 181 CCTGGTGGCTGGCAGAGTACGCCCTTCATCCGAGGGGGGGCCGANGCAAGGGCAAG 240
Db 308 CCTGGTGGCTGGCAGAGTACGCCCTTCATCCGAGAGGGGGGGCCGANGCAAGGGCAAG 367
QY 241 GAACCTGGGGCTGGGGGAGTGGCTTTCGAGATACCGAAG 286
Db 368 GAGCTGGGGCTGGGGGAGTGGCTTTCGAGATACCGAAG 413

RESULT 6
US-08-726-214-11
; Sequence 11, Application US/08726214
; Patent No. 6107076
; GENERAL INFORMATION:
; APPLICANT: Tang, Wei-Jen
; APPLICANT: Gilman, Alfred G.
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLIC CYCLASE
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,214
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005,498
; FILING DATE: 04-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSD:450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4131 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-726-214-11

Query Match 63.1%; Score 198.2; DB 3; Length 4131;
Best Local Similarity 79.9%; Pred. No. 1.2e-41;
Matches 246; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 1 ATGTCAGTTAGTGGCTCCTGCTCCCAAAAGTGGATGAACGAAGACAGCCCTGGGGT 60
Db 56 ATGTCAGTTAGTGGCTCCTGCTCCCAAAAGTGGATGAACGAAGACAGCCCTGGGGT 115
QY 61 GAACCAATGGCAGAACGTTTCGGGGGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120

Db 116 GAACCAATGGCAGAACGTTTCGGGGGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 172
QY 121 CCCGCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCCCCCTGCGGGCCCC 180
Db 173 CCCGCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCCCCCTGCGGGCCCC 232
QY 181 CCTGGTGGCTGGCAGAGTACGCCCTTCATCCGAGGGGGGGCCGANGCAAGGGCAAG 240
Db 233 ACTCGTGGCTGGCAGAGTACGCCCTTCATCCGAGGGGGGGCCGANGCAAGGGGGTGG 292
QY 241 GAACCTGGGGCTGGGGGAGTGGCTTTCGAGATACCGAAGTGCACACGACACCG 300
Db 293 GAGCTGGGGCTGGGGTGCAGTGGCTTGGTGTGATGACACTGAGGTGACCCACACCGATG 352
QY 301 GCGGGACC 308
Db 353 GGGACAGC 360

RESULT 7
US-09-404-650-12/c
; Sequence 12, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6503
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-404-650-12

Query Match 12.3%; Score 38.6; DB 4; Length 6503;
Best Local Similarity 55.2%; Pred. No. 0.31;
Matches 74; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 141 CCGGATGCAGAGCCACCCAGCCCTGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 200
Db 173 CCGGCTGGAGAGGAGGAGCCCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 114
QY 201 TGACGCTTCATCCGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 260
Db 113 GCGGG 1
QY 261 GCGGCTGGGGTTCG 274
Db 53 GCGGGGGGGGGTCCG 40

RESULT 8
US-07-793-961A-1/c
; Sequence 1, Application US/07793961A
; Patent No. 5334521
; GENERAL INFORMATION:
; APPLICANT: Yoshihiro Ishikawa
; TITLE OF INVENTION: Cloning and Character-
; TITLE OF INVENTION: ization of a Cardiac Adenylyl Cyclase
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Alan M. Gordon
; ADDRESSEE: American Cyanamid Company
; STREET: 1937 West Main Street,
; STREET: P.O. Box 60
; CITY: Stamford
; STATE: Connecticut
; COUNTRY: USA


```
;
; ZIP: 06904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII from DW4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/793,961A
; FILING DATE: 19911118
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,705
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203 321 2719
; TELEFAX: 203 321 2971
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4046 base pairs listed
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-793-961A-1

Query Match 12.0%; Score 37.6; DB 1; Length 4046;
Best Local Similarity 49.2%; Pred. No. 0.52;
Matches 97; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 90 CCGTGGCAGCTCGGCGAGGTGGCTTCTGCACGCCCGCCGCTATATGAGCTGCCTCCGGGATGC 149
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 462 CCGGGGGTCACTGTCAGGCGCCACCTCCAGCTGCCCGCCCAACCGCTGACATGGCCTCAGTGTC 403
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 150 AGAGCCACCCAGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCTT 209
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 402 TCAGAGCCCGAGGCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCTC 343
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 210 CATCCGGAGGGGGCGGCCANGCAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 269
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 342 CGGATGAAGGCCCTCATCTCCAGGGGACCCGAGGGGGACCCGAGGGGGACCCGAGGGGGTGGG 283
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 270 CTTTGAAGATACCGAAG 286
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 282 GGCTGCGCATCCCGGAG 266
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
US-08-240-357-1/G
; Sequence 1, Application US/08240357
; Patent No. 5578481
; GENERAL INFORMATION:
; APPLICANT: Ishikawa, Yoshihiro
; TITLE OF INVENTION: Cloning and Characterization of a
; TITLE OF INVENTION: Cardiac Adenylyl Cyclase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/240,357
; FILING DATE: 10-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,705-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4046 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 131..3625
; US-08-240-357-1

Query Match 12.0%; Score 37.6; DB 1; Length 4046;
Best Local Similarity 49.2%; Pred. No. 0.52;
Matches 97; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 90 CCGTGGCAGCTCGGCGAGGTGGCTTCTGCACGCCCGCCGCTATATGAGCTGCCTCCGGGATGC 149
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 462 CCGGGGGTCACTGTCAGGCGCCACCTCCAGCTGCCCGCCCAACCGCTGACATGGCCTCAGTGTC 403
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 150 AGAGCCACCCAGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCTT 209
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 402 TCAGAGCCCGAGGCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCTC 343
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 210 CATCCGGAGGGGGCGGCCANGCAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 269
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 342 CGGATGAAGGCCCTCATCTCCAGGGGACCCGAGGGGGACCCGAGGGGGACCCGAGGGGGTGGG 283
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 270 CTTTGAAGATACCGAAG 286
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 282 GGCTGCGCATCCCGGAG 266
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
5498529-5
; Patent No. 5498529
; APPLICANT: BERKA, THOMAS R.; FORNWALD, JAMES A.; CORNIAT,
; JOSEFINA G.; ROSENBERG, MARTIN; STRICKLER, JAMES E.; TAYLOR, DEAN P.
; TITLE OF INVENTION: PROTEIN PROTEASE INHIBITORS FROM
; STREPTOMYCES
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,506
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 894,167
; FILING DATE: 03-JUN-1992
; APPLICATION NUMBER: 346,119
; FILING DATE: 16-FEB-1989
; APPLICATION NUMBER: 897,245
; FILING DATE: 18-AUG-1986
; SEQ ID NO: 5
; LENGTH: 668
; 5498529-5

Query Match 11.8%; Score 37.2; DB 6; Length 668;
Best Local Similarity 49.4%; Pred. No. 0.49;
Matches 126; Conservative 0; Mismatches 121; Indels 8; Gaps 1;

QY 57 GGGTGAACGCAATGGGAGAGAGCGTTTCGGCGCCCGCTGGGCACTGCGGCGAGGTGGCTTCTG 116
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 130 GGATGCACAAATGCGGAACACCGCGCGCTGGGCAAGCCCGCTGCGCCCTCAGCGCCACCG 189
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RESULT 13
US-08-231-193A-44/c
; Sequence 44, Application US/08231193A
; Patent No. 5849895
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie P.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
; TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231.193A
; FILING DATE: 20-APR-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/052,459
; FILING DATE: 20-APR-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3243 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...3243
; US-08-231-193A-44

Query Match      11.7%; Score 36.6; DB 2; Length 3243;
Best Local Similarity    45.7%; Pred. No. 0.89;
Matches 126; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

Qy   13  AGTGGCCTCTCGGTGCCCTAAAGTGATGGAACGAAAACAAGCCCTGGGGTGAAGCAATGGG  72
     || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   2926  AGAGCCCCCAGGCGCGGAGAGCCGAGAGCGGTGCCTGTCTCACAGSGTGAAGGTGAGG  2867

Qy   73  CAGAAGCGTTTCGGGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACGCCCGCGCTATATG  132
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   2866  CAGACAGCCCCCAGCACAAATGAGGTGGGGCTGGGGCGTCAGGCAGACGCTGCTGCTG  2807

Qy   133  ACGTGCCTCCGGGATGCAGACCACCCAGCCCACCCCTCGCGGGCCCCCTCGGTGCCCC  192
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   2806  TGCCTGCCAGCGGGGGCCCTCGCTGCTGCGCCCTCTTGGCAGSCCTCCCGGTAATCGGC  2747

Qy   193  TGGCAGGATGACGCTTCATCCGAGGGGGCGCCCCANGCAAGGCAAGGAACCTGGGGCTG  252
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   2746  AAGNCATCGACTGCGCTTGCGCCCAAGCGCTTGCAGGCGAGTGGCCGTGGGGCGGGCG  2687

Qy   253  CGGGCATGGGCCCTGGGCTTTCGAAGATAACCGAAGTG  288
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db      2686   CAGCGGGGCCGTGTCACCCAGCGGCACCGAGCTG 2651

RESULT 14
; Sequence 44, Application US/08486273A
US-08-486-273A-44/c
; Patent No. 5985586
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie P.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA
; TITLE OF INVENTION: ENCODING SAME AND USES THEREFOR
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,273A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/231,193
; FILING DATE: 20-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9383B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3243 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...3243
US-08-486-273A-44

Query Match          11.7%; Score 36.6; DB 2; Length 3243;
Best Local Similarity 45.7%; Pred. No. 0.89;
Matches 126; Conservative 0; Mismatches 150; Indels 0; Gaps

Qy    13   AGTGGCCTCTGTGTCCTTAATGGATGAACGAAACACACCTGGGGTGACAGCAATGGG 72
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     2926  AGAGCCCCCAGCGCGGGAGAGCCAGGACCGGTGGCGGTGCACAGSGTGGAAGGTGAGGA 2867
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy    73   CAGAAGCGTTTCGCGGCGCGGTGCACCTCGGGCAGTGGCTTCTGCACGCCCCCCTCATATG 132
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     2866  CAGACACCCCCCAGGACAATGCAAGTGGGGGTGGCGGTGCAGGCACACGTGTGCTG 132
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy    133  AGCTGCTCTCGGGATGCAGAGCCACCACCCACCCCTCGGGGCCCCCTCGGTGCCCC 192
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     2806  TGCTGCCAGCGGGGGCCCCCTGCTGCTCGCCCTCTTCCAGGCCCTCCCGGTAGATCGGC 2747
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy    193  TGGCAGGATGACGCCCTTCATCCGGAGGGGCGGCCCANCAAGGCAAGGAACTGGGGCTG 252
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Gb     2746  AAGCACATGCATCGCCCTCGCGCAAGCGCCCTGCAGGCCGACTGCAGCGCGACTGCGCTGCGGCGCG 2687
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 20:52:08 ; Search time 57.983 Seconds
(without alignments)
12194.743 Million cell updates/sec

Title: US-09-750-240-1

Perfect score: 314

Sequence: 1 atgtcatgttttagtgctt.....acaccgcggaccgctgaa 314

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21:	/SID22/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22:	/SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23:	/SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24:	/SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	313	99.7	314	22	Human partial card
2	313	99.7	2127	19	Human adenylyl cycl
3	295.2	94.0	3549	22	Human cardiac aden
4	295.2	94.0	3552	22	Human cardiac aden
5	295.2	94.0	3582	22	Human modified car
6	295.2	94.0	4942	20	Human type VI aden
7	227.4	72.4	4046	14	Cardiac adenylyl c
8	199.2	63.4	5841	24	Mouse ischaemic co
9	198.2	63.1	4131	21	Type VI adenylyl c

C 10	39.8	12.7	236303	22	AAS11614	Human genomic DNA
C 11	38.2	12.2	3050	22	AAS06036	Angiotensin conver
C 12	38.2	12.2	3174	21	AAC77370	Human ORFX ORF2925
C 13	38.2	12.2	3243	15	AAO79401	Human NMDAR2 recep
C 14	38.2	12.2	3698	15	AAO79400	Human NMDAR2 recep
C 15	38.2	12.2	4274	15	AAO79407	Human NMDAR2 recep
C 16	38.2	12.2	4289	15	AAO79405	Human NMDAR2 recep
C 17	38.2	12.2	4325	15	AAO79404	Human NMDAR2 recep
C 18	38.2	12.2	4340	15	AAO79372	Human N-methyl-D-a
C 19	38.2	12.2	4349	15	AAO79406	Human NMDAR2 recep
C 20	38.2	12.2	4354	15	AAO79403	Human NMDAR2 recep
C 21	38.2	12.2	160771	24	AQ88179	Human osteoblast d
C 22	37.6	12.0	4046	14	AQ842525	Cardiac adenylyl c
C 23	37.2	11.8	668	9	AAN80926	Longisporus Trypsi
C 24	37.2	11.8	1438	18	AAT91179	Human apoptosis pr
C 25	37	11.8	1700	21	AAC69681	Novel human protei
C 26	36.8	11.7	5317	23	ABL17087	Drosophila melanog
C 27	36.8	11.7	5558	23	ABL19835	Drosophila melanog
C 28	36.8	11.7	9579	23	ABL17086	Drosophila melanog
C 29	36.8	11.7	9579	23	ABL19834	Drosophila melanog
C 30	36.6	11.7	1734	22	ABD10196	Pseudorabies virus
C 31	36.6	11.7	3243	20	AAV82910	Human N-methyl-D-a
C 32	36.6	11.7	3243	21	AA95033	Human N-methyl-D-a
C 33	36.6	11.7	3243	21	AAZ38724	Human clone NMDA22
C 34	36.6	11.7	3243	24	AAZ47377	Human NMDAR2C codi
C 35	36.6	11.7	3243	24	ABA05910	Human NMDA recepto
C 36	36.6	11.7	3698	20	AAV82909	Human N-methyl-D-a
C 37	36.6	11.7	3698	21	AA95032	Human N-methyl-D-a
C 38	36.6	11.7	3698	21	AAZ38723	Human clone NMDA22
C 39	36.6	11.7	3698	24	AAZ47376	Human NMDAR2C codi
C 40	36.6	11.7	3698	24	AB199189	Human NMDA recepto
C 41	36.6	11.7	4002	20	AAV82915	Human N-methyl-D-a
C 42	36.6	11.7	4002	21	AA95038	Human N-methyl-D-a
C 43	36.6	11.7	4002	21	AAZ38729	Human NMDAR2 subun
C 44	36.6	11.7	4002	24	AAZ47382	Human NMDAR2C codi
C 45	36.6	11.7	4002	24	AB199194	Human NMDAR2C enco

ALIGNMENTS

RESULT 1

AA08561

ID AA08561 standard; cDNA; 314 BP.

XX AC

XX AAC08561;

XX DT 04-SEP-2001 (first entry)

XX Human partial cardiac adenylylase VI (ACVI) isoform #1 cDNA.

XX Human; cardiant; beta-adrenergic signalling protein; beta-ASP;

XX myocardiun; gene therapy; beta-adrenergic receptor; beta-AR;

KW adenylylase; adenylylase; adenylylase; adenylylase;

KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;

KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ss.

XX Homo sapiens.

XX Key

XX CDS

XX Location/Qualifiers

FT 1..312

FT /*tag= a

FT /product= "Human partial cardiac ACVI isoform #1"

FT /transl_except= (pos:229..231, aa:Xaa)

FT /note= "Xaa is an unknown amino acid; CDS does not

include stop codon"

FT /EC_number= "4.6.1.1"

XX WO200148164-A2.

XX 05-JUL-2001.

XX 26-DEC-2000; 2000WO-US35411.

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XX 27-DEC-1999; 99US-0472667.
XX (RECG ) UNIV CALIFORNIA.
XX Hammond HK, Gao M;
XX WPI; 2001-418260/44.
XX P-PSDB; AAE04308.
XX Novel polynucleotide encoding a modified adenylylcyclase polypeptide
XX useful for enhancing cardiac function in mammalian hearts, and for
XX treating heart disease, especially congestive heart failure -
XX Example 5; Page 114; 153pp; English.
XX The present invention relates to methods and compositions for enhancing
XX cardiac function in mammalian hearts by inserting transgenes encoding
XX beta-adrenergic signalling proteins (beta-ASP) which increase
XX beta-adrenergic responsiveness within the myocardium using in vivo
XX gene therapy. The beta-ASPs of the invention include beta-adrenergic
XX receptors (beta-AR), adenylylcyclases (also referred as adenylylcyclase,
XX adenylylate cyclase and cAMP synthetase) and G-protein receptor kinase
XX (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
XX in mammalian hearts and for treating heart disease, especially
XX congestive heart failure. The present cDNA sequence encodes human
XX partial cardiac adenylylcyclase VI (ACVI) isoform which is used for
XX generating a third beta-ASP transgene, used in the exemplification
XX of the invention.
XX Sequence 314 BP; 60 A; 98 C; 108 G; 47 T; 1 other;

Query Match          99.7%; Score 313; DB 22; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.7e-69;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTAGTGGCTCTCTGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60
Db 1 ATGTCATGTTTAGTGGCTCTCTGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60
QY 61 GAACGCAATGGCAGAAAGCGTTCCGGCGCGCGTGGGCACATCGGGCAGGTGCTTCGCACG 120
Db 61 GAACGCAATGGCAGAAAGCGTTCCGGCGCGCGTGGGCACATCGGGCAGGTGCTTCGCACG 120
QY 121 CCCCCTATATGAGTGCCTCTCGGGATGCAGAGCCACCCAGCCGCCCTCGGGGCCCCC 180
Db 121 CCCCCTATATGAGTGCCTCTCGGGATGCAGAGCCACCCAGCCGCCCTCGGGGCCCCC 180
QY 181 CCTCGTGGCCCTCGCAGGATGACGCTTTCATCCGAGGGGGGGCCCGCANGAAGGCAAG 240
Db 181 CCTCGTGGCCCTCGCAGGATGACGCTTTCATCCGAGGGGGGGCCCGCANGAAGGCAAG 240
QY 241 GAACTGGGGCTGGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACACGACACCG 300
Db 241 GAACTGGGGCTGGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACACGACACCG 300
QY 301 GCGGGACCGCTGAA 314
Db 301 GCGGGACCGCTGAA 314

RESULT 2
AAV23246
ID AAV23246 standard; cDNA; 2127 BP.
AC AAV23246;
XX 17-JUL-1998 (first entry)
XX Human adenylylcyclase isoform VI encoding cDNA.
XX Human; adenylylcyclase VI; AC-VI; beta-adrenergic signalling protein;
XX transgene; gene therapy; congestive heart failure; cardiac function;
KW

```

```

KW adenovirus; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 1..2127
XX FT /*tag= a
XX FT /*product= "adenylylcyclase isoform VI"
XX FT /*transl_except= (pos:229..231,aa:Xaa)
XX FT /*transl_except= (pos:315..317,aa:Xaa)
XX FT /*note= "no stop codon given; Xaa = unknown"
XX FT misc_difference 315
XX FT /*tag= b
XX FT /*note= "n indicates a gap of about 0.5 kb"
XX WO9810085-A2.
XX 12-MAR-1998.
XX 05-SEP-1997; 97WO-US15610.
XX 16-JUN-1997; 97US-0048933.
XX 05-SEP-1996; 96US-0708661.
XX (COLL-) COLLATERAL THERAPEUTICS.
XX (RECG ) UNIV CALIFORNIA.
XX Gao M, Hammond HK, Insel PA, Ping P, Post SR;
XX WPI; 1998-193633/17.
XX P-PSDB; AAW53345.
XX Vectors containing transgene(s) encoding beta-adrenergic signalling
XX proteins - useful for gene therapy of congestive heart failure
XX Claim 60; Fig 12A; 114pp; English.
XX The present sequence encodes human adenylylcyclase isoform VI (AC-VI)
XX from the present invention. The present invention describes a
XX recombinant replication-defective viral particle (I) comprising a gene
XX encoding a beta-adrenergic signalling protein (beta-ASP) operably
XX linked to a promoter. Also described are: (1) a recombinant pro-viral
XX plasmid (Ia) comprising a gene encoding a beta-ASP, as above, operably
XX linked to a promoter and further comprising a replication-defective
XX viral genome; (2) a (mammalian) cell transfected with (I) or (Ia); (3)
XX an isolated polynucleotide comprising a sequence encoding a human
XX adenylylcyclase isoform VI (AC-VI), or a variant having AC activity;
XX (4) a human AC-VI encoded by (3); (5) an isolated polynucleotide
XX sequence which hybridises at high stringency to (3); and (6) a vector
XX comprising the polynucleotide of (3). (I) can be used to form a
XX filtered adenovirus particle preparation. (I) is used to enhance
XX cardiac function in mammals.
XX Sequence 2127 BP; 421 A; 637 C; 615 G; 452 T; 2 other;

Query Match          99.7%; Score 313; DB 19; Length 2127;
Best Local Similarity 100.0%; Pred. No. 2.2e-69;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTAGTGGCTCTCTGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60
Db 1 ATGTCATGTTTAGTGGCTCTCTGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60
QY 61 GAACGCAATGGCAGAAAGCGTTCCGGCGCGCGTGGGCACATCGGGCAGGTGCTTCGCACG 120
Db 61 GAACGCAATGGCAGAAAGCGTTCCGGCGCGCGTGGGCACATCGGGCAGGTGCTTCGCACG 120
QY 121 CCCCCTATATGAGTGCCTCTCGGGATGCAGAGCCACCCAGCCGCCCTCGGGGCCCCC 180
Db 121 CCCCCTATATGAGTGCCTCTCGGGATGCAGAGCCACCCAGCCGCCCTCGGGGCCCCC 180
QY 181 CCTCGTGGCCCTCGCAGGATGACGCTTTCATCCGAGGGGGGGCCCGCANGAAGGCAAG 240

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Db 181 CCTCGGTCCCTGGCAGGATGACGCCTTCATCCGAGGGCGGCCCAAGCAAG 240
 QY 241 GAACTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACACACACCG 300
 Db 241 GAACTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACACACACCG 300
 QY 301 GCGGACCGGTGAA 314
 Db 301 GCGGACCGGTGAA 314

RESULT 3
 AAD08563
 ID AAD08563 standard; DNA; 3549 BP.
 XX
 AC AAD08563;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human cardiac adenylyclase VI (ACVI) isoform #1 DNA.
 XX
 KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;
 KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;
 KW adenylyclase; adenylate cyclase; cAMP synthetase;
 KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;
 KW cardiac adenylyclase VI; ACVI isoform; beta-ASP transgene; ds.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT CDS 1..3504
 FT /*tag= a
 FT /product= "Human cardiac adenylyclase VI isoform #1"
 FT /EC_number= "4.6.1.1"
 XX
 PN WO200148164-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US35411.
 XX
 PR 27-DEC-1999; 99US-0472667.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Hammond HK, Gao M;
 XX
 DR WPI; 2001-418260/44.
 DR P-PSDB; AAE04310.
 XX
 PT Novel polynucleotide encoding a modified adenylyclase polypeptide
 PT useful for enhancing cardiac function in mammalian hearts, and for
 PT treating heart disease, especially congestive heart failure -
 XX
 PS Example 5; Page 122-129; 153pp; English.
 XX
 CC The present invention relates to methods and compositions for enhancing
 CC cardiac function in mammalian hearts by inserting transgenes encoding
 CC beta-adrenergic signalling proteins (beta-ASP) which increase
 CC beta-adrenergic responsiveness within the myocardium using in vivo
 CC gene therapy. The beta-ASPs of the invention include beta-adrenergic
 CC receptors (beta-AR), adenylyclases (also referred as adenylyclase,
 CC adenylate cyclase and cAMP synthetase) and G-protein receptor kinase
 CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
 CC in mammalian hearts and for treating heart disease, especially
 CC congestive heart failure. The present DNA sequence encodes human
 CC cardiac adenylyclase VI (ACVI) isoform which is used for generating
 CC a third beta-ASP transgene, used in the exemplification
 CC of the invention.
 XX
 SQ Sequence 3549 BP; 699 A; 1025 C; 1061 G; 764 T; 0 other;

Query Match 94.0%; Score 295.2; DB 22; Length 3549;

Best Local Similarity 97.1%; Pred. No. 7.1e-65;
 Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGGTTTACTTGGCCTCCTGCTCCCTAAAGTGGATGAACGAAACAGCCTGGGGT 60
 Db 1 ATGTCATGGTTTACTTGGCCTCCTGCTCCCTAAAGTGGATGAACGAAACAGCCTGGGGT 60
 QY 61 GAACGCAATGGGCAGAACGCTTCGCGGCGCGCTGCACCTCGGGAGGTGGCTTCTGCACG 120
 Db 61 GAACGCAATGGGCAGAACGCTTCGCGGCGCGCTGCACCTCGGGAGGTGGCTTCTGCACG 120
 QY 121 CCCGCTATATGAGCTGCCTCCGGGATGCAGAGCACCCACCCCTGCGGGGCCCC 180
 Db 121 CCCGCTATATGAGCTGCCTCCGGGATGCAGAGCACCCACCCCTGCGGGGCCCC 180
 QY 181 CCTCGTCCCTCGCAGGATGACGCTTCATCCGAGGGCGGCCCAAGGCAAG 240
 Db 181 CCTCGTCCCTCGCAGGATGACGCTTCATCCGAGGGCGGCCCAAGGCAAG 240
 QY 241 GAACTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACACACCG 300
 Db 241 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACACACCG 300
 QY 301 GCGGACCG 309
 Db 301 GCGGACCG 309

RESULT 4
 AAD08567
 ID AAD08567 standard; DNA; 3552 BP.
 XX
 AC AAD08567;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human cardiac adenylyclase VI (ACVI) isoform #2 DNA.
 XX
 KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;
 KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;
 KW adenylyclase; adenylate cyclase; cAMP synthetase;
 KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;
 KW cardiac adenylyclase VI; ACVI isoform; beta-ASP transgene; ds.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT CDS 1..3507
 FT /*tag= a
 FT /product= "Human cardiac adenylyclase VI isoform #2"
 FT /EC_number= "4.6.1.1"
 XX
 PN WO200148164-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US35411.
 XX
 PR 27-DEC-1999; 99US-0472667.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Hammond HK, Gao M;
 XX
 DR WPI; 2001-418260/44.
 DR P-PSDB; AAE04311.
 XX
 PT Novel polynucleotide encoding a modified adenylyclase polypeptide
 PT useful for enhancing cardiac function in mammalian hearts, and for
 PT treating heart disease, especially congestive heart failure -
 XX
 PS Claim 6; Page 134-140; 153pp; English.
 XX

CC The present invention relates to methods and compositions for enhancing
 CC cardiac function in mammalian hearts by inserting transgenes encoding
 CC beta-adrenergic signalling proteins (beta-ASP) which increase
 CC beta-adrenergic responsiveness within the myocardium using in vivo
 CC gene therapy. The beta-ASPs of the invention include beta-adrenergic
 CC receptors (beta-AR), adenylyl cyclases (also referred as adenylyl cyclase,
 CC adenylylate cyclase and cAMP synthetase) and G-protein receptor kinase
 CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
 CC in mammalian hearts and for treating heart disease, especially
 CC congestive heart failure. The present DNA sequence encodes human
 CC cardiac adenylyl cyclase VI (ACVI) isoform which is used for generating
 CC a fourth beta-ASP transgene, used in the exemplification
 CC of the invention.
 XX
 SQ Sequence 3552 BP; 686 A; 1037 C; 1068 G; 761 T; 0 other;
 Query Match 94.0%; Score 295.2; DB 22; Length 3552;
 Best Local Similarity 97.1%; Pred. No. 7.1e-65;
 Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 ATGTCATGTTAGTGGCTCCTGCTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60
 DB 1 ATGTCATGTTAGTGGCTCCTGCTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60
 QY 61 GAACGCAATGGGAGAGGTTTCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
 DB 61 GAACGCAATGGGAGAGGTTTCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
 QY 121 CCCCCTATATGAGCTGCTCCGGGATGACAGCCACCCAGCCCTCGGGGCCCC 180
 DB 121 CCCCCTATATGAGCTGCTCCGGGATGACAGCCACCCAGCCCTCGGGGCCCC 180
 QY 181 CCTCGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGGGGGCCANGCAAGGCAAG 240
 DB 181 CCTCGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGGGGGCCANGCAAGGCAAG 240
 QY 241 GAACCTGGGCTGGGCGACGTGGCCCTGGGCTTCGGAAGATACCGAAGTGACAGCACCG 300
 DB 241 GAGCTGGGCTGGGCGACGTGGCCCTGGGCTTCGGAAGATACCGAAGTGACAGCACCG 300
 QY 301 GCGGGACCG 309
 DB 301 GCGGGACCG 309
 RESULT 5
 ID AAD08568 standard; cDNA; 3582 BP.
 XX
 AC AAD08568;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human modified cardiac adenylyl cyclase VI (ACVI) isoform cDNA.
 XX
 KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;
 KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;
 KW adenylyl cyclase; adenylylate cyclase; cAMP synthetase;
 KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;
 KW cardiac adenylyl cyclase VI; ACVI isoform; beta-ASP transgene; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 22..3525
 FT /*tag= a
 FT /product= "Human modified cardiac ACVI isoform"
 XX
 PN W0200148164-A2.
 XX
 PD 05-JUL-2001.
 XX

PF 26-DEC-2000; 2000WO-US35411.
 XX
 PR 27-DEC-1999; 99US-0472667.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Hammond HK, Gao M;
 XX
 DR WPI; 2001-418260/44.
 DR P-PSDB; ARE04312.
 XX
 PT Novel polynucleotide encoding a modified adenylyl cyclase polypeptide
 PT useful for enhancing cardiac function in mammalian hearts, and for
 PT treating heart disease, especially congestive heart failure -
 XX
 PS Claim 4; Page 143-150; 153pp; English.
 XX
 CC The present invention relates to methods and compositions for enhancing
 CC cardiac function in mammalian hearts by inserting transgenes encoding
 CC beta-adrenergic signalling proteins (beta-ASP) which increase
 CC beta-adrenergic responsiveness within the myocardium using in vivo
 CC gene therapy. The beta-ASPs of the invention include beta-adrenergic
 CC receptors (beta-AR), adenylyl cyclases (also referred as adenylyl cyclase,
 CC adenylylate cyclase and cAMP synthetase) and G-protein receptor kinase
 CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
 CC in mammalian hearts and for treating heart disease, especially
 CC congestive heart failure. The present cDNA sequence encodes human
 CC modified cardiac adenylyl cyclase VI (ACVI) isoform which is used for
 CC generating a beta-ASP transgene, used in the exemplification of the
 CC invention.
 XX
 SQ Sequence 3582 BP; 703 A; 1036 C; 1067 G; 776 T; 0 other;
 Query Match 94.0%; Score 295.2; DB 22; Length 3582;
 Best Local Similarity 97.1%; Pred. No. 7.1e-65;
 Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 ATGTCATGTTAGTGGCTCCTGCTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60
 DB 22 ATGTCATGTTAGTGGCTCCTGCTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 81
 QY 61 GAACGCAATGGGAGAGGTTTCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
 DB 61 GAACGCAATGGGAGAGGTTTCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 141
 QY 121 CCCCCTATATGAGCTGCTCCGGGATGACAGCCACCCAGCCCTCGGGGCCCC 180
 DB 121 CCCCCTATATGAGCTGCTCCGGGATGACAGCCACCCAGCCCTCGGGGCCCC 201
 QY 181 CCTCGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGGGGGCCANGCAAGGCAAG 240
 DB 181 CCTCGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGGGGGCCANGCAAGGCAAG 261
 QY 241 GAACCTGGGCTGGGCGACGTGGCCCTGGGCTTCGGAAGATACCGAAGTGACAGCACCG 300
 DB 241 GAGCTGGGCTGGGCGACGTGGCCCTGGGCTTCGGAAGATACCGAAGTGACAGCACCG 321
 QY 301 GCGGGACCG 309
 DB 301 GCGGGACCG 330
 RESULT 6
 ID AAX00461 standard; cDNA; 4942 BP.
 XX
 AC AAX00461;
 XX
 DT 21-MAY-1999 (first entry)
 XX
 DE Human type VI adenylyl cyclase cDNA.
 XX
 KW Adenylyl cyclase type VI; human; hAC6; therapy; diagnosis; ds.

XX OS Homo sapiens.
 XX PH Key Location/Qualifiers
 XX FT CDS 145..3651
 XX FT /*tag= a
 XX PN WO9901547-A1.
 XX PD 14-JAN-1999.
 XX PF 01-JUL-1998; 98WO-US13694.
 XX PR 01-JUL-1997; 97US-0886350.
 XX PR 01-JUL-1997; 97US-0070904.
 XX PA (CORT-) COR THERAPEUTICS INC.
 XX PI Tomlinson JA;
 XX WPI; 1999-106049/09.
 XX P-PSDB; AAW30599.
 XX Newly isolated and purified human type VI adenylyl cyclase (hAC6)
 XX polypeptide - useful for identifying potential therapeutic agents
 XX that modulate hAC6 activity, and for the diagnosis of
 XX hAC6-associated diseases and disorders
 XX Claim 3; Fig 1A-I; 42pp; English.
 XX This DNA sequence encodes human type VI adenylyl cyclase (hAC6, see
 XX AAW30599) that is expressed mainly in the heart and brain. hAC6 has
 XX a similar putative structure to other adenylyl cyclase isoforms
 XX but, like type V, is distinguishable in that it has a larger
 XX N-terminus and a relatively shorter C-terminus as it lacks the C2b
 XX region. hAC6 cDNA was initially isolated from a human heart cDNA
 XX library using an adenylyl cyclase PCR fragment as probe. It was
 XX used to design primers that were used in a PCR-based RACE to obtain
 XX the full-length cDNA sequence. The invention relates to the hAC6
 XX gene, methods for the recombinant production of purified hAC6 and
 XX the proteins made by these methods, antibodies against hAC6,
 XX vectors, probes and host cells (especially HEK-293) transformed by
 XX genes encoding polypeptides having hAC6 activity, along with
 XX diagnostic and therapeutic uses for these various reagents. hAC6
 XX can be used as a tool to screen for agonists and antagonists that
 XX stimulate/inhibit hAC6. Such compounds have therapeutic utility
 XX in treating diseases caused by aberrant activity of this enzyme,
 XX and diseases whose symptoms can be ameliorated by stimulating or
 XX inhibiting the activity of hAC6.
 XX
 XX SQ Sequence 4942 BP; 953 A; 1404 C; 1512 G; 1073 T; 0 other;
 Query Match 94.0%; Score 295.2; DB 20; Length 4942;
 Best Local Similarity 97.1%; Pred. No. 7.5e-65;
 Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 ATGTCATGGTTTACTGGCTCCTGGTCCCTAAAGTGATGAACGGAACAGCCTGGGT 60
 Db 145 ATGTCATGGTTTACTGGCTCCTGGTCCCTAAAGTGATGAACGGAACAGCCTGGGT 204
 QY 61 GAACGCAATGGCAGAGAGCGTTCGCGGCGCGTGGCACTCGGGCAGGTGCTTCGCACG 120
 Db 205 GAACGCAATGGCAGAGAGCGTTCGCGGCGCGTGGCACTCGGGCAGGTGCTTCGCACG 264
 QY 121 CCGCGCTATATGATGCTCCGCGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180
 Db 265 CCGCGCTATATGATGCTCCGCGATGCAGAGCCACCCAGCCCTCGGGGCCCC 324
 QY 181 CCTCGGTGCCCTGGCAGGATGACGCTTCATCCGAGGGCGGCCCCANGCAAGGGCAAG 240
 Db 325 CCTCGGTGCCCTGGCAGGATGACGCTTCATCCGAGGGCGGCCCCAGGCAAGGGCAAG 384
 QY 241 GAACTGGGGTGGCGGGCAGTGGCCCTTGGGCTTCGAAGATACCGAAGTGACAACGACACCG 300

Db 385 GAGCTGGGGTGGCGGAGTGGCTTCCGAGGATACCGAGGTGACCAACGACACGCG 444
 QY 301 GCGGGACCG 309
 Db 445 GCGGGACG 453
 RESULT 7
 AAQ42525
 ID AAQ42525 standard; DNA; 4046 BP.
 XX AC AAQ42525;
 XX DT 14-SEP-1993 (first entry)
 XX DE Cardiac adenylyl cyclase gene.
 XX KW Regulation; cardiac function; heart; heart failure; ss.
 XX OS Canis familiaris.
 XX PH Key Location/Qualifiers
 XX FT CDS 131..3627
 XX FT /*tag= a
 XX PN EP543137-A.
 XX PD 26-MAY-1993.
 XX PF 12-OCT-1992; 92EP-0117374.
 XX PR 18-NOV-1991; 91US-0793961.
 XX PA (AMCY) AMERICAN CYANAMID CO.
 XX PI Ishikawa Y;
 XX WPI; 1993-168873/21.
 XX P-PSDB; AAR37309.
 XX Purified DNA encoding cardiac adenylyl cyclase - useful to screen
 XX for cpds. which stimulate activity of the cyclase
 XX Claim 1; Fig 2; 34pp; English.
 XX A canine heart cDNA library was constructed in lambda gt10 and was
 XX screened with a 970 bp AatI-HincII fragment from type I adenylyl
 XX cyclase cDNA probe (encodes the first cytoplasmic domain of adenylyl
 XX cyclase, which has significant homology to other previously known
 XX types of adenylyl cyclase). One positive clone, of 5.4 kb was obtd.
 XX Positive colonies were subcloned into pUC18 and further subcloned
 XX and sequenced bidirectionally. The 5.4 kb clone was used to
 XX rescreen the library and on overlapping clone contg. the 5' end of
 XX the gene was isolated. Together the two clones cover the complete
 XX canine cardiac adenylyl cyclase gene. The gene is suspected of
 XX being involved in the regulation of cardiac function and it is thought
 XX that decreased activity of adenylyl cyclase in the heart may be a
 XX major factor in the development of heart failure. Thus the adenylyl
 XX cyclase gene is useful to screen cpds. which stimulate the activity
 XX of the cyclase.
 XX SQ Sequence 4046 BP; 743 A; 1206 C; 1254 G; 843 T; 0 other;
 Query Match 72.4%; Score 227.4; DB 14; Length 4046;
 Best Local Similarity 89.5%; Pred. No. 7.7e-48;
 Matches 256; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
 QY 1 ATGTCATGGTTTACTGGCTCCTGGTCCCTAAAGTGATGAACGGAACAGCCTGGGT 60
 Db 131 ATGTCATGGTTTACTGGCTCCTGGTCCCTAAAGTGATGAACGGAACAGCCTGGGT 190
 QY 61 GAACGCAATGGCAGAGAGCGTTCGCGGCGCGTGGCACTCGGGCAGGTGCTTCGCACG 120

Db 191 GAACGCAATGGCAGAACGCT---CCACGCCGGGACTCGGACCAAGTGGCTTCTGCACG 247
 QY 121 CCCCGCTATATGAGCTGCTCCGGGATGAGAGCCACCCAGCCCGCCCTCGGGGCCCC 180
 Db 248 CCCCGCTATATGAGCTGCTCCGGGATGAGAGCCCGCCCGCCCTCGGGGCCCC 307
 QY 181 CCTCGTGCCCTGGCAGGATGACGCTTTCATCCGGAGGGGGCCCGCCANGCAAGGCAAG 240
 Db 308 CCTCGTGCCCTGGCAGGATGAGGCTTTCATCCGGAGAGGGCCCGCCCGGCAAGGCAAG 367
 QY 241 GAACGCGGCTGGGCACTGGCCCTGGGCTTCGAAAGATACCAAG 286
 Db 368 GAGCTGGGCTGGGCGCTGGCCCTGGGCTTCGAGGACACTGAGG 413

RESULT 8

ABI99680
ID ABI99680 standard; cDNA; 5841 BP.

AC ABI99680;

XX
XX
XX 07-MAR-2002 (first entry)

DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:716.

XX
KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.

XX
OS Mus musculus.

XX
PN WO20018188-A2.

XX
PD 22-NOV-2001.

XX
PF 18-MAY-2001; 2001WO-JP04192.

XX
PR 18-MAY-2000; 2000JP-0145977.

XX
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX
DR WPI; 2002-034733/04.

DR
P-PSDB; ABB57257.

XX
PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
expression levels of particular genes defined in the specification or
PT by determining the expression profile of a gene group comprising these
PT genes -

XX
PS Claim 2; Page 1771-1780; 2690pp; English.

XX
CC The present invention describes a method for examining ischaemic
conditions, comprising measuring the expression levels of particular
CC genes (I) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (I). The method
CC is useful for examining the ischaemic condition (e.g. compressive
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC expression levels of particular genes (ABI99202 to ABI99912, encoding
CC the protein sequences in ABB57020 to ABB57374) or by determining the
CC expression profile of a gene group comprising these genes. The
CC expression levels or expression profiles produced by these genes are
CC used as an indicator when screening for ischaemic condition-improving
CC drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914
CC represent PCR primers for a mouse ischaemic condition related sequence,
CC which are used in the exemplification of the present invention.

XX
SQ Sequence 5841 BP; 1214 A; 1558 C; 1673 G; 1396 T; 0 other;

Query Match

63.4%; Score 199.2; DB 24; Length 5841;

Best Local Similarity 82.3%; Pred. No. 9.8e-41;

Matches 241; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

QY 1 ATGTCATGTTTAGTGGCTCCTGCTCCCTAAAGTGGATGAACGAAACAGCCTGGGGT 60
 Db 96 ATGTCATGTTTAGTGGCTCCTGCTCCCAAGTGGATGAACGAAACAGCCTGGGG 155
 QY 61 GAACGCAATGGCAGAACGCTTCGGGGCCGCTGGGCACTCGGGCAGGTGGCTTCTGCACG 120
 Db 156 GAACGCAATGGCAGAACGCTTCGGGGCCGCTGGGCACTCGGGCAGGTGGCTTCTGCACG 212
 QY 121 CCCCGCTATATGAGCTGCTCCGGGATGAGAGCCACCCAGCCCGCCCTCGGGGCCCC 180
 Db 213 CCTCGCTATATGAGCTGCTCCCAAGTGGAGGCCACCCAGCCCGCCCTCGGAGCTCAC 272
 QY 181 CCTCGTGCCCTGGCAGGATGACGCTTTCATCCGGAGGGGGCCCGCCANGCAAGGCAAG 240
 Db 273 ACTCGTGCCCTGGCAGGATGAAGCTTTCATCAGGAGGGGGCCCGCCAGGGGTGTG 332
 QY 241 GAACGCGGCTGGGCACTGGCCCTGGGCTTCGAAAGATACCAAGTGAACAAC 293
 Db 333 GAGCTGGGCTGGGCTCAGTGGCTTGGGGTTTGACGACACTGAGGTGACCAC 385

RESULT 9

AAA53923
ID AAA53923 standard; cDNA; 4131 BP.

AC AAA53923;

XX
XX 03-JAN-2001 (first entry)

DE Type VI adenylyl cyclase coding sequence.

XX
KW Adenylyl cyclase; type I; type II; recombinant; enzyme; CAMP;
cyclic AMP; adenosine monophosphate; screening; stimulation;
KW inhibition; treatment; cholera; pituitary tumour; heart failure;
KW ischaemia; endocrine disorder; cell necrosis;
KW pseudohypoparathyroidism; endocrine deficiency; human; ss.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers

FT CDS 14..3556

FT /*tag= a

FT /product= Type VI adenylyl cyclase

XX
PN US6107076-A.

XX
PD 22-AUG-2000.

XX
PF 04-OCT-1996; 960S-0726214.

XX
PR 04-OCT-1995; 950S-0005498.

XX
PA (TEXA) UNIV TEXAS SYSTEM.

XX
PI Gilman AG, Tang W;

XX
XX WPI; 2000-578539/54.

XX
DR P-PSDB; AAB02010.

XX
PT Novel soluble mammalian polypeptide composition comprising adenylyl
cyclase activity for screening stimulators and inhibitors of adenylyl
cyclase, is activated by Gsalpha

XX
PS Disclosure; Columns 75-78; 73pp; English.

XX
CC A recombinant Adenylyl cyclase is described which lacks membrane
bound domains. Separation and purification of the recombinant
CC enzyme is much easier compared with wild type enzymes and the
CC recombinant enzyme is more stable than the wild type enzyme which
CC allows easier screening of compounds that stimulate and inhibit
CC Adenylyl cyclase activity. The recombinant adenylyl cyclase comprises
CC a chimera of adenylyl cyclase C_1 and C_2 domains linked covalently.

CC The domains may be linked by a linker peptide. The recombinant
CC adenylyl cyclase is useful for screening inhibitors and stimulators
CC of adenylyl cyclase activity. Inhibitors of the enzyme are useful for
CC treating cholera, pituitary tumors, heart failure, ischaemia,
CC endocrine disorders and cell necrosis. Stimulators of adenylyl
CC cyclase are useful for treating pseudohypoparathyroidism and other
CC endocrine deficiencies.

XX
SQ Sequence 4131 BP; 835 A; 1190 C; 1182 G; 924 T; 0 other;

Query Match 63.1%; Score 198.2; DB 21; Length 4131;
Best Local Similarity 79.9%; Pred. No. 1.7e-40;
Matches 246; Conservative 0; Mismatches 59; Indels 3; Gaps 1;
QY 1 ATGTCATGGTTTGTAGTGGCTCCCTGCTCCCTAAAGTGTGATGAACGAAACAGCCTGGCGT 60
DB 56 ATGTCATGGTTTGTAGTGGCTCCCTGCTCCCTAAAGTGTGATGAACGAAACAGCCTGGCGC 115
QY 61 GAACGCAATGGGAGAGAGCTTCGCGCGCCGCTGGGCACTCGGCGAGGTGGCTTCTGCAACG 120
DB 116 GAACGCAATGGGAGAGAGCG---CCACGCGCAGCGCAGCGCCCTGGCTTCTGCGCG 172
QY 121 CCCGCTATATAGCTGCTCCCGGATGACAGCCACCCAGCCCTGCGGCGCC 180
DB 173 CCCGCTATATAGCTGCTCCCGGATGACAGCCACCCAGCCCTGCGGCTCGC 232
QY 181 CCTCGGTGCCCCCTGGCAGGATGACGCTTCATCGGAGGGCGGCCCAAGGCGCAAG 240
DB 233 ACTCGGTGCCCCCTGGCAGGATGACGCTTCATCAGGAGGCTGGCCGGAAGGGGTGTG 292
QY 241 GAACGCGGTGGCGGCGAGTGGCCCTGGGCTTCGAAGATACCGAAGTACACACGACACCG 300
DB 293 GAGCTGGGGCTGGGCTCAGTGGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 352
QY 301 GCGGGACC 308
DB 353 GGGACAGC 360

RESULT 10
AAS11614/C
ID AAS11614 standard; DNA; 236303 BP.

XX AAS11614;

XX 24-OCT-2001 (first entry)

DE Human genomic DNA containing exons 2-17 of the CRIM1 gene.

XX
KW CRIM-1; Human; human chromosome 2p21-16.3; ophthalmological;
KW neuroprotective; renal; osteopathic; dental; vulnary; immunogen;
KW antibody; gene therapy; neurodegenerative disease; eye disorder;
KW cataract; bone morphogenic protein; BMG; renal disease; bone abnormality;
KW tooth abnormality; wound; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
FH exon 33104..33277

FT /tag= a

FT /number= 2

FT /tag= b

FT /number= 2

FT /tag= c

FT /number= 3

FT /tag= d

FT /number= 3

FT /tag= e

FT /number= 4

FT intron 79225..101022
FT /tag= f
FT /number= 4
FT exon 101023..101144
FT /tag= g
FT /number= 5
FT intron 101145..113377
FT /tag= h
FT /number= 5
FT exon 113378..113560
FT /tag= i
FT /number= 6
FT intron 113561..115985
FT /tag= j
FT /number= 6
FT exon 115986..116183
FT /tag= k
FT /number= 7
FT intron 116184..135707
FT /tag= l
FT /number= 7
FT exon 135708..135836
FT /tag= m
FT /number= 8
FT intron 135837..146471
FT /tag= n
FT /number= 8
FT exon 146472..146628
FT /tag= o
FT /number= 9
FT intron 146629..148761
FT /tag= p
FT /number= 9
FT exon 148762..148883
FT /tag= q
FT /number= 10
FT intron 148884..150044
FT /tag= r
FT /number= 10
FT exon 150045..150254
FT /tag= s
FT /number= 11
FT intron 150255..153815
FT /tag= t
FT /number= 11
FT exon 153816..154031
FT /tag= u
FT /number= 12
FT intron 154032..158580
FT /tag= v
FT /number= 12
FT exon 158581..158802
FT /tag= w
FT /number= 13
FT intron 158803..173982
FT /tag= x
FT /number= 13
FT exon 173983..174177
FT /tag= y
FT /number= 14
FT intron 174178..181006
FT /tag= z
FT /number= 14
FT exon 181007..181129
FT /tag= aa
FT /number= 15
FT intron 181130..183612
FT /tag= ab
FT /number= 15
FT exon 183613..183800
FT /tag= ac
FT /number= 16
FT intron 183801..185152

```
FT      /*tag= ad
FT      /number= 16
FT      exon      185153..187765
FT      /*tag= ae
FT      /number= 17
XX
XX      WO200138519-A1.
PN      31-MAY-2001.
XX
XX      24-NOV-2000; 2000WO-AU01435.
XX
XX      26-NOV-1999; 99AU-0004348.
XX
XX      (UYQU ) UNIV QUEENSLAND.
XX
XX      Little M, Yamada T, Holmes G, Georgas K, Kolle G, Wilkinson L;
XX      WPI; 2001-343951/36.
XX
XX      Nucleic acids from human chromosome 2p21-16.3 and the encoded peptide,
XX      especially cataract formation -
XX
XX      Claim 4; Fig 3; 169pp; English.
XX
XX      The invention relates to nucleic acids from human chromosome 2p21-16.3
XX      and the encoded peptide (and mouse and chicken orthologues) that
XX      comprises a PGECCPLP group, an insulin-like growth factor binding protein
XX      (IGFBP)-like domain, cysteine-rich domains, an RGD (undefined) group
XX      and a transmembrane domain. The protein, e.g. CRIM1, interacts with
XX      peptides of the transforming growth factor superfamily. A composition
XX      comprising an expression construct comprising the nucleic acids of the
XX      invention or a mimetic which antagonises or mimics an activity of a CRIM1
XX      polypeptide may be used in a method for modulating the biological
XX      activity of a polypeptide of the bone morphogenic protein (BMP) family.
XX      In this way they may be used to prevent or treat an eye disease,
XX      especially cataract formation. They may also be used to treat
XX      neurodegenerative diseases, renal and kidney disease, bone and tooth
XX      abnormalities, wounds and skin damage, e.g. by use of the nucleic acid in
XX      gene therapy by using antibodies directed against CRIM1 polypeptides.
XX      The present sequence is a Human genomic DNA containing exons 2-17 of
XX      the CRIM1 gene.
XX
XX      Sequence 236303 BP; 70199 A; 46544 C; 47996 G; 71563 T; 1 other;
XX
XX      Query Match      12.7%; Score 39.8; DB 22; Length 236303;
XX      Best Local Similarity 55.4%; Pred. No. 1.8;
XX      Matches 77; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
XX
XX      QY      78 GCGTTCCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCGCCGCTATATGAGCTG 137
XX      Db 234505 GAGTCGGGGCCCGCGGGAGTGGGGGAGCCTCCCTACCCCTCGCCGCCGCGCAG 234446
XX
XX      QY      138 CCTCGGGATGACAGACCCACCCAGCCCTCGGGGCCCTCGGTGCCCTCGGCA 197
XX      Db 234445 CCTACGGCCGAGCTCTCTCCCTGCGCCCTCTCCGCCGCCGAGTCCCGGCC 234386
XX
XX      QY      198 GGATGACGCGCTTCATCCGG 216
XX      Db 234385 TCTCGCTCTCTTCCTCCGG 234367
XX
XX      RESULT 11
XX      AAS06036/c
XX      ID AAS06036 standard; DNA; 3050 BP.
XX
XX      AC AAS06036;
XX
XX      DT 12-SEP-2001 (first entry)
XX
XX      DE Angiotensin converting enzyme (ACEV) splice variant DNA #36.
XX
```

```
KW      Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW      granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW      platelet-derived endothelial cell growth factor; cardiovascular disease;
KW      cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; ds;
KW      vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW      myocardial infarction; coronary arterial thrombosis; renal disease;
KW      diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW      multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW      nonaroidotic pulmonary granulomatous disease; endothelial abnormality;
KW      vascular disorder; asbestosis.
XX
XX      Homo sapiens.
OS
XX
XX      WO200136632-A2.
PN
XX
XX      25-MAY-2001.
PD
XX
XX      17-NOV-2000; 2000WO-IL00766.
PF
XX
XX      17-NOV-1999; 99IL-0132978.
PR
XX      10-DEC-1999; 99IL-0133455.
PR
XX
XX      (COMP-) COMPUGEN LTD.
PA
XX
XX      Levine Z, David A, Azar I, Khosravi R, Bernstein J;
PI
XX
XX      WPI; 2001-336004/35.
DR
XX      P-PSDB; AAU02936.
XX
XX      Novel alternative splicing variants e.g. variant of angiotensin
XX      converting enzyme (ACEV), useful in identifying candidate compounds
XX      capable of binding to the variant and to detect anti-variant antibodies
XX
XX      Claim 1; Page 335-336; 519pp; English.
XX
XX      The sequence represents a DNA encoding an angiotensin converting enzyme
XX      splice variant (ACEV) polypeptide. The polypeptides of the invention
XX      include variants of granulocyte colony stimulating factor receptor,
XX      glucagon, interleukin 6, platelet-derived endothelial cell growth factor,
XX      cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and
XX      vasoactive intestinal polypeptide receptor 2. The polypeptides and their
XX      associated nucleic acids are useful for identification of variant
XX      sequences and detection of candidate compounds capable of binding the
XX      molecules. The sequences of the invention can be used in the treatment
XX      and diagnosis of various disorders including cardiovascular diseases such
XX      as arteriosclerosis, myocardial infarction and coronary arterial
XX      thrombosis, renal diseases such as diabetic nephropathy, muscular
XX      diseases such as hypertrophy, immune disorders such as immune complex
XX      nephritis, multiple sclerosis, cancer, sarcoidosis, nonaroidotic
XX      pulmonary granulomatous diseases such as asbestosis and vascular
XX      pathologies involving an endothelial abnormality such as deep vein
XX      thrombosis.
XX
XX      Sequence 3050 BP; 520 A; 1032 C; 942 G; 555 T; 1 other;
XX
XX      Query Match      12.2%; Score 38.2; DB 22; Length 3050;
XX      Best Local Similarity 46.0%; Pred. No. 2.4;
XX      Matches 127; Conservative 0; Mismatches 149; Indels 0; Gaps 0;
XX
XX      QY      13 AGTGGCCCTCGTCCCTAAAGTGGATGAACGGAACAGCCTGGGTGAACCAATGG 72
XX      Db 2623 AGAGGCCCTCCAGCGCCGAGGAGCCGCTGGTGGACAGGTGAAGAGGA 2564
XX
XX      QY      73 CAGAAGCGTTTCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCGCCCTATATG 132
XX      Db 2563 CAGACAGCCCCCAGCAAAATGGCAGGTGGCGCTGCAGGACAGACGTCTCTCTG 2504
XX
XX      QY      133 AGCTGCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGCGGGCCCCCTCGGTGCCCC 192
XX      Db 2503 TGCTGCCAGCGGGGCCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2444
XX
XX      QY      193 TGGCAGGATGACGCCCTTCATCCGGAGGGCGGCCCCANGCAAGGCAAGCACTGGGGCTG 252
```

```
Db 2443 AAGCACATCGACTCGCTGGCGGCAAGCGCTGACGCCGAGTGGCGTGGCGGGCG 2384
QY 253 CGGGCACTGGCCCTGGCTTCGAGATACCGAAGTG 288
Db 2383 CAGCGGGGGCGGGTGCACCCAGCGGGCAGCGAGCTG 2348

RESULT 12
AAC77370
ID AAC77370 standard; cDNA; 3174 BP.
XX
AC AAC77370;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human ORFX ORF2925 polynucleotide sequence SEQ ID NO:5849.
XX
KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive; ss.
XX
OS Homo sapiens.
XX
PN W0200058473-A2.
XX
PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US08621.
XX
PR 31-MAR-1999; 99US-0127607.
PR 02-APR-1999; 99US-0127636.
PR 05-APR-1999; 99US-0127728.
PR 30-MAR-2000; 2000US-0540763.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
WPI; 2000-602362/57.
XX
P-PSDB; AAB43161.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
XX
PS Claim 5; Page 5022-5024; 5507pp; English.
XX
CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC antithyroid; and antianemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder. The
CC nucleic acids can be used to express ORFX proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
```

```
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX
SQ Sequence 3174 BP; 737 A; 897 C; 904 G; 620 T; 16 other;

Query Match 12.2%; Score 38.2; DB 21; Length 3174;
Best Local Similarity 53.4%; Pred. No. 2.4;
Matches 79; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 137 GCCTCGGGATGACAGCCACCCAGCCCGCTGCGGGCCCGCTCGGTGCCCTGGC 196
Db 2049 GCCCCTCCAGGCTCAGCTTCCAAACCCACAGCTCCCGGTGGCCACATTGCCCTCAGC 2108
QY 197 AGGATGACGCTTTCATCCGGAGGGCGGCCGAGGCGAAGCAAGCAACTGGGCTCGGG 256
Db 2109 AGGCTTAGTCCAGTTCCTGGGTGGGGGAGGAGGAGTGGCCAGTGGCCAGTGGCCAGG 2168
QY 257 CAGTGGCCCTGGGCTTCGAAAGATACCGA 284
Db 2169 CAGGCGCCTGGCTAGCTGGACATCCA 2196

RESULT 13
AAQ79401/c
ID AAQ79401 standard; cDNA; 3243 BP.
XX
AC AAQ79401;
XX
DT 06-JUL-1995 (first entry)
XX
DE Human NMDAR2 receptor subunit clone NMDA24 gene.
XX
KW N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel;
KW glutamate; hippocampus; rat; pcDNA1; NMDA receptor; antagonist; ds.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FH Key 1..822
FT CDS /tag= a
FT /product= part of the NMDAR2C receptor subunit
FT misc_feature 540..551
FT /tag= b
FT /note= "11 bp insertion found in clone NMDA24"
FT misc_feature 1501..1525
FT /tag= c
FT /note= "24 bp insertion found in clone NMDA24"
XX
PN W09424284-A.
XX
PD 27-OCT-1994.
XX
PF 20-APR-1994; 94WO-US04387.
XX
PR 20-APR-1993; 93US-0052449.
XX
PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
XX
PI Daggett LP, Ellis SB, Liaw CW, Lu C;
XX
WPI; 1994-341863/42.
XX
P-PSDB; AAR66059.
XX
PT Isolated DNA encoding a human N-methyl-D-aspartate receptor
PT subunit - used as probes in the identification and isolation of
PT nucleic acids encoding related receptor subunits.
XX
PS Claim 11; Page 99-104; 156pp; English.
```

XX The nucleotide sequence of the novel N-methyl-D-aspartate (NMDA)
CC receptor 2C (NMDAR2C) gene clone NMDA24. This clone covers bases
CC 861-4068 of the complete NMDAR2C gene (AAQ79372) with an insertion of 11
CC bp between bases 1300-1 and an insertion of 24 bp between bases 2350-1.
CC The 11 bp insert adds an extra 3 a.a. to the peptide sequence but causes
CC a reading frame shift which terminates the peptide at residue 494 of the
CC NMDAR2C sequence. The NMDA receptor contains two subunits: subunit R1
CC (AAQ79370) and subunit R2 selected from the subunits 2A (AAQ79375), 2B
CC (AAQ79377), 2C and 2D (AAQ79378). The receptor forms part of a family of
CC NMDA receptors which have cation-selective channels and bind glutamate
CC and NMDA. The NMDAR2C gene was obtained by amplifying cDNA derived from
CC human brain tissues with primers corresponding to sequences in the rat
CC NMDAR2A receptor DNA and using the resultant fragments as probes to
CC screen a cDNA library derived from human hippocampal RNA. 4 basic clones
CC were isolated: NMDA21 (AAQ79399), NMDA22 (AAQ79400), NMDA24 (AAQ79401)
CC and NMDA26 (AAQ79402). The clones are thought to be splice variants of
CC each other. Based on the sequence of the 4 clones, a series of variants
CC (AAQ79403-7) of the NMDAR2C receptor were constructed. The expression of
CC the genes allows the reconstruction of the NMDA receptor. The complete
CC receptor can be used to identify compounds which bind or are antagonistic
CC to the human NMDA receptor.
XX
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Best Local Similarity 46.0%; Pred. No. 2.5;
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QY 73 CAGAAAGCGTTCCGCGCGCGCTGGCACTCGGCAGGTGGCTTCTGCACGCCCGCTATATG 132
DB 2866 CAGACAGCCCCCAGCAAAATGGCAGGTGGCGGTGCGAGCAGAGGTGCTGTCTG 2807
QY 133 AGCTGCTCCGGGATGCAGACCCAGCCAGCCCTGCGGGGCCCTCGGTGCCCC 192
DB 2806 TGCTGCCAGGGGGGGCGGCGCTGCTGCGCCCTCTGGCAGGCGCTCCCGTAGATCGGC 2747
QY 193 TGGCAGGATGACGCGCTTCATCCGAGGGGGGCCCGCCANGCAAGGCAAGCAACTGGGGCTG 252
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QY 253 CGGCGAGTGGCCCTGGGCTTGAAGATACCCGAAGTG 288
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ID AAQ79400 standard; cDNA; 3698 BP.
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AC AAQ79400;
XX
DT 06-JUL-1995 (first entry)
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XX
KW N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel;
KW glutamate; hippocampus; rat; pcDNA1; NMDA receptor; antagonist; ds.
XX
OS Homo sapiens.
XX
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XX
PN W09424284-A.
XX
PD 27-OCT-1994.
XX
PF 20-APR-1994; 94WO-US04387.
XX
PR 20-APR-1993; 93US-0052449.
XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX
XX Daggett LP, Ellis SB, Liaw CW, Lu C;
XX WPI: 1994-341863/42.
XX P-PSDB; AAR66058.
XX
XX Isolated DNA encoding a human N-methyl-D-aspartate receptor
XX subunit - used as probes in the identification and isolation of
XX nucleic acids encoding related receptor subunits.
XX
XX Claim 11; Page 99-104; 156pp; English.
XX
CC The nucleotide sequence of the novel N-methyl-D-aspartate (NMDA)
CC receptor 2C (NMDAR2C) gene clone NMDA22. This clone covers bases
CC 367-4068 of the complete NMDAR2C gene (AAQ79372) with an insertion of 11
CC bp between bases 1300-1 and a 15 bp deletion of bases 1960-74. The 11 bp
CC insert adds an extra 3 a.a. to the peptide sequence but causes a reading
CC frame shift which terminates the peptide at residue 494 of the NMDAR2C
CC sequence. The NMDA receptor contains two subunits: subunit R1 (AAQ79370)
CC and subunit R2 selected from the subunits 2A (AAQ79375), 2B (AAQ79377),
CC 2C and 2D (AAQ79378). The receptor forms part of a family of NMDA
CC receptors which have cation-selective channels and bind glutamate and
CC NMDA. The NMDAR2C gene was obtained by amplifying cDNA derived from
CC human brain tissues with primers corresponding to sequences in the rat
CC NMDAR2A receptor DNA and using the resultant fragments as probes to
CC screen a cDNA library derived from human hippocampal RNA. 4 basic clones
CC were isolated: NMDA21 (AAQ79399), NMDA22 (AAQ79400), NMDA24 (AAQ79401)
CC and NMDA26 (AAQ79402). The clones are thought to be splice variants of
CC each other. Based on the sequence of the 4 clones, a series of variants
CC (AAQ79403-7) of the NMDAR2C receptor were constructed. The expression of
CC the genes allows the reconstruction of the NMDA receptor. The complete
CC receptor can be used to identify compounds which bind or are antagonistic
CC to the human NMDA receptor.
XX
SQ Sequence 3698 BP; 610 A; 1280 C; 1164 G; 644 T; 0 other;

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Best Local Similarity 46.0%; Pred. No. 2.5;
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QY 73 CAGAAAGCGTTCCGCGCGCGCTGGCACTCGGCAGGTGGCTTCTGCACGCCCGCTATATG 132
DB 3321 CAGACAGCCCCCAGCAAAATGGCAGGTGGCGGTGCGAGCAGACAGTGTCTGTG 3262
QY 133 AGCTGCTCCGGGATGCAGACCCAGCCAGCCCTGCGGGGCCCTCGGTGCCCC 192
DB 3261 TGCTGCCAGGGGGGGCGGCGCTGCTGCGCCCTCTGGCAGGCGCTCCCGTAGATCGGC 3202
QY 193 TGGCAGGATGACGCGCTTCATCCGAGGGGGGCCCGCCANGCAAGGCAAGCAACTGGGGCTG 252
DB 3201 AAGCACATCGACTGCGCTGCGCCAGGCGCTGAGGCGGAGTGTCCGTGCGGGCGGGCG 3142
QY 253 CGGCGAGTGGCCCTGGGCTTGAAGATACCCGAAGTG 288
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RESULT 15
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XX DT 06-JUL-1995 (first entry)
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XX XX N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel;
KW glutamate; hippocampus; rat; pcdNA1; NMDA receptor; antagonist; ds.
XX XX Homo sapiens.
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XX FT 1959..1960
XX FT /*tag= b
XX FT /note= "15 bp deletion of NMDAR2C sequence between
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XX FT misc_feature 2335..2336
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XX FT /note= "51 bp deletion of NMDAR2C sequence between
XX FT these bases"
XX PN MO9424284-A.
XX XX
XX PD 27-OCT-1994.
XX XX
XX PE 20-APR-1994; 94WO-0504387.
XX XX
XX PR 20-APR-1993; 93US-0052449.
XX XX
XX PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX XX
XX PI Daggett LP, Ellis SB, Liaw CW, Lu C;
XX XX
XX DR WPI; 1994-341863/42.
XX DR P-PSDB; AAR66065.
XX XX
XX PT Isolated DNA encoding a human N-methyl-D-aspartate receptor
XX PT subunit - used as probes in the identification and isolation of
XX PT nucleic acids encoding related receptor subunits.
XX XX
XX PS Claim 11; Page 99-104; 156pp; English.
XX XX
XX CC The nucleotide sequence of the novel N-methyl-D-aspartate (NMDA)
XX CC receptor 2C (NMDAR2C) gene clone NMDAR2C-delta15-delta51. This clone
XX CC contains bases 1-1959, 1975-2350 and 2402-4068 of the complete NMDAR2C
XX CC sequence (AAQ79372). The variant differs from the full length sequence by
XX CC a 15 bp deletion of bases 1960-74 and a 51 bp deletion of bases
XX CC 2351-2401. A series of variants (AAQ79403-7) of the NMDAR2C receptor
XX CC were constructed, by recombination, based on the sequence of the 4 basic
XX CC clones: NMDA21 (AAQ79399), NMDA22 (AAQ79400), NMDA24 (AAQ79401) and
XX CC NMDA26 (AAQ79402). The NMDA receptor contains two subunits: subunit R1
XX CC (AAQ79370) and subunit R2 selected from the subunits 2A (AAQ79375), 2B
XX CC (AAQ79377), 2C and 2D (AAQ79378). The receptor forms part of a family of
XX CC NMDA receptors which have cation-selective channels and bind glutamate
XX CC and NMDA. The expression of the genes allows the reconstruction of the
XX CC NMDA receptor. The complete receptor can be used to identify compounds
XX CC which bind or are antagonistic to the human NMDA receptor.
XX XX
XX SQ Sequence 4274 BP; 713 A; 1462 C; 1331 G; 768 T; 0 other;

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Best Local Similarity 46.0%; Pred. No. 2.6;
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QY 133 AGCTGCTCCGGGATGCAGAGCCACCCAGCCACCCTGCGGGCCCCCCTCGGTGCCCC 192
Db 3565 TGCTGCCAGGGGGGGCCCTGCTGCTCGCCCTCTCTGGCAGGCTCCCGTAGATCGGC 3506
QY 193 TGGCAGGATGACCGCTTTCATCCCGAGGGGGGGCCCAANGCAAGGGCAAGAACTGGGGCTG 252
Db 3505 AAGCACATCGACTCGGCTGCGCCAAAGCGCTGCAGGCCGAGTGTCCGTGCGGGCGGGCG 3446
QY 253 CGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTG 288
Db 3445 CAGGCGGGGCGGTGCACCCAGCGGGCAGCGAGCTG 3410

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Run on: February 22, 2003, 20:53:24 ; Search time 776.507 Seconds
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Listing first 45 summaries

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23: em_pat:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	313	99.7	314	6	AR189757	AR189757 Sequence
3	295.2	94.0	3549	6	AR174473	AR174473 Sequence
4	295.2	94.0	3549	6	AR189761	AR189761 Sequence
5	295.2	94.0	3552	6	AR189766	AR189766 Sequence
6	295.2	94.0	3582	6	AR189768	AR189768 Sequence
7	295.2	94.0	5877	9	AB007882	AB007882 Homo sapi
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9	293.6	93.5	193283	2	AC021647	AC021647 Homo sapi
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19	196.6	62.6	6036	10	RATADC	L01115 Rattus norv
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21	186.2	59.3	108689	2	AC096835	AC096835 Rattus no
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23	57.8	18.4	61901	5	U72484	U72484 Fugu rubrip
24	46.6	14.8	125020	9	AF429315	AF429315 Homo sapi
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27	43	13.7	318696	2	AC102953	AC102953 Rattus no
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AUTHORS		Hammond H.Kirk., Insel, P.A., Ping, P., Post, S.R. and Gao, M.						
TITLE		Gene therapy for congestive heart failure						
JOURNAL		Patent: US 6306830-A 1 23-OCT-2001;						
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ACCESSION AX189757
VERSION AX189757.1 GI:15143133
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 314)
AUTHORS Hammon, H. K. and Gao, M.
TITLE Gene therapy for congestive heart failure
JOURNAL THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
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VERSION AX189761.1 GI:15143135
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SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3549)
AUTHORS Hammon, H. K., Insel, P. A., Ping, P., Post, S. R. and Gao, M.
TITLE Gene therapy for congestive heart failure
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DEFINITION Sequence 5 from Patent WO0148164.
ACCESSION AX189761
VERSION AX189761.1 GI:15143135
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SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3549)
AUTHORS Hammon, H. K., Insel, P. A., Ping, P., Post, S. R. and Gao, M.
TITLE Gene therapy for congestive heart failure
JOURNAL Patent: US 6306830-A 5 23-OCT-2001;
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REFERENCE 1 (bases 1 to 3549)
AUTHORS Hammond,H.K. and Gao,M.
TITLE Gene therapy for congestive heart failure
JOURNAL Patent: WO 0148164-A 5 05-JUL-2001.
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
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VERSION AX189766.1 GI:15143139
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SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3552)
AUTHORS Hammond,H.K. and Gao,M.
TITLE Gene therapy for congestive heart failure
JOURNAL Patent: WO 0148164-A 10 05-JUL-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
FEATURES
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        Location/Qualifiers
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                /organism="Homo sapiens"
                /db_xref="taxon:9606"
BASE COUNT 686 a 1037 c 1068 g 761 t
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Query Match 94.0%; Score 295.2; DB 6; Length 3552;
Best Local Similarity 97.1%; Pred. No. 4.8e-56;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 ATGTCATGGTTTAGTGCCCTCCTGGTCCCTAAAGTGATGAACGGAAACAGCCTGGGGT 60
Db 1 ATGTCATGGTTTAGTGCCCTCCTGGTCCCTAAAGTGATGAACGGAAACAGCCTGGGGT 60
QY 61 GAACGCAATGGCAGAGAGCGTTCCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120
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Db 61 GAACGCAATGGCAGAGAGCGTTCCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120
QY 121 CCGCGCTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCCTCGGGGGCCCC 180
Db 121 CCGCGCTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCCTCGGGGGCCCC 180
QY 181 CCTCGGTGCCCTCGGGCAGTGCCTTTCATCCGAGGGCGGCCANGCAAGGGCAAG 240
Db 181 CCTCGGTGCCCTCGGGCAGTGCCTTTCATCCGAGGGCGGCCANGCAAGGGCAAG 240
QY 241 GAACCTGGGGTGGCGGCGAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGACACCG 300
Db 241 GAGCTGGGGTGGCGGCGAGTGGCCCTGGGCTTCGAGGATACCGAAGTGACAACGACACCG 300
QY 301 GCGGGACCG 309
Db 301 GCGGGACCG 309
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RESULT 6
AX189768
LOCUS AX189768 3582 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 12 from Patent WO0148164.
ACCESSION AX189768
VERSION AX189768.1 GI:15143140
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 3582)
AUTHORS Hammond,H.K. and Gao,M.
TITLE Gene therapy for congestive heart failure
JOURNAL Patent: WO 0148164-A 12 05-JUL-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
FEATURES
    source
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            1..3582
                /organism="synthetic construct"
                /db_xref="taxon:32630"
                /note="Modified AC-VI"
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Best Local Similarity 97.1%; Pred. No. 4.8e-56;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 ATGTCATGGTTTAGTGCCCTCCTGGTCCCTAAAGTGATGAACGGAAACAGCCTGGGGT 60
Db 22 ATGTCATGGTTTAGTGCCCTCCTGGTCCCTAAAGTGATGAACGGAAACAGCCTGGGGT 81
QY 61 GAACGCAATGGCAGAGAGCGTTCCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120
Db 82 GAACGCAATGGCAGAGAGCGTTCCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 141
QY 121 CCGCGCTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCCTCGGGGGCCCC 180
Db 142 CCGCGCTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCCTCGGGGGCCCC 201
QY 181 CCTCGGTGCCCTCGGGCAGTGCCTTTCATCCGAGGGCGGCCANGCAAGGGCAAG 240
Db 202 CCTCGGTGCCCTCGGGCAGTGCCTTTCATCCGAGGGCGGCCANGCAAGGGCAAG 261
QY 241 GAACCTGGGGTGGCGGCGAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGACACCG 300
Db 262 GAGCTGGGGTGGCGGCGAGTGGCCCTGGGCTTCGAGGATACCGAAGTGACAACGACACCG 321
QY 301 GCGGGACCG 309
Db 322 GCGGGACCG 330
RESULT 7
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AB007882
LOCUS AB007882 5877 bp mRNA linear PRI 10-MAY-2002
DEFINITION Homo sapiens KIAA0422 mRNA, partial cds.
ACCESSION AB007882
VERSION AB007882.2 GI:20521044
KEYWORDS KIAA0422.
SOURCE Homo sapiens male brain cDNA to mRNA, clone_lib:pBluescriptII SK
plus clone:hh01205sl.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Ishikawa, K., Nagase, T., Nakajima, D., Seki, N., Ohira, M.,
Miyajima, N., Tanaka, A., Kotani, H., Nomura, N. and Ohara, O.
Prediction of the coding sequences of unidentified human genes.
VIII. 78 new cDNA clones from brain which code for large proteins
in vitro
DNA Res. 4 (5), 307-313 (1997)
MEDLINE 98116655
PUBMED 9455477
REFERENCE 2 (bases 1 to 5877)
AUTHORS Ohara, O.
TITLE Direct Submission
JOURNAL Submitted (06-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
292-0812, Japan (E-mail:cdna@info.kazusa.or.jp, Tel:+81-438-52-3913,
Fax:+81-438-52-3914)
COMMENT On May 9, 2002 this sequence version replaced gi:2887418.
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Location/Qualifiers
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/tissue_type="brain"
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/note="This sequence was obtained by subcloning of the DNA
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hh01205)."
1..5877
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BASE COUNT
ORIGIN

1148 a 1612 c 1782 g 1335 t
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-- Query Match

Best Local Similarity 97.1%; Pred. No. 4.4e-56;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 ATGTCATGTTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60
|||||
DB 137 ATGTCATGTTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 196
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QY 61 GAACGCAATGGGCACAGAGCGTTGCGGGCGCGTGGGCACATCGGGCAGGTGGCTTCTGCACG 120
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DB 197 GAACGCAATGGGCACAGAGCGTTGCGGGCGCGTGGGCACATCGGGCAGGTGGCTTCTGCACG 256
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QY 121 CCCCGCTATATGAGTGCCTCCGGGATGCAGCCACCCAGCCCGCCCTCGGGGCCCC 180
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QY 181 CCTCGGTGCCCCCTGGCAGATGACGCCCTTCATCCGAGGGGGCCCGCANGCAGGCAAG 240
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DB 317 CCTCGGTGCCCCCTGGCAGATGACGCCCTTCATCCGAGGGGGCCCGCANGGCAAG 376
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QY 241 GAACGCGGCTCGGGCAGTGGCCCTGGGCTTCGAAGATACGAACTGACACGACACCG 300
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DB 377 GAGCTGGGGCTCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACGACACCG 436
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QY 301 GCGGGGACCG 309
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DB 437 GCGGGGACG 445
RESULT 8
AC117498/c
LOCUS AC117498 205248 bp DNA linear, HTG 31-JUL-2002
DEFINITION Homo sapiens clone RP11-422021, *** SEQUENCING IN PROGRESS ***, 20
unordered pieces.
ACCESSION AC117498
VERSION AC117498.4 GI:22002346
KEYWORDS HTG: HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 205248)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Albrooks, S.L., Amarantunge, H.C., Are, J.R., Ayale, M., Banks, T.,
Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonin, D.,
Bowley, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Dellane, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, J., Johnson, R., Jollivet, S., Joudah, S.,
Karlssoon, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kuchta, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louised, H.,
Lorado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwar, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Mel, G., Metzger, M.,
Moser, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, N., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
Oragunye, N., Oviado, R., Pace, A., Payton, B., Peary, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rivers, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,

Sodergren, E., Sonaika, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 205248)
Worley, K.C.

Direct Submission
Submitted (10-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 205248)
Worley, K.C.

Direct Submission
Submitted (31-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 29, 2002 this sequence version replaced gi:21956504.

COMMENT

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Drafting Center Code: WUGSC
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HEAU
Center clone name: RP11-422021
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 216840 bases at least Q40
Consensus quality: 220255 bases at least Q30
Consensus quality: 222408 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 2025: contig of 2025 bp in length
* 2026 2125: gap of unknown length
* 2126 4437: contig of 2312 bp in length
* 4438 4537: gap of unknown length
* 4538 6633: contig of 2096 bp in length
* 6634 9149: gap of unknown length
* 9149 9249: gap of unknown length
* 9249 11635: contig of 2387 bp in length
* 11636 11735: gap of unknown length
* 11736 13780: contig of 2045 bp in length
* 13781 13880: gap of unknown length
* 13881 16697: contig of 2817 bp in length
* 16698 16797: gap of unknown length
* 16798 20089: contig of 3292 bp in length
* 20090 20189: gap of unknown length
* 20190 23014: contig of 2825 bp in length
* 23015 23114: gap of unknown length
* 23115 25345: contig of 2231 bp in length
* 25346 25445: gap of unknown length
* 25446 31033: contig of 5588 bp in length
* 31034 31133: gap of unknown length
* 31134 35863: contig of 4730 bp in length

* 35864 35963: gap of unknown length
* 35964 49814: contig of 13851 bp in length
* 49815 49914: gap of unknown length
* 49915 64385: contig of 14471 bp in length
* 64386 64485: gap of unknown length
* 64486 81100: contig of 16615 bp in length
* 81101 97966: contig of 16766 bp in length
* 97967 98066: gap of unknown length
* 98067 115533: contig of 17467 bp in length
* 115534 115633: gap of unknown length
* 115634 139873: contig of 24240 bp in length
* 139874 139973: gap of unknown length
* 139974 175364: contig of 35391 bp in length
* 175365 175464: gap of unknown length
* 175465 205248: contig of 29784 bp in length.

FEATURES
source

Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-422021"

BASE COUNT 51253 a 48444 c 48345 g 51200 t 6006 others
ORIGIN

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Best Local Similarity 97.1%; Pred. No. 2.6e-56;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGCTTTAGTGGCTTCCTGCTCCTAAAGTGGATGACGAAACAGCCTGGGGT 60
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Db 169119 ATGTCATGCTTTAGTGGCTTCCTGCTCCTAAAGTGGATGACGAAACAGCCTGGGGT 169060
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QY 61 GAACGCAATGGCGAAGAGCTTCGCGCGCGCTCGGCGAGTGGCTTCTGCGACG 120
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Db 168999 CCGCGTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCCTCGCGGGCCCC 168940
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QY 181 CCTCGGTGCCCCGGCAGGATGACGCTTCATCCGAGGGGGCGCCGCAAG 240
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Db 168939 CCTCGGTGCCCCGGCAGGATGACGCTTCATCCGAGGGGGCGCCGCAAG 168880
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QY 241 GAATCGGGGCTGCGGGCAGTGGCCCTCGGCTTCGAAGATACCAAGACACACACG 300
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QY 301 GCGGGACCG 309
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Db 168819 GCGGGACG 168811

RESULT 9
LOCUS

AC021647 193283 bp DNA linear HTG 09-MAY-2002
Homo sapiens chromosome 12 clone RP11-455122, WORKING DRAFT
SEQUENCE, 8 unordered pieces.

ACCESSION

AC021647.18 GI:20335444

VERSION

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

KEYWORDS

Homo sapiens

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 193283)

AUTHORS

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, E.R., Allen, C.,

Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,

Barbata, J., Benton, J., Bimane, K., Blankenburg, K., Bonnin, D.,

Bouck, J., Bowie, S., Brieval, M., Brown, E., Brown, M., Bryant, N.P.,

Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,

Carroll, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,

Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

thyroid tissues
Biochim. Biophys. Acta 1493 (1-2), 279-283 (2000)
20435313
PUBMED 10978539
REFERENCE 2 (bases 1 to 6463)
Wicker, R., Gascon Catalan, A., Caillieux, A.-F., Starenki, D.,
Stengel, D., Sarasin, A. and Suarez, H.G.
Direct Submission
Submitted (28-MAR-2000) Lab Etude des Relations - Instabilite
genetique et Cancer UPR 2169, Institut de Recherches sur le Cancer
CNRS IFR 1221, 7 rue Guy Moquet, Villejuif 94801, France
FEATURES
source Location/Qualifiers
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complement(19..447)
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695..4201
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BASE COUNT 1264 a 1795 c 1871 g 1533 t

ORIGIN

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Best Local Similarity 96.4%; Pred. No. 2.3e-55;
Matches 298; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGTCATGGTTTACTGGCTCCTCGTCCCTAACTGGATGAACGAAACAGCCTGGGT 60
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QY 61 GAACCGCAATGGCGAAGAGCGTTCGCGCGCGCTGGCACTCGGCGAGGTGGCTTCTGCACG 120
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QY 121 CCCCGCTATATGACTCGCTCCGGGATGCAGAGCCACCCACCCACCCCTGGCGGCC 180
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DB 815 CCCCGCTATATGACTCGCTCCGGGATGCAGAGCCACCCACCCACCCCTGGCGGCC 874
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QY 181 CCTCGGTGCCCTTGGCAGGATGACGCTTTCATCCGAGGCGCGCCGANGCAAGGCAAG 240
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DB 875 CCTCGGTGCCCTTGGCAGGATGACGCTTTCATCCGAGGCGCGCCGANGCAAGGCAAG 934
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QY 241 GAACCTGGGCTGGCGGAGTGGCCCTTGAAGATACCGAAGTGACACGACCG 300
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DB 935 GAGCTGGGCTGGCGGAGTGGCCCTTGAAGATACCGAAGTGACACGACCG 994
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QY 301 GCGGGACCG 309
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DB 995 GCGGGACG 1003
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RESULT 11
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LOCUS Homo sapiens chromosome 12 clone RP11-579D7, WORKING DRAFT
DEFINITION AC025557
ACCESSION AC025557.4 GI:7657832
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens
SOURCE Homo sapiens
ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 171945)
AUTHORS Waterston, R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 171945)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Apr 27, 2000 this sequence version replaced gi:7574970.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0579D07
----- Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing method: plasmid; 0%
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 166140 bases at least Q40
Consensus quality: 167959 bases at least Q30
Consensus quality: 168924 bases at least Q20
Insert size: 177000; agarose-fp
Insert size: 170345; sum-of-contigs
Quality coverage: 5.62 in Q20 bases; agarose-fp
Quality coverage: 5.86 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 1963: contig of 1774 bp in length
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* 72409 72508: gap of unknown length
* 72509 84743: contig of 12235 bp in length
* 84744 84843: gap of unknown length
* 84844 97522: contig of 12679 bp in length
* 97523 97622: gap of unknown length
* 97623 110884: contig of 13262 bp in length
* 110885 126977: gap of unknown length
* 126978 127077: contig of 15993 bp in length
* 127078 146137: gap of unknown length
* 146138 146237: gap of unknown length
* 146238 171945: contig of 25708 bp in length.

FEATURES

Location/Qualifiers

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72509..84743
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ORIGIN

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Best Local Similarity 96.8%; Pred. No. 1.3e-53;
Matches 299; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 1 ATGTCATGGTTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGGAACAAACAGCCTGGGT 60

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Db 79560 ATGTCATGGTTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGGAACAAACAGCCTGGGT 79501
QY 61 GAACCAATGGCAGAGCGTTTCGGGCGCCCTGGCACTCGGCAGGTGGCTTCTGCACG 120
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Db 79440 CCCCCTATATGAGCTGCTCCCGGATGACAGCCACCCAGCCACCCCTCGGGGCC 79382
QY 181 CCGTGGTCCCTGGCAGGATGACGCTTCATCCGAGGGGGCCGANGCAAGGCAAG 240
Db 79381 CCGTGGTCCCTGGCAGGATGACGCTTCATCCGAGGGGGCCGANGCAAGGCAAG 79322
QY 241 GAACCTGGGCTGGGCGAGTGGCTTCGAGATACGAGTGAACGACGACCG 300
Db 79321 GAGCTGGGCTGGGCGAGTGGCTTCGAGATACGAGTGAACGACGACCG 79262
QY 301 GCGGGACCG 309
Db 79261 GCGGGACG 79253
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RESULT 12
DOGADENCYC 4046 bp mRNA linear MAM 27-APR-1993
DEFINITION Canis familiaris adenylyl cyclase type VI mRNA sequence.
ACCESSION M94968
VERSION M94968.1 GI:163896
KEYWORDS adenylyl cyclase type VI.
SOURCE Canis familiaris cardiac muscle cDNA to mRNA.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 4046)
AUTHORS Katsushika,S., Chen,L., Kawabe,J., Nilakantan,R., Halnon,N.J.,
Homcy,C.J. and Ishikawa,Y.
TITLE Cloning and characterization of a sixth adenylyl cyclase isoform:
types V and VI constitute a subgroup within the mammalian adenylyl
cyclase family
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (18), 8774-8778 (1992)
MEDLINE 92409599
PUBMED 1528892
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/db_xref="taxon:9615"
/tissue_type="cardiac muscle"
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Best Local Similarity 89.5%; Pred. No. 6.2e-41;
Matches 256; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
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QY 61 GAACCAATGGCAGAGCGTTTCGGGCGCCCTGGCACTCGGCAGGTGGCTTCTGCACG 120
Db 191 GAACCAATGGCAGAGCGT---CCACGCGGGGACTCGGACAGTGGCTTCTGCACG 247
QY 121 CCCCCTATATGAGCTGCTCCCGGATGACAGCCACCCAGCCACCCCTCGGGGCC 180
Db 248 CCCCCTATATGAGCTGCTCCCGGATGACAGCCACCCAGTCCACCCCTCGGGCTCC 307
QY 181 CCGTGGTCCCTGGCAGGATGACGCTTCATCCGAGGGGGCCGANGCAAGGCAAG 240
Db 308 CCGTGGTCCCTGGCAGGATGACGCTTCATCCGAGGGGGCCGANGCAAGGCAAG 367
QY 241 GAACCTGGGCTGGGCGAGTGGCTTCGAGATACGAGTGAACGACGACCG 286

Db 368 GAGCTGGGGTGGGGGGTGGCCCTGGGCTTCGAGGACACTGAGG 413
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RESULT 13

129958
LOCUS 129958 4046 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5578481.
ACCESSION 129958
VERSION 129958.1 GI:1820749
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4046)
AUTHORS Ishikawa, Y.
TITLE Cloning and characterization of a cardiac adenylyl cyclase
JOURNAL Patent: US 5578481-A 1 26-NOV-1996;
FEATURES
Location/Qualifiers
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/organism="unknown"
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Matches 256; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

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QY 61 GAACGCAATGGCAGAGCGCTTCGCGCGCGCTGCGGCACTCGGCGAGGTGGCTTCGACG 120
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DB 191 GAGCGCAATGGCAGAGCGT---CCAGCGCGCGGACTCGGACCATGGCTTCGACG 247
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QY 121 CCGCGTATATAGTCCCTCCGGGATGACAGACCCAGCCGCCCTCGGGGCCCC 180
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DB 248 CCGCGTATATAGTCCCTCCGGGATGACAGACCCAGCCGCCCTCGGGGCCCC 307
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QY 181 CCGTGGTCCCTCGGAGGATGAGCGCTTCATCGGAGGCGCGCCCGCAACGAGGCAAG 240
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DB 308 CCGTGGTCCCTCGGAGGATGAGCGCTTCATCGGAGGCGCGCCCGCAACGAGGCAAG 367
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QY 241 GAATGGGGTGGCGGCGAGTGGCCCTGCGGCTTCGAGATACCCGAAG 286
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DB 368 GAGCTGGGGTGGGGGGTGGCCCTGGGCTTCGAGGACACTGAGG 413
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RESULT 14

AX305965
LOCUS AX305965 5841 bp DNA linear PAT 11-DEC-2001
DEFINITION Sequence 716 from Patent WO0188188.
ACCESSION AX305965
VERSION AX305965.1 GI:17645322
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Ishikawa, K., Asai, S., Takahashi, Y., Nagata, T. and Ishii, Y.
TITLE Method for examining ischemic conditions
JOURNAL Patent: WO 0188188-A 716 22-NOV-2001;
School Juridical Person Nihon University (JP)
FEATURES
Location/Qualifiers
1..5841
/organism="Mus musculus"
/db_xref="taxon:10090"
BASE COUNT 1214 a 1558 c 1673 g 1396 t
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Best Local Similarity 82.3%; Pred. No. 1.1e-34;
Matches 241; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

QY 1 ATGTCATGTTTAGTGGCCCTCCCTGTCCTAAAGTGGATGAACGGAAACAGCGCTGGGGT 60
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DB 96 ATGTCATGTTTAGTGGCCCTCCCTGTCCTCCCAAAAGTGGATGAACGGAAACAGCTGGGGG 155
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QY 61 GAACGCAATGGCAGAGCGCTTCGCGCGCGCTGCGGCACTCGGCGAGGTGGCTTCGACG 120
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DB 156 GAGCGCAATGGCAGAGCG---CCACGCGCACGCGAATCGAGCATGGCTTCGCGCA 212
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QY 121 CCGCGTATATAGTCCCTCCGGGATGACAGACCCAGCCGCCCTCGGGGCCCC 180
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DB 213 CCGCGTATATAGTCCCTCCAGAAATGCGGAGCCACCCAGCCGCTCGCTGACGCTCAC 272
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DB 273 ACTCGGTGGCCCTCGGAGGATGAAGCCTTCATCAGAGGCGCGCCCGGCGAGGGGTGTG 332
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QY 241 GAATGGGGTGGCGGCGAGTGGCCCTGCGGCTTCGAGATACCCGAAGTGACAAC 293
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DB 333 GAGCTGGGGTGGCGGTGAGTGGCTTCGCGCTTCGAGCAGACTGAGGTGACCAC 385
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RESULT 15

MUSADCYC
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DEFINITION Mouse adenylyl cyclase type VI mRNA, complete cds.
ACCESSION M93422
VERSION M93422.1 GI:191690
KEYWORDS adenylyl cyclase; adenylyl cyclase type VI.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 5841)
AUTHORS Yoshimura, M. and Cooper, D. M.
TITLE Cloning and expression of a Ca(2+)-inhibitable adenylyl cyclase
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (15), 6716-6720 (1992)
MEDLINE 92357702
PUBMED 1379717

FEATURES

Location/Qualifiers
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BASE COUNT      1214 a 1558 c 1673 g 1396 t
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Query Match      63.4%; Score 199.2; DB 10; Length 5841;
Best Local Similarity 82.3%; Pred. No. 1.1e-34;
Matches 241; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

Qy 1 ATGTCATGTTTAGTGGCTCCTGTGCTAAAGTGGATGAACGGAAAAACACCCCTGGGGT 60
Db 96 ATGTCATGTTTAGTGGCTCCTGTGCTCCAAAGTGGATGAACGGAAAAACAGCTTGGGG 155
Qy 61 GAACGCAATGGCAGAGGTTTCGGCGCCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
Db 156 GAACGCAATGGCAGAGG---CCACGCCACGGCAATCGAGCCAGTGGCTTCTGCACA 212
Qy 121 CCCCCGTATAGCTGCCCTCCGGGATGCAGAGCCAGCCAGCCGCCCTCGGGGCCCC 180
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Qy 181 CCTCGTGCCCTCGGAGGATGACGCCCTTCATCCGGAGGGGGGGCCCGCCANGCAAGGGCAAG 240
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Qy 241 GAACCTGGGGCTCGGGCAGTGGCCCTTGGGCTTCGAAGATACCGAAGTGACAAAC 293
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Job time : 953.507 secs

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3	84.5	14.8	174	6	O95J71	O95J71	macaca fasc
4	80.5	14.1	533	4	O96JK4	O96JK4	homo sapien
5	78.5	13.8	1492	4	O9NU93	O9NU93	homo sapien
6	78	13.7	2033	12	O9E940	O9E940	gallid herp
7	78	13.7	2033	12	O9E938	O9E938	gallid herp
8	77.5	13.6	1285	11	O7O305	O7O305	mus musculus
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10	77	13.5	389	6	O8SQ95	O8SQ95	nyctimene a
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12	75	13.2	4203	5	O96562	O96562	caenorhabdi
13	75	13.2	4219	5	O9NL87	O9NL87	caenorhabdi
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 EMBL: AL049698; CAB76849.1; -
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 InterPro: IPR002710; DIL.
 InterPro: IPR000253; FHA_domain.
 InterPro: IPR001478; PDZ.
 Pfam: PF01843; DIL; 1.
 Pfam: PF00498; FHA; 1.
 Pfam: PF00595; PDZ; 1.
 SMART: SM00240; FHA; 1.
 SMART: SM00228; PDZ; 1.
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 QY 61 PRCPWQDDAFIRGGPKXGKLGRLGRLAVALGFEDTEVTTTTPAGP 103
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 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE ICP4 protein.
 GN ICP4.
 OS Gallid herpesvirus 3.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Marek's disease-like viruses.
 OX NCBI_TaxID=35250;
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 RP SEQUENCE FROM N.A.
 RC STRAIN=HPRS24;
 RA Izumiya Y., Jang H., Ono M., Mikami T.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RT Strain HPRS24.;
 RL Curr. Top. Microbiol. Immunol. 0:0-0(2000).
 DR EMBL: AB049735; BAB16594.1; -
 DR InterPro: IPR005205; Herpes_ICP4_C.
 DR InterPro: IPR005206; Herpes_ICP4_N.
 DR Pfam: PF03585; Herpes_ICP4_C; 1.
 DR Pfam: PF03584; Herpes_ICP4_N; 1.
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 RN [1]
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 RA Nechiporuk T.T., Figueroa K., Sahba S., Nechiporuk A.V., Pulst S.M.;
 RT "Mouse homolog of the SCA2 gene."
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF041472; AAC09275.1; -
 DR MGD: MGI:127223; SCA2.
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 Williams S.;
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 HSSP: Q12923; 3PDZ.
 InterPro: IPR002710; DIL.
 InterPro: IPR000253; FHA_domain.
 InterPro: IPR001478; PDZ.
 Pfam: PF01843; DIL; 1.
 Pfam: PF00498; FHA; 1.
 Pfam: PF00595; PDZ; 1.
 SMART: SM00240; FHA; 1.
 SMART: SM00228; PDZ; 1.
 PROSITE: PS0106; PDZ; 1.
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 Best Local Similarity 27.2%; Pred. No. 7.9;
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 QY 13 DERKTAWNGRGKRSRR-----CTRAGGCTPRYMSCLRDAEPSPPTPA--GP 60
 Db 1316 EKRRQEGYYSRLAEARRQHQDEAARRLLEAPGLCRP---PLPRDYEPSPSPAPGAP 1372
 QY 61 PRCPWQDDAFIRGGPKXGKLGRLGRLAVALGFEDTEVTTTTPAGP 103
 Db 1373 PPPQORNASYLKTQVLSFDSPSLFTAKFVAYNEEEDCDSLAGP 1415
 RESULT 6
 QY9E940 PRELIMINARY; PRT; 2033 AA.
 ID QY9E940
 AC QY9E940
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE ICP4 protein.
 GN ICP4.
 OS Gallid herpesvirus 3.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Marek's disease-like viruses.
 OX NCBI_TaxID=35250;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HPRS24;
 RA Izumiya Y., Jang H., Ono M., Mikami T.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RT Strain HPRS24.;
 RL Curr. Top. Microbiol. Immunol. 0:0-0(2000).
 DR EMBL: AB049735; BAB16581.1; -
 DR InterPro: IPR005205; Herpes_ICP4_C.
 DR InterPro: IPR005206; Herpes_ICP4_N.
 DR Pfam: PF03585; Herpes_ICP4_C; 1.
 DR Pfam: PF03584; Herpes_ICP4_N; 1.
 DR PRINTS: PR01217; PRICHEXTENSN.
 SQ SEQUENCE 2033 AA; 217266 MW; CCF52D36BCC8C085 CRC64;
 Query Match 13.7%; Score 78; DB 12; Length 2033;
 Best Local Similarity 32.3%; Pred. No. 12;
 Matches 31; Conservative 5; Mismatches 34; Indels 26; Gaps
 QY 23 NGKRSRRRGTAGGCTPRYMSCLRDAEP-----SPTPAGPPRC-PWQDDAFIRRG- 74
 Db 1501 NRPRLGRSRTGAG---PPPVASCTRPPTPEACRDAGPPPKRRCFWRDPARIMDGS 1557
 QY 75 ---GPXKGKLGRLAVALGFEDTEVTTTTP-----AGP 103

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Db 854 PPPVC---RAFGGRGGLDAQGGLPGGGRDVLGVQLVTMG 889

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Job time : 96 secs

GenCore version 5.1.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 19, 2003, 15:22:28 ; Search time 12 Seconds
(without alignments)
359.462 Million cell updates/sec

Title: US-09-750-240-2

Perfect score: 570

Sequence: 1 MSWFGSLLPVKYDKRTAWG.....RAVALGFEDTEVTTPAGPL 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	428	75.1	1166	1	CYA6_RAT
5	75	13.2	289	1	KLFD_MOUSE
6	73.5	12.9	719	1	DEND_RAT
7	73	12.8	512	1	IE63_HSV11
8	73	12.8	1168	1	MYSC_ACACA
9	72	12.6	232	1	VEGA_HUMAN
10	71.5	12.5	1816	1	AF6_HUMAN
11	69.5	12.2	1061	1	RNE_ECOLI
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18	68	11.9	1323	1	NME4_RAT
19	67.5	11.8	511	1	IE63_HSV1E
20	67	11.8	425	1	I450_HUMAN
21	66.5	11.7	283	1	IPF1_HUMAN
22	66.5	11.7	365	1	IB01_SAGOE
23	66	11.6	251	1	HXB4_HUMAN
24	66	11.6	489	1	ACHE_XENLA
25	66	11.6	778	1	TAST_HUMAN
26	65.5	11.5	283	1	IPF1_MESAU
27	65.5	11.5	284	1	IPF1_MOUSE
28	65.5	11.5	365	1	IA01_SAGOE
29	65.5	11.5	659	1	VST2_HEVME
30	65.5	11.5	946	1	IP3L_HUMAN
31	65	11.4	269	1	CEBD_HUMAN
32	65	11.4	340	1	NIF1_HUMAN
33	65	11.4	376	1	VASP_MOUSE

ALIGNMENTS

RESULT 1

ID	CYA6_HUMAN	STANDARD;	PRT;	1168 AA.
AC	O43306; Q9NR75;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-OCT-2001 (Rel. 40, Last sequence update)			
DE	Adenylylate cyclase, type VI (EC 4.6.1.1) (ATP pyrophosphate-lyase)			
DE	(Ca(2+)-inhibitable adenylyl cyclase).			
GN	ADCY6 OR KIAA0422.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Thyroid;			
RA	Wicker R., Gascon Catalan A., Cailleux A.-F., Starenki D., Stengel D.,			
RA	Sarasin A., Suarez H.G.;			
RT	"Cloning and expression of human adenylyl cyclase type VI from normal			
RT	thyroid tissues.";			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE OF 142-1168 FROM N.A.			
RC	TISSUE=Brain;			
RA	MEDLINE=98116655; PubMed=9455477;			
RA	Ishikawa K.-I., Nagase T., Nakajima D., Seki N., Ohira M.,			
RA	Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;			
RT	"Prediction of the coding sequences of unidentified human genes. VIII.			
RT	78 new cDNA clones from brain which code for large proteins in			
RT	vitro.";			
RL	DNA Res. 4:307-313(1997).			
CC	-I- FUNCTION: THIS A MEMBRANE-BOUND, CA(2+)-INHIBITABLE ADENYLYL			
CC	CYCLASE (BY SIMILARITY).			
CC	-I- CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.			
CC	-I- ENZYME REGULATION: INHIBITION BY CA(2+) IN THE SUBMICROMOLAR			
CC	CONCENTRATION RANGE (BY SIMILARITY).			
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-I- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.			
CC	-I- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE			
CC	FAMILY.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF250226; AAP82478.1; -			
DR	EMBL; AB007882; BAA24852.1; -			
DR	HSSP; P19754; IAWK.			
DR	Genew; HGNC:237; ADCY6.			
DR	MIM; 600294; -			
DR	InterPro; IPR001054; G_cyclase.			

60 TRCPQDEAIFIRAGPGRGVGLGRSLVALGDFDDTEV--TTPMG 100

Db

RESULT 4

CYA6_RAT

ID CYA6_RAT STANDARD; PRT; 1166 AA.

AC Q03343;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Adenylate cyclase, type VI [EC 4.6.1.1] (ATP pyrophosphate-lyase)

DE (Ca(2+)-inhibitable adenyl cyclase).

DE ADCY6.

GN Rattus norvegicus (Rat).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OC NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=93077589; PubMed=1332969;

RX Krupinski J., Lehman T.C., Frankenfield C.D., Zwaagstra J.C.,

RA Watson P.A.;

RA "Molecular diversity in the adenylate cyclase family. Evidence for

RT eight forms of the enzyme and cloning of type VI.";

RT J. Biol. Chem. 267:24858-24862(1992).

RL [2]

RN SEQUENCE FROM N.A.

RP RP

RP TISSUE=Liver;

RC MEDLINE=93028552; PubMed=1409703;

RC Premont R.T., Chen J., Ma H.-W., Ponnappalli M., Iyengar R.;

RA "Two members of a widely expressed subfamily of hormone-stimulated

RT adenyl cyclases.";

RT Proc. Natl. Acad. Sci. U.S.A. 89:9809-9813(1992).

RL -1- FUNCTION: THIS A MEMBRANE-BOUND, CA(2+)-INHIBITABLE ADENYLYL

CC CYCLASE.

CC -1- CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.

CC -1- ENZYME REGULATION: INHIBITION BY CA(2+) IN THE SUBMICROMOLAR

CC CONCENTRATION RANGE.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.

CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE

CC FAMILY.

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EMBL; L01115; AAA40676.1; -

DR EMBL; M96160; AAA40678.1; ALT_INIT.

DR PIR; A45145; A45145.

DR HSP; P19754; IAWK.

DR InterPro; IPR001054; G_cyclase.

DR Pfam; PF00211; guanylate_cyc; 2.

DR SMART; SM00044; CYCC; 2.

DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; 2.

DR PROSITE; PSS01125; GUANYLATE_CYCLASES_2; 2.

KW Lyase; CAMP synthesis; Transmembrane; Glycoprotein; Repeat.

FT DOMAIN 1 149 CYTOPLASMIC (POTENTIAL).

FT FT 166 POTENTIAL.

FT TRANSMEM 179 195 POTENTIAL.

FT TRANSMEM 212 228 POTENTIAL.

FT TRANSMEM 237 253 POTENTIAL.

FT TRANSMEM 257 273 POTENTIAL.

FT TRANSMEM 287 303 POTENTIAL.

FT DOMAIN 304 671 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 672 689 POTENTIAL.

FT TRANSMEM 700 716 POTENTIAL.

FT TRANSMEM 741 757 POTENTIAL.

FT DOMAIN 758 817 EXTRACELLULAR (POTENTIAL).

FT FT

```
FT TRANSMEM 818 834 POTENTIAL.
FT TRANSMEM 837 853 POTENTIAL.
FT TRANSMEM 895 911 POTENTIAL.
FT DOMAIN 912 1166 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 791 791 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 876 876 K -> E (IN REF. 2).
FT CONFLICT 80 130 R -> P (IN REF. 2).
FT CONFLICT 130 130 R -> P (IN REF. 2).
FT CONFLICT 538 538 G -> A (IN REF. 2).
FT CONFLICT 790 790 I -> L (IN REF. 2).
SQ SEQUENCE 1166 AA; 130506 MW; 5042C650546E4E79 CRC64;

Query Match 75.1%; Score 428; DB 1; Length 1166;
Best Local Similarity 78.4%; Pred. No. 2.6e-34;
Matches 80; Conservative 8; Mismatches 12; Indels 2; Gaps 2;

QY 1 MSWESGLLVKPKVDERTKANGERSRRCTRAGGCTPRYMSCLRDAPSPPTPACG 60
Db 1 MSWESGLLVKPKVDERTKANGERSRRCTRAGGCTPRYMSCLRDAPSPPTPACG 59
QY 61 PRCPQDDAFIRRGPGPKKGLRAVALGFEDTEVTTTPAG 102
Db 60 TRCPQDEAFIRRGPGKGLRLSVALGFEDTEV-TTPMG 100

RESULT 5
KLFID_MOUSE
ID KLFID_MOUSE STANDARD; PRT; 289 AA.
AC Q9JZ6: Q9JH9: Q9EX3;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Kruessel-like factor 13 (Transcription factor BTEB3) (Basic
DE transcription element binding protein 3) (BTE-binding protein 3)
DE (RANTES factor of late activated T lymphocytes-1) (RFLAT-1) (Erythroid
DE transcription factor FKLF-2).
GN KLF13 OR BTEB3 OR FKLF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=20115087; PubMed=10642511;
RA Martin K.M., Cooper W.N., Metcalfe J.C., Kemp P.R.;
RT "Mouse BTEB3, a new member of the basic transcription element binding
RT protein (BTEB) family, activates expression from GC-rich minimal
RT promoter regions";
RL Biochem. J. 345:529-533(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=B6D2F2; TISSUE=Yolk;
RX MEDLINE=20287401; PubMed=10828046;
RA Asano H., Li X.S., Stamatoyanopoulos G.;
RT "FKLF-2: a novel Kruppel-like transcriptional factor that activates
RT globin and other erythroid lineage genes.";
RL Blood 95:3578-3584(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=20541714; PubMed=11087666;
RA Schohy S., Gabant P., Van Reeth T., Hertveldt V., Dreze P.-L.,
RA Van Vooren P., Riviere M., Szpirer J., Szpirer C.;
RT "Identification of KLF13 and KLF14 (SP6), novel members of the SP/XKLF
RT transcription factor family.";
RL Genomics 70:93-101(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Song A., Thamatrakoln K., Krensky A.M.;
RT "Identification of Mus musculus cDNA for RANTES factor of late
RT activated T lymphocytes-1.";
```

```
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Transcription factor that activates expression from GC-
CC rich minimal promoter regions, including genes in the cells of the
CC erythroid lineage.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: BELONGS TO THE SP1 FAMILY OF C2H2-TYPE ZINC-FINGER
CC PROTEINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ245644; CAB75887.1; -.
CC EMBL; AF251796; AAF73964.1; -.
CC EMBL; AJ275987; CAC06697.1; -.
CC EMBL; AF252285; AAF65826.1; -.
CC HSP; P08047; 1SP2.
CC TRANSFAC; T05052; -.
CC MGD; MGI:1354948; Klf13.
CC InterPro; IPR000822; Znf_C2H2.
CC Pfam; PF00096; zf-C2H2; 6.
CC ProDom; PD00003; Znf_C2H2; 1.
CC SMART; SM00355; Znf_C2H2; 3.
CC PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
CC PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
CC Repeat; Zinc-finger; Metal-binding.
KW Repeat; Zinc-finger; Metal-binding.
FT DOMAIN 2 146 ALA/PRO-RICH.
FT DOMAIN 149 169 ARG/LYS-RICH (BASIC).
FT DOMAIN 168 250 ZINC FINGERS.
FT ZN_FING 168 192 C2H2-TYPE.
FT ZN_FING 198 222 C2H2-TYPE.
FT ZN_FING 228 250 C2H2-TYPE.
FT DOMAIN 265 288 SER-RICH.
FT CONFLICT 13 30 ECLVSMSSRAVYVHEPREG -> SASCPQPSRARAAGR
FT CONFLICT 32 32 E -> R (IN REF. 1).
FT CONFLICT 43 43 P -> L (IN REF. 1).
SQ SEQUENCE 289 AA; 31136 MW; E248EF12890DA090 CRC64;

Query Match 13.2%; Score 75; DB 1; Length 289;
Best Local Similarity 27.6%; Pred. No. 1.9;
Matches 29; Conservative 7; Mismatches 41; Indels 28; Gaps 4;

QY 9 VPKVDERTKA-----WGERNGQ-----KSRRRGTGAGGCTPRYMSCLRDAP 51
Db 45 LPRVDERRDGKDSALFVVVARILADLNQAPAPAPAEERREGAARAKARTPCRLPPAPPAP 104
QY 52 PPSP-----TPAGPRCPQDD--AFIRRGPKKGLR 85
Db 105 PPGPEPSPGQAGAPAAPSPAWSEPEAALEQEPGAGSGEPLR 149

RESULT 6
DEND_RAT
ID DEND_RAT STANDARD; PRT; 719 AA.
AC P50617;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Dendrin (Fragment).
GN DDN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
```

RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=97073143; PubMed=8915891;
RA Neuner-Jehle M., Denizot J.P., Borbely A.A., Mallet J.;
RT "Characterization and sleep deprivation-induced expression modulation
of dendrin, a novel dendritic protein in rat brain neurons.";
RL J. Neurosci. Res. 46:138-151(1996).
CC -/- MISCELLANEOUS: MODULATED BY SLEEP DEPRIVATION.
CC
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CC
CC EMBL: X96589; CAA65407.1; --
DR NON_TER 1
FT SEQUENCE 719 AA; 77208 MW; 89E2ED094514EAFB CRC64;
SQ
Query Match 12.9%; Score 73.5; DB 1; Length 719;
Best Local Similarity 28.9%; Pred. No. 6.5;
Matches 26; Conservative 7; Mismatches 30; Indels 27; Gaps 3;
QY 13 DERKTAWGERNGOKRRRRTRAGG-----FCTPRYMSCLRDAP----- 52
Db 124 EKRAASQEREAKETKRR-KKAGDGVPSAPPRAPELRRAAQPTGPFVFSRPERFGQ 182
QY 53 -----PSPTPAGPPRCPWQDDAFIRRGPP 76
Db 183 VGRAPRPSALPOGDGPGVANAGWGDRRPGP 212
RESULT 7
IE63_HSV11
ID IE63_HSV11 STANDARD; PRT; 512 AA.
AC P10238;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transcriptional regulator IE63 (VIM63) (ICP27).
GN UL54.
GN Herpes simplex virus (type 1 / strain 17).
OS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88274327; PubMed=2839594;
RA McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
RA McNab D., Perry L.J., Scott J.E., Taylor P.;
RT "The complete DNA sequence of the long unique region in the genome of
herpes simplex virus type 1.";
RL J. Gen. Virol. 69:1531-1574(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89036163; PubMed=2846760;
RA Perry L.J., McGeoch D.J.;
RT "The DNA sequences of the long repeat region and adjoining parts of
the long unique region in the genome of herpes simplex virus type
1.";
RL J. Gen. Virol. 69:2831-2846(1988).
RN [3]
RP FUNCTION: INVOLVED IN THE DOWN-REGULATION OF VIRAL IMMEDIATE-EARLY
GENES AND ACTS IN COMBINATION WITH ICP0 AND ICP4 AS AN ACTIVATOR
OF LATE GENES.
CC
CC -/- PTM: PHOSPHORYLATED.
CC
CC -/- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL54,
CC HSV-2 UL54, EBV-1 5, VZV 4, EBV BMLF1, HCMV UL69, AND HVS-1 57.
CC
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CC
CC EMBL: D10879; BAA01700.1; --
DR EMBL: X14112; CAA32290.1; --
DR PIR: I30089; WMBEY4.
KW Early protein; Transcription regulation; DNA-binding; Phosphorylation.
SQ SEQUENCE 512 AA; 55252 MW; 97DF74A2B7E63A85 CRC64;
Query Match 12.8%; Score 73; DB 1; Length 512;
Best Local Similarity 27.5%; Pred. No. 5.2;
Matches 30; Conservative 8; Mismatches 53; Indels 18; Gaps 4;
QY 8 LVPKVDKRTAWGERNGOKRRRRG--TRAGGCTPRYMSCLRDAPSPPTPAGP-PRCP 64
Db 127 LQPPPTKAQPARGRRGRGRRGCGCAADGLSDPR-----RRAPTRNRPGGPRPGAG 181
QY 65 WQDDAFIRRGPPXKGKE-----LGLRAVALGFEDTEVTTTPAGP 103
Db 182 WTDGPGAPHGCEAWRGSEQDPDPGGQRTGRGVRAQPPPLMTLAIAPPPADP 230
RESULT 8
MYSC_ACACA
ID MYSC_ACACA STANDARD; PRT; 1168 AA.
AC P10569;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myosin IC heavy chain.
GN MIC.
OS Acanthamoeba castellanii (Amoeba).
OC Eukaryota; Acanthamoebidae; Acanthamoeba.
OX NCBI_TaxID=5755;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88016163; PubMed=3477803;
RA Jung G., Korn E.D., Hammer J.A. III;
RT "The heavy chain of Acanthamoeba myosin IB is a fusion of myosin-like
and non-myosin-like sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6720-6724(1987).
RN [2]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE=86259656; PubMed=3014500;
RA Hammer J.A. III, Jung G., Korn E.D.;
RT "Genetic evidence that Acanthamoeba myosin I is a true myosin.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:4655-4659(1986).
RN [3]
RP PHOSPHORYLATION SITE.
RX MEDLINE=90037074; PubMed=2530230;
RA Brzeska H., Lynch T.J., Martin B., Korn E.D.;
RT "The localization and sequence of the phosphorylation sites of
Acanthamoeba myosins I. An improved method for locating the
phosphorylated amino acid.";
RL J. Biol. Chem. 264:19340-19348(1989).
RN [4]
RP FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAS ATPASE
ACTIVITY THAT IS ACTIVATED BY F-ACTIN.
CC
CC -/- SUBUNIT: MYOSIN I HEAVY CHAIN IS SINGLE-HEADED. DIMER OF A HEAVY
CC AND A LIGHT CHAIN. INABILITY TO SELF-ASSEMBLE INTO FILAMENTS.
CC
CC -/- DOMAIN: TH.1 BINDS DIRECTLY TO ANIONIC PHOSPHOLIPID MEMBRANES;
CC MYOSIN I CAN THEREFORE MOVE ACTIN RELATIVE TO MEMBRANES AND VICE
CC VERSA. TH.2 AND SH3 BIND TIGHTLY TO F-ACTIN; THIS TOGETHER WITH
CC THE NUCLEOTIDE-SENSITIVE SITE IN THE HEAD, ALLOWS SINGLE MOLECULES
CC OF MYOSIN I TO CROSS-LINK ACTIN FILAMENTS.
CC
CC -/- MISCELLANEOUS: THIS ORGANISM EXPRESSES AT LEAST THREE ISOFORMS OF
CC MYOSIN I HEAVY-CHAIN, ENCODED BY GENES MIA, MIB, AND MIT.
CC
CC -/- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
CC
CC -/- CAUTION: WAS ORIGINALLY THOUGHT TO BE MYOSIN IB.
CC
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DR EMBL: J02974; AAA27707.1; -
 DR PIR: A33891; MWAXIC.
 DR HSSP: P08799; 1MND.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001609; myosin_head.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00063; myosin_head; 1.
 DR PRINTS: PR00193; MYOSINHEAVY.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000355; myosin_head; 1.
 DR SMART: SM00242; MYSC; 1.
 DR SMART: SM00326; SH3; 1.
 DR PROSITE: PS0002; SH3; 1.
 KW Myosin; ATP-binding; Phosphorylation; Multigene family; SH3 domain.
 FT DOMAIN 1 670
 FT MYOSIN HEAD-LIKE.
 FT TAIL HOMOLGY REGION 1 (TH.1).
 FT GLY/PRO/ALA-RICH (TH.2).
 FT SH3.
 FT DOMAIN 923 975
 FT MYOSIN HEAD-LIKE.
 FT SH3.
 FT DOMAIN 976 1035
 FT MYOSIN HEAD-LIKE.
 FT SH3.
 FT BIND 101 108
 FT ATP (POTENTIAL).
 FT MOD_RES 311 311
 FT PHOSPHORYLATION.
 SQ SEQUENCE 1168 AA; 127309 MW; D07084B373A37A32 CRC64;

Query Match 12.8%; Score 73; DB 1; Length 1168;
 Best Local Similarity 25.8%; Pred. NO. 12;
 Matches 24; Conservative 13; Mismatches 32; Indels 24; Gaps 4;

QY 1 MSWFSGLLPVKYDERKTAH--GERNGKSRRTGFRAGGCTPRYMNSCLRDAPSPPTA 58
 DB 995 LTFNEGAVTVINKSPNDWWEGLNGQR-----GVFPASVVELIPRAAAPGPGS 1044

QY 59 GPPR-----CPWODDAFIR-RGGPKRG 79
 DB 1045 GGPAPPGGKSGRAAPMGPGMRGGGPAFG 1077

RESULT 9

ID VEGA_HUMAN STANDARD; PRT: 232 AA.
 AC P15692; Q16889; O60720; O75875; Q9UL23; Q9UH58; Q9H1W9; Q9H1W8;
 AC O96NW5;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
 DE permeability factor) (VPF).
 GN VEGF OR VEGFA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS VEGF189 AND VEGF165).
 RX MEDLINE=90069608; PubMed=2479986;
 Leung D.W., Cachianes G., Kuang W.-J., Goeddel D.V., Ferrara N.;
 RT "Vascular endothelial growth factor is a secreted angiogenic
 RT mitogen.";
 RT Science 246:1306-1309(1989).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM VEGF189), AND PARTIAL SEQUENCE.
 RX MEDLINE=90069609; PubMed=2479987;
 Keck P.J., Hauser S.D., Krivi G., Sanzo K., Warren T., Feder J.,
 RA Connolly D.T.;
 RT "Vascular permeability factor, an endothelial cell mitogen related to
 RT PDGF.";
 RT Science 246:1309-1312(1989).
 RL

RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM VEGF189).
 RX MEDLINE=91268072; PubMed=1711045;
 Tischer E., Mitchell R., Hartman T., Silva M., Gospodarowicz D.,
 RA Fiddes J.C., Abraham J.A.;
 RT "The human gene for vascular endothelial growth factor. Multiple
 RT protein forms are encoded through alternative exon splicing.";
 RT J. Biol. Chem. 266:11947-11954(1991).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM VEGF206).
 RX MEDLINE=92168017; PubMed=1791831;
 Houck K.A., Ferrara N., Winer J., Cachianes G., Li B., Leung D.W.;
 RT "The vascular endothelial growth factor family: identification of a
 RT fourth molecular species and characterization of alternative splicing
 RT of RNA.";
 RL Mol. Endocrinol. 5:1806-1814(1991).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM VEGF165).
 RX MEDLINE=92231879; PubMed=1567395;
 Weindel K., Marne D., Welch H.A.;
 RT "AIDS-associated Kaposi's sarcoma cells in culture express vascular
 RT endothelial growth factor.";
 RL Biochem. Biophys. Res. Commun. 183:1167-1174(1992).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM VEGF145).
 RX MEDLINE=97207275; PubMed=9054410;
 Poltorak Z., Cohen T., Sivan R., Kandellis Y., Spira G., Vlodavsky I.,
 RA Keshet E., Neufeld G.;
 RT "VEGF145, a secreted vascular endothelial growth factor isoform that
 RT binds to extracellular matrix.";
 RL J. Biol. Chem. 272:7151-7158(1997).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM VEGF183).
 RC TISSUE=Kidney;
 RX MEDLINE=99096474; PubMed=9878851;
 Lei J., Jiang A., Pei D.;
 RT "Identification and characterization of a new splicing variant of
 RT vascular endothelial growth factor: VEGF183.";
 RL Biochim. Biophys. Acta 1443:400-406(1998).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM VEGF165).
 RC TISSUE=Breast;
 RX MEDLINE=98119755; PubMed=9450968;
 Claffey K.P., Shih S.-C., Mullen A., Dziennis S., Cusick J.L.,
 RA Abrams K.R., Lee S.W., Detmar M.;
 RT "Identification of a human VPE/VEGF 3' untranslated region mediating
 RT hypoxia-induced mRNA stability.";
 RL Mol. Biol. Cell 9:469-481(1998).
 RN [9]
 RP SEQUENCE OF 114-209 FROM N.A. (ISOFORM VEGF183).
 RC TISSUE=Retina;
 RX MEDLINE=99165303; PubMed=10067980;
 Jingjing L., Xue Y., Agarwal N., Roque R.S.;
 RT "Human Muller cells express VEGF183, a novel spliced variant of
 RT vascular endothelial growth factor.";
 RL Invest. Ophthalmol. Vis. Sci. 40:752-759(1999).
 RN [10]
 RP SEQUENCE FROM N.A. (ISOFORM VEGF165).
 RC TISSUE=Hemangioendothelioma;
 RA Murata H., Fukushima J., Hattori S., Okuda K., Yanagi H.;
 RT "Human cDNA for the vascular endothelial growth factor isoform
 RT VEGF165.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP SEQUENCE FROM N.A. (ISOFORM VEGF148).
 RC TISSUE=Renal glomerulus;
 RX MEDLINE=99394945; PubMed=10464055;
 Whittle C.J., Gillespie K.M., Harrison R., Mathieson P.W.,
 RA Harper S.J.;
 RT "Heterogeneous vascular endothelial growth factor (VEGF) isoform mRNA
 RT and receptor mRNA expression in human glomeruli, and the
 RT identification of VEGF148 mRNA, a novel truncated splice variant.";
 RL Clin. Sci. 97:303-312(1999).

RT [12] SEQUENCE FROM N.A. (ISOFORM VEGF121).
RP Sato J.D., Whitney R.G.;
RA "Human cDNA for vascular endothelial growth factor isoform VEGF121.";
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [13]
RN SEQUENCE FROM N.A.
RA Williams S.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [14]
RN SEQUENCE OF 23-232 FROM N.A. (VEGF165).
RA Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [15]
RN PRELIMINARY SEQUENCE OF 27-36; 43-50 AND 59-81.
RX MEDLINE-90062112; PubMed-2584205.
RA Connolly D.T., Olander J.V., Heuvelman D., Nelson R., Monsell R.,
RA Siegel N., Haymore B.L., Lelmgruber R., Feder J.;
RT "Human vascular permeability factor. Isolation from U937 cells.";
RL J. Biol. Chem. 264:20017-20024(1989).
RN [16]
RN SEQUENCE OF 27-41.
RX MEDLINE-93145946; PubMed-7678805;
RA Fiebig B.L., Jaeger B., Schoellmann C., Weindel K., Wilting J.,
RA Kochs G., Marne D., Hug H., Weich H.A.;
RT "Synthesis and assembly of functionally active human vascular
endothelial growth factor homodimers in insect cells.";
RL Eur. J. Biochem. 211:19-26(1993).
RN [17]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 34-135.
RX MEDLINE-97352774; PubMed-9207067;
RA Muller Y.A., Li B., Christinger H.W., Wells J.A., Cunningham B.C.,
RA de Vos A.M.;
RT "Vascular endothelial growth factor: crystal structure and functional
mapping of the kinase domain receptor binding site.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:7192-7197(1997).
RN [18]
RN X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 34-135.
RX MEDLINE-98035455; PubMed-9351807;
RA Muller Y.A., Christinger H.W., Keyt B.A., de Vos A.M.;
RT "The crystal structure of vascular endothelial growth factor (VEGF)
refined to 1.93-A resolution: multiple copy flexibility and receptor
binding.";
RL Structure 5:1325-1338(1997).
RN [19]
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 39-134.
RX MEDLINE-99119204; PubMed-9922142;
RA Wiesmann C., Christinger H.W., Cochran A.G., Cunningham B.C.,
RA Fairbrother W.J., Keenan C.J., Meng G., de Vos A.M.;
RT "Crystal structure of the complex between VEGF and a receptor-blocking
peptide.";
RL Biochemistry 37:17765-17772(1998).
RN [20]
RN STRUCTURE BY NMR OF 34-135.
RX MEDLINE-97477915; PubMed-9336848;
RA Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
RA Starovasnik M.A.;
RT "1H, 13C, and 15N backbone assignment and secondary structure of the
receptor-binding domain of vascular endothelial growth factor.";
RL Protein Sci. 6:2250-2260(1997).
RN [21]
RN STRUCTURE BY NMR OF 137-215.
RX MEDLINE-98298440; PubMed-9634701;
RA Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
RA Starovasnik M.A.;
RT "Solution structure of the heparin-binding domain of vascular
endothelial growth factor.";
RL Structure 6:637-648(1998).
RN [22]
RN FUNCTION.
RX MEDLINE-21320570; PubMed-11427521;
RA Murphy J.F., Fitzgerald D.J.;

RT "Vascular endothelial growth factor induces cyclooxygenase-dependent
proliferation of endothelial cells via the VEGF-2 receptor.";
RL FASEB J. 15:1667-1669(2001).
CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
endothelial cell growth. It induces endothelial cell
proliferation, promotes cell migration, inhibits apoptosis, and
induces permeabilization of blood vessels. It binds to the
CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC heparin. Neuropilin-1 binds isoforms VEGF-165 and VEGF-145.
CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC with PlGF (By similarity).
CC -!- SUBCELLULAR LOCATION: VEGF121 is acidic and freely secreted.
CC VEGF165 is more basic, has heparin-binding properties and,
CC although a significant proportion remains cell-associated, most is
CC freely secreted. VEGF189 is very basic; it is cell-associated
CC after secretion and is bound avidly by heparin and the
CC extracellular matrix, although it may be released as a soluble
CC form by heparin, heparinase or plasmin.
CC -!- ALTERNATIVE PRODUCTS: 7 isoforms; VEGF206 (shown here), VEGF189,
CC VEGF183, VEGF165/VEGF, VEGF148, VEGF145 and VEGF121; may be
CC produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: The VEGF189, VEGF-165 and VEGF-121 isoforms
CC are widely expressed, whereas the VEGF206 and VEGF-145 are
CC uncommon.
CC -!- INDUCTION: Regulated by growth factors, cytokines, gonadotropins,
CC nitric oxide, hypoxia, hypoglycemia and oncogenic mutations.
Query Match 12.6%; Score 72; DB 1; Length 232;
Best Local Similarity 32.8%; Pred. NO. 3.1;
Matches 21; Conservative 5; Mismatches 16; Indels 22; Gaps 3;
QY 10 PKVD---ERKTAWGERNGKRRRRRTRAGGCTPRYMS-----CLROAEPSPPT 56
DB 132 PKDRARQEKSVGKGGKGRKRRKS-----RYKSWSVYVGARCCMLPWSLPGPH 182
QY 57 PAGP 60
DB 183 PCGP 186
RESULT 10
AF6_HUMAN
ID AF6_HUMAN STANDARD; PRT; 1816 AA.
AC P55196; O75087; O75088; O75089; Q9NU92;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE AF-6 protein.
GN MLLT4 OR AF6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE-94061833; PubMed-8242616;
RA Prasad R., Gu Y., Alder H., Nakamura T., Canaani O., Saito H.,
RA Huebner K., Gale R.P., Nowell P.C., Kuriyama K., Miyazaki Y.,
RA Croce C.M., Canaani E.;
RT "Cloning of the ALL-1 fusion partner, the AF-6 gene, involved in
RT acute myeloid leukemias with the t(6;11) chromosome translocation.";
RL Cancer Res. 53:5624-5628(1993).
RN [2]
RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RP TISSUE=Fetal brain;
RX MEDLINE-98344142; PubMed-9679199;
RA Saito S., Matsushima M., Shirahama S., Minaguchi T., Kanamori Y.,
RA Minami M., Nakamura Y.;
RT "Complete genomic structure, DNA polymorphisms, and alternative
RT splicing of the human AF-6 gene.";
RL DNA Res. 5:115-120(1998).
RN [3]
RN SEQUENCE OF 337-1816 FROM N.A. (ISOFORM 2).

RA Williams S.;

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: MAY ACT AS AN INTRACELLULAR SIGNALING COMPONENT

CC CONTROLLED BY RAS SIGNALING PATHWAYS.

CC -!- SUBUNIT: BINDS DIRECTLY TO ZO-1 AND OCCLUDIN.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).

CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1, 2 (SHOWN HERE) AND 3; ARE

CC PRODUCED BY ALTERNATIVE SPLICING.

CC -!- DISEASE: INVOLVED IN ACUTE LEUKEMIAS BY A CHROMOSOMAL

CC TRANSLOCATION T(6;11)(Q27;Q23) THAT INVOLVES MLLT4 AND MLL/HRX.

CC THE RESULT IS A ROGUE ACTIVATOR PROTEIN.

CC -!- SIMILARITY: CONTAINS 1 DILUTE DOMAIN.

CC -!- SIMILARITY: CONTAINS 1 FHA DOMAIN.

CC -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AB011399; BAA32484.1; -;

DR EMBL; AB011399; BAA32483.1; -;

DR EMBL; AB011399; BAA32485.1; -;

DR EMBL; U02478; AAC50059.1; -;

DR EMBL; AL049698; CAB76850.1; -;

DR HSSP; Q12923; 3PDZ.

DR Genew; HGNC:7137; MLLT4.

DR MIM; 159559; -;

DR InterPro; IPR002710; DIL.

DR InterPro; IPR000253; FHA_domain.

DR InterPro; IPR001478; PDZ.

DR InterPro; IPR000159; RA_domain.

DR Pfam; PF00498; FHA; 1.

DR Pfam; PF00595; PDZ; 1.

DR Pfam; PF00788; RA; 2.

DR Pfam; PF01843; DIL; 1.

DR ProDom; PD003376; DIL; 1.

DR SMART; SM00240; FHA; 1.

DR SMART; SM00228; PDZ; 1.

DR SMART; SM00314; RA; 2.

DR PROSITE; PS0106; PDZ; 1.

KW Chromosomal translocation; Proto-oncogene; Alternative splicing.

FT DOMAIN 36 206

FT DOMAIN 425 491

FT DOMAIN 804 910

FT DOMAIN 991 1077

FT DOMAIN 162 174

FT DOMAIN 1349 1356

FT DOMAIN 1371 1376

FT DOMAIN 1561 1571

FT SITE 26 26

FT VARSPLIC 1588 1611

FT VARSPLIC 1612 1816

FT VARSPLIC 1666 1743

FT VARSPLIC 1744 1816

FT CONFLICT 373 373

FT CONFLICT 391 391

FT CONFLICT 744 744

FT CONFLICT 1031 1031

FT CONFLICT 1408 1408

FT CONFLICT 1816 AA; 205604 MW; EB1FE7F04879CE8F CRC64;

Query Match 12.5%; Score 71.5; DB 1; Length 1816;

Best Local Similarity 26.5%; Pred. NO. 25;

Matches 27; Conservative 15; Mismatches 45; Indels 15; Gaps 3;

OY 13 DERKTAWGERNGOKRRRR-----GTRAGGCTPRYMSCLRDAPPSPPTA--cp 60

DB 1631 EKARQEEGYSLAEARRRQHDAAARRLLEPAAGLCRP---PLPRDYEPSPSPAPGAP 1687

OY 61 PRCPWQDDAFIRRGPGXKGLGLRAVALGFEDTEVTTTPAG 102

DB 1688 PPPQPNASYLKTQVLSPDLSFTAKFVAYNEEEDDCSLAG 1729

RESULT 11

RNE_ECOLI

ID RNE_ECOLI STANDARD; PRT: 1061 AA.

AC P21513; P77591;

DT 01-MAY-1991 (Rel. 18, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Ribonuclease E (EC 3.1.4.-) (RNase E).

GN RNE OR AMS OR HMP1 OR B1084.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1474(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=K12;

RX MEDLINE=97061202; PubMed=8905232;

RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,

RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,

RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,

RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,

RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,

RA Yano M., Horiuchi T.;

RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome

RT corresponding to the 12.7-28.0 min region on the linkage map.";

RL DNA Res. 3:137-155(1996).

RN [3]

RP SEQUENCE OF 1-1025 FROM N.A.

RC STRAIN=K12;

RX MEDLINE=93078265; PubMed=1447789;

RA Casaregola S., Jacq A., Lacudj D., McGurk G., Margaron S.,

RA Tempete M., Norris V., Holland I.B.;

RT "Cloning and analysis of the entire Escherichia coli ams gene. ams is

RT identical to hmp1 and encodes a 114 kDa protein that migrates as a

RT 180 kDa protein.";

RL J. Mol. Biol. 228:30-40(1992).

RN [4]

RP SEQUENCE OF 1-844 FROM N.A.

RC STRAIN=K12;

RX MEDLINE=91131576; PubMed=1704367;

RA Claverie-Martin F., Diaz-Torres M., Yancey S.D., Kushner S.R.;

RT "Analysis of the altered mRNA stability (ams) gene from Escherichia

RT coli. Nucleotide sequence, transcriptional analysis, and homology of

RT its product to MRP3, a mitochondrial ribosomal protein from

RT Neurospora crassa.";

RL J. Biol. Chem. 266:2843-2851(1991).

RN [5]

RP PARTIAL SEQUENCE FROM N.A., AND SEQUENCE OF 1-27.

RC STRAIN=K12;

RX MEDLINE=91187608; PubMed=2011493;

RA Chauhan A.K., Miczak A., Taraseviciene L., Aprillon D.;

RT "Sequencing and expression of the rne gene of Escherichia coli.";

RL Nucleic Acids Res. 19:125-129(1991).
RN [6]
RP SEQUENCE OF 844-1061 FROM N.A., AND CHARACTERIZATION.
RC STRAIN-K12;
RX MEDLINE=94022304; PubMed=8415644;
RA Cornack R.S., Genereaux J.L., Mackie G.A.;
RT "Rnase E activity is conferred by a single polypeptide:
RT overexpression, purification, and properties of the ams/rne/hmp1 gene
RT product.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:9006-9010(1993).
RN [7]
RP CHARACTERIZATION.
RX PubMed=11328869;
RA Walsh A.P., Tock M.R., Mallen M.H., Kaberdin V.R., Gabain Av A.,
RA McDowall K.J.;
RT "Cleavage of poly(A) tails on the 3'-end of RNA by ribonuclease E of
RT Escherichia coli.";
RL Nucleic Acids Res. 29:1864-1871(2001).
CC -!- FUNCTION: MATURES 5S RNA FROM ITS PRECURSORS FROM ALL THE RRNA
CC GENES. IT ALSO CLEAVES RNA I, A MOLECULE THAT CONTROLS THE
CC REPLICATION OF COLEI PLASMID DNA. IT IS THE MAJOR ENDOURIBONUCLEASE
CC PARTICIPATING IN MRNA TURNOVER IN E.COLI. IT INITIATES THE DECAY
CC OF RNAS BY CUTTING THEM INTERNALLY NEAR THEIR 5'-END. IT IS ABLE
CC TO REMOVE POLY(A) TAILS BY AN ENDONUCLEOTIC PROCESS.
CC -!- SUBUNIT: ORGANIZED INTO A STRUCTURE (PROCESSOME OR RNA
CC DEGRADOSOME) CONTAINING A NUMBER OF RNA-PROCESSING ENZYMES.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE RNE FAMILY.
CC -!- SIMILARITY: CONTAINS 1 SI MOTIF DOMAIN.
CC -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 1003
CC ONWARD AND IS SHORTER (1025 AA) DUE TO A FRAMESHIFT.
CC -!- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN IN THE C-TERMINUS
CC AND IS SHORTER (815 AA) DUE TO A FRAMESHIFT.
CC -!- CAUTION: REF.5 SEQUENCE WAS ALSO INCORRECT IN MANY POSITIONS DUE
CC TO FRAMESHIFTS.
CC
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CC
CC EMBL; AE000209; AAC74168.1; -
CC EMBL; D90744; BAA35893.1; -
CC EMBL; X67470; CAA47818.1; ALT.FRAME.
CC EMBL; M62747; AAZ23443.1; ALT.FRAME.
CC EMBL; X54309; CAA38206.1; ALT.FRAME.
CC EMBL; L23942; AAA03347.1; -
CC PIR; JG0009; JG0009.
CC PIR; A23747; A23747.
CC PIR; S25116; S25116.
CC PIR; S27311; S27311.
CC EcoGene; EGI0859; rne.
CC InterPro; IPR004659; RNaseEG.
CC InterPro; IPR003029; S1.
CC Pfam; PF00575; S1; 1.
CC SMART; SM00316; S1; 1.
CC TIGRFAWS; TIGR00757; RNaseEG; 1.
CC PROSITE; PS50126; S1; 1.
KW Hydrolase; Nuclease; Endonuclease; RNA-binding; Complete proteome.
FT DOMAIN 39 119
FT S1 MOTIF.
FT CONFLICT 390 390 Q -> H (IN REF. 4).
FT CONFLICT 487 487 V -> L (IN REF. 1 AND 2).
FT CONFLICT 564 564 A -> R (IN REF. 3).
FT CONFLICT 784 784 N -> K (IN REF. 3).
FT CONFLICT 838 838 A -> R (IN REF. 4).
FT CONFLICT 905 905 P -> R (IN REF. 3).
FT CONFLICT 1048 1048 H -> R (IN REF. 6).
SQ SEQUENCE 1061 AA; 118182 MW; B911877DF03E79A8 CRC64;

Query Match

12.2%; Score 69.5; DB 1; Length 1061;

Best Local Similarity 26.4%; Pred. No. 23;
Matches 29; Conservative 9; Mismatches 41; Indels 31; Gaps 4;
QY 8 LVPKVDERTAW-GERNGQKRRRRGTRAGGCTTPRYMSCLRDAPPSPTPAGP-----60
DB 501 MLPKHEEAMALPSEEEFAERKRPQPALATFAMPDV-----PPAPTAEAPAPVA 552
QY 61 -----PRCQWQDAFIRRGCPKXKGLGRAVALGFEDTEVTTPA 101
DB 553 PAPKAAPATPAAPAOGLLSRRFG-----ALKALFSGGEETKPTQPA 595
RESULT 12
POLN_RUBVT
ID POLN_RUBVT STANDARD; PRT; 2205 AA.
AC P13889;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Nonstructural polyprotein [Contains: Nonstructural protein NSP1;
DE Nonstructural protein NSP2; Nonstructural protein NSP3; Nonstructural
DE protein NSP4].
OS Rubella virus (strain Therien).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Rubivirus.
OX NCBI_TaxID=11045;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90281585; PubMed=2353453;
RA Dominguez G., Wang C.Y., Frey T.K.;
RT "Sequence of the genome RNA of rubella virus: evidence for genetic
RT rearrangement during togavirus evolution.";
RL Virology 177:225-258(1990).
RN [2]
RP SEQUENCE OF 1737-2205 FROM N.A.
RX MEDLINE=88226020; PubMed=2836271;
RA Frey T.K., Marr L.D.;
RT "Sequence of the region coding for virion proteins C and E2 and the
RT carboxy terminus of the nonstructural proteins of rubella virus:
RT comparison with alphaviruses.";
RL Gene 62:85-99(1989).
CC -!- PTM: SPECIFIC ENZYMTIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
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CC
CC EMBL; M15240; AAA88528.1; -
CC PIR; A35320; MNWVRN.
CC MEROPS; C27.001; -
CC InterPro; IPR002589; Alpp.
CC InterPro; IPR001788; RNA_dep_RNapol2.
CC InterPro; IPR000606; Viral_helicase1.
CC Pfam; PF00978; RNA_dep_RNapol2; 1.
CC Pfam; PF01443; Viral_helicase1; 1.
CC Pfam; PF01661; Alpp; 1.
CC SMART; SM00506; Alpp; 1.
KW Polyprotein; Nonstructural protein.
FT CHAIN 1 ? NONSTRUCTURAL PROTEIN NSP1.
FT CHAIN ? ? NONSTRUCTURAL PROTEIN NSP2.
FT CHAIN ? ? NONSTRUCTURAL PROTEIN NSP3.
FT CHAIN ? 2205 NONSTRUCTURAL PROTEIN NSP4.
SQ SEQUENCE 2205 AA; 240220 MW; 15A95F55E34C0B03 CRC64;
Query Match 12.2%; Score 69.5; DB 1; Length 2205;
Best Local Similarity 30.5%; Pred. No. 47;
Matches 25; Conservative 5; Mismatches 33; Indels 19; Gaps 3;
QY 22 RNSQKRRRRGTRAGGCTTPRYMSCLRDAPPSPTPAGPRCPWQDDAFIRRGPKXGKE 81

RA Guichard S., Rodier M., Meyrier A., Caron P., Vantghem M.-C.,
RA Assayag M., Peix J.-L., Pugeat M., Rohmer V., Vallotton M., Lenolr G.,
RA Gaudray P., Proye C., Conte-Devolx B., Chanson P., Shugart Y.Y.,
RA Goldgar D., Murat A., Calender A.,
RT "Germline mutation analysis in patients with multiple endocrine
neoplasia type 1 and related disorders.";
RL Am. J. Hum. Genet. 63:455-467(1998).
RN [6]
RP VARIANT FIHP LYS-260.
RX MEDLINE=99011276; PubMed=9792884;
RA Teh B.T., Esapa C.T., Houlston R., Grandell U., Farnebo F.,
RA Nordenskjöld M., Pearce C.J., Carmichael D., Larsson C., Harris P.E.;
RT "A family with isolated hyperparathyroidism segregating a missense
MEN1 mutation and showing loss of the wild-type alleles in the
parathyroid tumors.";
RL Am. J. Hum. Genet. 63:1544-1549(1998).
RN [7]
RP VARIANT FIHP GLU-189.
RX MEDLINE=990517176; PubMed=9843042;
RA Fujimori M., Shirahama S., Sakurai A., Hashizume K., Hama Y., Ito K.,
RA Shingu K., Kobayashi S., Amano J., Fukushima Y.;
RT "Novel V184E MEN1 germline mutation in a Japanese kindred with
familial hyperparathyroidism.";
RL Am. J. Med. Genet. 80:221-222(1998).
RN [8]
RP VARIANTS FMEN1.
RX MEDLINE=98334342; PubMed=9671267;
RA Agarwal S.K., Debelenko L.V., Kester M.B., Guru S.C., Manickam P.,
RA Olufemi S.E., Skarulis M.C., Heppner C., Crabtree J.S.,
RA Lubensky I.A., Zhuang Z., Kim Y.S., Chandrasekharappa S.C.,
RA Collins F.S., Liotta L.A., Spiegel A.M., Burns A.L., Emmert-Buck M.R.,
RA Marx S.J.;
RT "Analysis of recurrent germline mutations in the MEN1 gene encountered
in apparently unrelated families.";
RL Hum. Mutat. 12:75-82(1998).
RN [9]
RP VARIANTS FMEN1 ILB-135 AND LYS-364.
RX MEDLINE=98410971; PubMed=9740255;
RA Boeni R., Vormeyer A.O., Pack S., Park W.-S., Burg G., Hofbauer G.,
RA Darling T., Liotta L., Zhuang Z.;
RT "Somatic mutations of the MEN1 tumor suppressor gene detected in
sporadic angiofibromas.";
RL J. Invest. Dermatol. 111:539-540(1998).
RN [10]
RP VARIANTS FMEN1 LYS-119 DEL AND 171-GLN--LEU-173 DEL.
RX MEDLINE=98419173; PubMed=9747036;
RA Sakurai A., Shirahama S., Fujimori M., Katai M., Itakura Y.,
RA Kobayashi S., Amano J., Fukushima Y., Hashizume K.;
RT "Novel MEN1 gene mutations in familial multiple endocrine neoplasia
type 1.";
RL J. Hum. Genet. 43:199-201(1998).
RN [11]
RP VARIANT FMEN1 GLY-45.
RX MEDLINE=99048878; PubMed=9832038;
RA Sato M., Matsubara S., Miyauchi A., Ohye H., Imachi H., Murao K.,
RA Takahara J.;
RT "Identification of five novel germline mutations of the MEN1 gene in
Japanese multiple endocrine neoplasia type 1 (MEN1) families.";
RL J. Med. Genet. 35:915-919(1998).
RN [12]
RP VARIANTS FMEN1 TRP-39; TYR-177; ASP-184; PRO-269 AND PRO-272.
RX MEDLINE=99103464; PubMed=9888389;
RA Poncin J., Abs R., Velkeniers B., Bonduelle M., Abramowicz M.,
RA Legros J.-J., Verloes A., Meurisse M., van Gaal L., Verellen C.,
RA Koulschier L., Beckers A.;
RT "Mutation analysis of the MEN1 gene in Belgian patients with multiple
endocrine neoplasia type 1 and related diseases.";
RL Hum. Mutat. 13:54-60(1998).
RN [13]
RP VARIANTS MEN1 ASP-161 AND ARG-246.
RX MEDLINE=99188881; PubMed=10090472;
RA Mutch M.G., Dilley W.G., Sanjurjo F., Debenedetti M.K., Doherty G.M.,
RA Wells S.A. Jr., Goodfellow P.J., Lairmore T.C.;

RT "Germline mutations in the multiple endocrine neoplasia type 1 gene:
evidence for frequent splicing defects.";
Hum. Mutat. 13:175-185(1999).
CC -!- FUNCTION: NOT KNOWN.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: UBIQUITOUS.
CC -!- DISEASE: DEFECTS IN MEN1 ARE THE CAUSE OF FAMILIAL MULTIPLE
ENDOCRINE NEOPLASIA TYPE 1 (FMEN1); WERNER SYNDROME, AN AUTOSOMAL
DOMINANT DISORDER CHARACTERIZED BY TUMORS OF THE PARATHYROID
GLANDS, GASTRO-INTESTINAL ENDOCRINE TISSUE, THE ANTERIOR PITUITARY
AND OTHER TISSUES. CUTANEOUS LESIONS AND NERVOUS-TISSUE TUMORS CAN
EXIST. PROGNOSIS IN FMEN1 PATIENTS IS RELATED TO HORMONAL
HYPERSECRETION BY TUMORS, SUCH AS HYPERGASTRINEMIA CAUSING SEVERE
PEPTIC ULCER DISEASE (ZOLLINGER-ELISON SYNDROME, ZES), PRIMARY
HYPERPARATHYROIDISM, AND ACUTE FORMS OF HYPERINSULINEMIA.
CC -!- DISEASE: DEFECTS IN MEN1 ARE THE CAUSE OF FAMILIAL ISOLATED
HYPERPARATHYROIDISM (FIHP OR HRPT1). FIHP IS AN AUTOSOMAL DOMINANT
DISORDER CHARACTERIZED BY HYPERCALCEMIA, ELEVATED PARATHYROID
HORMONE (PTH) LEVELS, AND UNIGLANDULAR OR MULTIGLANDULAR
PARATHYROID TUMORS.
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U932236; AAC51228.1; -;
DR EMBL: U932237; AAC51229.1; -;
DR EMBL: U932237; AAC51229.1; -;
DR Genew: HGNC:7010; MEN1.
DR MIM: 131100; -;
DR MIM: 145000; -;
DR Nuclear protein; Disease mutation; Alternative splicing; Polymorphism.
KW VARSPLIC 149 153
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FT L -> R (IN FMEN1).
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FT E -> K (IN PARATHYROID ADENOMA).
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Best Local Similarity 25.9%; Pred. No. 15;
Matches 28; Conservative 9; Mismatches 31; Indels 40; Gaps 5;
QY 14 ERKTAWGERNGKRRRRGTRAGGCTPRYMNSCLRDAAEPSPPTP----- 57

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 19, 2003, 15:32:08 ; Search time 17 seconds
(without alignments)
588.116 Million cell updates/sec

Title: US-09-750-240-2

Perfect score: 570

Sequence: 1 MSWFSGLLVPKVDERKTAMG.....RAVALGFEDTEVTTPAGPL 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	472.5	82.9	1165	2 A46180	adenyllyl cyclase t
2	432	75.8	1180	2 A47202	adenylate cyclase
3	431	75.6	1166	2 A49201	adenylate cyclase
4	77.5	13.6	1285	2 T14171	ataxin-2 - mouse
5	76	13.3	285	2 E5507	hypothetical prote
6	74	13.0	1173	2 T31421	C-terminal domain-
7	73	12.8	512	1 WMBEY4	UL54 protein - hum
8	73	12.8	550	2 C75557	hypothetical prote
9	73	12.8	1168	1 MWAXIC	myosin heavy chain
10	72	12.6	232	2 A41551	vascular endothell
11	72	12.6	406	2 T36632	probable oxidoredu
12	72	12.6	576	2 T36729	probable serine/th
13	70.5	12.4	357	2 S11137	class I histocompa
14	70.5	12.4	357	2 S11134	class I histocompa
15	69.5	12.2	138	2 C96734	hypothetical prote
16	69.5	12.2	337	2 S11136	class I histocompa
17	69.5	12.2	1061	1 S27311	ribonuclease E (EC
18	69.5	12.2	2205	1 MNWVRN	nonstructural poly
19	69	12.1	948	2 A57640	retinoblastoma bin
20	69	12.1	1621	2 T15264	hypothetical prote
21	68.5	12.0	144	2 E86364	hypothetical prote
22	68.5	12.0	303	2 T19289	hypothetical prote
23	68.5	12.0	357	2 S11135	class I histocompa
24	68.5	12.0	1061	2 F90811	RNase E [imported]
25	68.5	12.0	1061	2 B85671	RNase E [similarit
26	68.5	12.0	1147	2 T42627	ADP-ribosylation f
27	68	11.9	162	2 T49420	hypothetical prote
28	68	11.9	212	2 T35187	hypothetical prote
29	68	11.9	294	2 T22639	hypothetical prote

ALIGNMENTS

RESULT 1

A46180

adenyllyl cyclase type VI - dog

C:Species: Canis lupus familiaris (dog)

C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 04-Sep-1998

C:Accession: A46180

R:Katsushika S.; Chen, L.; Kawabe, J.; Nalakantan, R.; Halnon, N.J.; Homcy, C.J.; I

Proc. Natl. Acad. Sci. U.S.A. 89, 8774-8778, 1992

A:Title: Cloning and characterization of a sixth adenyllyl cyclase isoform: types V a

A:Reference number: A46180; MUID:92409599; PMID:1528892

A:Accession: A46180

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-1165 <NAI>

A:Experimental source: cardiac

A>Note: sequence extracted from NCBI backbone (NCBIN:114249, NCBIPI:114250)

C:Superfamily: human adenylate cyclase; guanylate cyclase catalytic domain homology

C:Keywords: transmembrane protein

F:319-553/Domain: guanylate cyclase catalytic domain homology <GCC>

F:924-1163/Domain: guanylate cyclase catalytic domain homology <GCC>

Query Match	82.9%	Score	472.5	DB	2	Length	1165
Best Local Similarity	83.2%	Pred. No.	2.3e-39				
Matches	89	Conservative	2	Mismatches	11	Indels	5
						Gaps	2
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QY	61	PRCPWQDDAFIRRGPGKXKELGLRAVALG	PEDETE- ---VTTTPAGP	103			
Db	60	PRCPWQDDAFIRRGPGKXKELGLRAVALG	FEDETEAMS	AVGAGGGP	106		

RESULT 2

A47202

adenylate cyclase (EC 4.6.1.1) type 6 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999

C:Accession: A47202; A5145

R:Premont, R.T.; Chen, J.; Ma, H.W.; Ponnappalli, M.; Iyengar, R.

Proc. Natl. Acad. Sci. U.S.A. 89, 9809-9813, 1992

A:Title: Two members of a widely expressed subfamily of hormone-stimulated adenyllyl

A:Reference number: A47202; MUID:93028552; PMID:1409703

A:Accession: A47202

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-1180 <PRE>

A:Experimental source: liver, kidney

A>Note: sequence extracted from NCBI backbone (NCBIPI:115851)

R:Krupinski, J.; Lehman, T.C.; Frankenfield, C.D.; Zwaagstra, J.C.; Watson, P.A.

J. Biol. Chem. 267, 24858-24862, 1992

hypothetical prote
hypothetical prote
2-aminobenzoyl-CoA
N-methyl-D-asparta
N-methyl-D-asparta
N-methyl-D-asparta
conserved hypothet
class I histocompa
UL54 protein - hum
hypothetical prote
hypothetical prote
insulin promoter f
hypothetical prote
class I histocompa
hypothetical prote

30 68 11.9 310 2 T22641
31 68 11.9 572 2 T52520
32 68 11.9 730 2 S24376
33 68 11.9 1323 2 I78557
34 68 11.9 1323 2 S27224
35 68 11.9 1356 1 C45219
36 67.5 11.8 259 2 B87314
37 67.5 11.8 357 2 S11133
38 67.5 11.8 511 1 A48560
39 67 11.8 140 2 E72503
40 67 11.8 304 2 T23801
41 67 11.8 418 2 F82638
42 66.5 11.7 283 2 G01926
43 66.5 11.7 310 2 T29731
44 66.5 11.7 364 2 I72217
45 66.5 11.7 1410 2 T47137

RESULT 15
C96734

Search completed: February 19, 2003, 15:35:39
Job time : 18 secs

RESULT 15
C96734

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: February 19, 2003, 15:33:43 ; Search time 23 Seconds
(without alignments)
384,520 Million cell updates/sec

Title: US-09-750-240-2
Perfect score: 570
Sequence: 1 MSWFGLLVPKVDERTAWG.....RAVALGFEDTEVTTPAGPL 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 433615 seqs, 85038156 residues

Total number of hits satisfying chosen parameters: 433615

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	545	95.6	453	1	PCT-US02-36759-36
2	73.5	12.9	442	5	US-09-724-676-58592
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4	73.5	12.9	678	5	US-09-724-676-58592
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6	73.5	12.9	1234	1	PCT-US02-14905-12
7	73.5	12.9	1239	6	US-10-218-140-4986
8	72.5	12.7	1129	1	PCT-US02-36151-44
9	72	12.6	126	5	US-09-724-676-58587
10	72	12.6	126	5	US-09-724-676-58587
11	72	12.6	126	5	US-09-724-676-58587
12	72	12.6	126	5	US-09-724-676-58587
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17	72	12.6	232	1	PCT-US02-26246A-7
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Sequence 58592, A
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Sequence 58593, A
Sequence 58590, A
Sequence 58590, A
Sequence 58591, A
Sequence 58591, A
Sequence 16, Appl
Sequence 348, Appl
Sequence 9, Appl
Sequence 58582, A
Sequence 58583, A
Sequence 58582, A
Sequence 58583, A
Sequence 58586, A
Sequence 58587, A
Sequence 58587, A

ALIGNMENTS

RESULT 1
PCT-US02-36759-36
; Sequence 36, Application PC/TUS0236759
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DUGGAN, Brendan M.
; APPLICANT: YANG, Junming
; APPLICANT: GIETZEN, Kimberly J.
; APPLICANT: LEE, Soo Yeun
; APPLICANT: TANG, Y. Tom
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: WALIA, Narinder K.
; APPLICANT: WARREN, Bridget A.
; APPLICANT: BARROSO, Ines
; APPLICANT: BECHA, Shanya D.
; APPLICANT: YUE, Henry
; APPLICANT: LEHR-MASON, Patricia M.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: LEE, Sally
; APPLICANT: EMERLING, Brooke M.
; APPLICANT: KABLE, Amy E.
; APPLICANT: KHARE, Reena
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: GANDHI, Ameeta R.
; APPLICANT: TRAN, Uyen K.
; APPLICANT: RICHARDSON, Thomas W.
; APPLICANT: MARQUIS, Joseph P.
; APPLICANT: LAL, Preeti G.
; APPLICANT: FORSYTHE, Ian J.
; APPLICANT: LEE, Ernestine A.
; APPLICANT: SWARNAKAR, Anita.
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: GORVAD, Ann E.
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: ISON, Craig H.
; APPLICANT: JIN, Pei
; APPLICANT: JIANG, Xin
; APPLICANT: JACKSON, Alan
; APPLICANT: BHATIA, Umesh
; APPLICANT: BURRILL, John D.
; APPLICANT: BLAKE, Julie J.
; APPLICANT: HO, Ann
; APPLICANT: ZHENG, Wenjin
; APPLICANT: GAO, Jing
; TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS
; FILE REFERENCE: PF-1279 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/36759

RESULT 3
US-09-724-676A-76996
; Sequence 76996, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222

RESULT 6
PCT-US02-14905-12
; Sequence 12, Application PC/TUS0214905
; GENERAL INFORMATION:
; APPLICANT: Research Corporation Tech. Inc.

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; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ASSOCIATED WITH PROSTATE CANCER
; FILE REFERENCE: AND MELANOMA IMMUNODETECTION
; CURRENT APPLICATION NUMBER: PCT/US02/14905
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 08/869,285
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 08/654,641
; PRIOR FILING DATE: 1996-05-28
; PRIOR APPLICATION NUMBER: 07/829,855
; PRIOR FILING DATE: 1992-01-31
; PRIOR APPLICATION NUMBER: 09/255,533
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1234
; LENGTH: 1234
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-14905-12

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Db 331 SGRAP-LEIRPSPPTSRG-SSRGTAILLTGLEORAGLITPRHLAQAADPPRSM 386
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OY 53 -----PSPTPAGPCPCWODAFIRGCPYKKEKEL-GLRAVALGFEDTEVTTT 102
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 387 SLAVVGTSPSAPPA-PPSPAFDPDRFL--NSPQRGTGGGCVSPDFPEAEAAHTPCS 443
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OY 103 PL 104
Db 444 AL 445

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RESULT 7

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US-10-218-140-4986
; Sequence 4986, Application US/10218140
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 15966-543 CON
; CURRENT APPLICATION NUMBER: US/10/218,140
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/127,728
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/127,636
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/127,607
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 6322
; SOFTWARE: Curator Version 1.0
; SEQ ID NO 4986
; LENGTH: 1239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-218-140-4986

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Query Match          12.9%  Score 73.5;  DB 6;  Length 1239;
Best Local Similarity 27.9%;  Pred. No. 2.8e+02;
Matches 34;  Conservative 13;  Mismatches 46;  Indels 29;  Gaps 7;

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Db 336 SGRAP-LEIRPSPPTSRG-SSRGTAILLTGLEORAGLITPRHLAQAADPPRSM 391
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OY 53 -----PSPTPAGPCPCWODAFIRGCPYKKEKEL-GLRAVALGFEDTEVTTT 102
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Db 392 SLAVVGTSPSAPPA-PPSPAFDPDRFL--NSPQRGTGGGCVSPDFPEAEAAHTPCS 448
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OY 103 PL 104
Db 449 AL 450

```

RESULT 8

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PCT-US02-36151-44
; Sequence 44, Application PC/TUS0236151
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: KABLE, Amy E.; SMARNARAR, Anita
; APPLICANT: GORVAD, Ann E.; HAFALIA, April J.A.
; APPLICANT: DUGGAN, Brendan M.; WARREN, Bridget A.
; APPLICANT: EMERLING, Brooke E.; ISON, Craig H.
; APPLICANT: NGUYEN, Danielle B.; LINDQUIST, Erika A.
; APPLICANT: LEE, Ernestine A.; YUE, Henry
; APPLICANT: YUE, HuiBin; FORSYTHE, Ian J.
; APPLICANT: RAMKUMAR, Jayalaxmi; GRIFFIN, Jennifer A.
; APPLICANT: LI, Joanna X.; MARQUIS, Joseph P.
; APPLICANT: GLETZEN, Kimberly J.; BAUGHN, Mariah R.
; APPLICANT: BOROMSKY, Mark L.; YAO, Monique G.
; APPLICANT: CHAWLA, Narinder K.; LEHR-MASON, Patricia M.
; APPLICANT: LAI, Preeti G.; GURURAJAN, Rajagopal
; APPLICANT: KHARE, Reena; BATRA, Sajeiv
; APPLICANT: BECHA, Shanya D.; LEE, Soo Yeun
; APPLICANT: TRAN, Uyen K.; ELLIOTT, Vicki S.
; APPLICANT: SPRAGUE, William W.; TANG, Y. Tom
; APPLICANT: ZEBARJADIAN, Yeganeh; JIANG, Xin
; APPLICANT: JACKSON, Alan A.; BHATIA, Umesh G.
; APPLICANT: BURRILL, John D.; LEE, Sally
; APPLICANT: BLAKE, Julie J.; HO, Anne
; APPLICANT: ZHENG, WenJin
; TITLE OF INVENTION: INTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: PF-1275 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/36151
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/344,472
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/334,558
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/340,296
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/343,557
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/350,420
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/351,927
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PERL Program
; SEQ ID NO 44
; LENGTH: 1129
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No: 71746949CD1
PCT-US02-36151-44

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Query Match          12.7%  Score 72.5;  DB 1;  Length 1129;
Best Local Similarity 32.8%;  Pred. No. 3.1e+02;
Matches 19;  Conservative 6;  Mismatches 24;  Indels 9;  Gaps 3;

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OY 50 AEPSPTPAGP--CPWODAFIRGCPYKKEKEL-GLRAVALGFE-DTEVTTT 103
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Db 839 SDPSPPLPHGPRNKGAVPWGND-----GPFSSSKTKTKKFGLSQGSTSSAKTALGP 891
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RESULT 9

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US-09-724-676-63223
: Sequence 63223, Application US/09724676
: GENERAL INFORMATION:
:   APPLICANT: Compugen LTD
:   TITLE OF INVENTION: Variants of alternative splicing
:   FILE REFERENCE: 129181.4 Compugen
:   CURRENT APPLICATION NUMBER: US/09/724,676
:   CURRENT FILING DATE: 2000-11-28
:   NUMBER OF SEQ ID NOS: 97222
:   SOFTWARE: PatentIn version 3.2
:   LENGTH: 126
:   TYPE: PRT
:   ORGANISM: Homo sapiens
US-09-724-676-63223

Query Match
Best Local Similarity 32.8%; Score 72; DB 5; Length 126;
Matches 21; Conservative 5; Mismatches 16; Indels 22; Gaps 3

QY 10 PKVD---EKTATCERNQKRSRRRGTRAGGCTPRWMS-----CLRDAEPPSFT 56
      |||  :  :  :  ||||  :  :  :  |||  :  :  :  |||  :  :  :  |||
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 26 PKKDRAOEKKSXSVRGKGQKRRKRKS-----RYKSWSVYVGARCLPWSLPGPH 76

QY 57 PAGP 60
      |||
DB 77 PCGP 80

RESULT 10
US-09-724-676-63224
: Sequence 63224, Application US/09724676
: GENERAL INFORMATION:
:   APPLICANT: Compugen LTD
:   TITLE OF INVENTION: Variants of alternative splicing
:   FILE REFERENCE: 129181.4 Compugen
:   CURRENT APPLICATION NUMBER: US/09/724,676
:   CURRENT FILING DATE: 2000-11-28
:   NUMBER OF SEQ ID NOS: 97222
:   SOFTWARE: PatentIn version 3.2
:   SEQ ID NO 63224
:   LENGTH: 126
:   TYPE: PRT
:   ORGANISM: Homo sapiens
US-09-724-676-63224

Query Match
Best Local Similarity 32.8%; Score 72; DB 5; Length 126;
Matches 21; Conservative 5; Mismatches 16; Indels 22; Gaps 3

QY 10 PKVD---EKTATCERNQKRSRRRGTRAGGCTPRWMS-----CLRDAEPPSFT 56
      |||  :  :  :  ||||  :  :  :  |||  :  :  :  |||  :  :  :  |||
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 26 PKKDRAOEKKSXSVRGKGQKRRKRKS-----RYKSWSVYVGARCLPWSLPGPH 76

QY 57 PAGP 60
      |||
DB 77 PCGP 80

RESULT 11
US-09-724-676-63227
: Sequence 63227, Application US/09724676
: GENERAL INFORMATION:
:   APPLICANT: Compugen LTD
:   TITLE OF INVENTION: Variants of alternative splicing
:   FILE REFERENCE: 129181.4 Compugen
:   CURRENT APPLICATION NUMBER: US/09/724,676
:   CURRENT FILING DATE: 2000-11-28
:   NUMBER OF SEQ ID NOS: 97222
:   SOFTWARE: PatentIn version 3.2
:   SEQ ID NO 63227
:   LENGTH: 126
:   TYPE: PRT

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: ORGANISM: Homo sapiens
US-09-724-676-63227

Query Match
Best Local Similarity 12.6%; Score 72; DB 5; Length 126;
Matches 21; Conservative 5; Mismatches 16; Indels 22; Gaps 3

QY 10 PKVD---EERTAMGERNGKRRRRGTRAGGCTPRYMS-----CLRDAEPPSPT 56
      ||| | : | : | ||| | : | ||| | : |
DB 26 PKKDRARQEKKSVMKGGKGGKRRKRKS-----RYKSMVVYGARCLMPWSLPGPH 76
      ||| | : | : | ||| | : | ||| | : |

QY 57 PAGP 60
      |||
DB 77 PCGP 80

RESULT 12
US-09-724-676-63228
: Sequence 63228, Application US/09724676
: GENERAL INFORMATION:
: APPLICANT: Compugen LTD
: TITLE OF INVENTION: Variants of alternative splicing
: FILE REFERENCE: 129181.4 Compugen
: CURRENT APPLICATION NUMBER: US/09/724,676
: NUMBER OF SEQ ID NOS: 97222
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 63228
: LENGTH: 126
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-724-676-63228

Query Match
Best Local Similarity 12.6%; Score 72; DB 5; Length 126;
Matches 21; Conservative 5; Mismatches 16; Indels 22; Gaps 3

QY 10 PKVD---EERTAMGERNGKRRRRGTRAGGCTPRYMS-----CLRDAEPPSPT 56
      ||| | : | : | ||| | : | ||| | : |
DB 26 PKKDRARQEKKSVMKGGKGGKRRKRKS-----RYKSMVVYGARCLMPWSLPGPH 76
      ||| | : | : | ||| | : | ||| | : |

QY 57 PAGP 60
      |||
DB 77 PCGP 80

RESULT 13
US-09-724-676A-63223
: Sequence 63223, Application US/09724676A
: GENERAL INFORMATION:
: APPLICANT: Compugen LTD
: TITLE OF INVENTION: Variants of alternative splicing
: FILE REFERENCE: 129181.4 Compugen
: CURRENT APPLICATION NUMBER: US/09/724,676A
: NUMBER OF SEQ ID NOS: 97222
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 63223
: LENGTH: 126
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-724-676A-63223

Query Match
Best Local Similarity 12.6%; Score 72; DB 5; Length 126;
Matches 21; Conservative 5; Mismatches 16; Indels 22; Gaps 3;

QY 10 PKVD---EERTAMGERNGKRRRRGTRAGGCTPRYMS-----CLRDAEPPSPT 56
      ||| | : | : | ||| | : | ||| | : |
DB 26 PKKDRARQEKKSVMKGGKGGKRRKRKS-----RYKSMVVYGARCLMPWSLPGPH 76
      ||| | : | : | ||| | : | ||| | : |

QY 57 PAGP 60
      |||
DB 77 PCGP 80

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 19, 2003, 15:32:58 ; Search time 354 Seconds
(without alignments)
189.413 Million cell updates/sec

Title: US-09-750-240-2

Perfect score: 570

Sequence: 1 MSWFGSLVVKYDERKTAMG.....RAVALGFEDTEVTTTAPAGPL 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 64473110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

- 1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
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- 9: /cgn2_6/ptodata/1/paa/US085_COMB.pep.*
- 10: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
- 11: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
- 12: /cgn2_6/ptodata/1/paa/US088_COMB.pep.*
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- 22: /cgn2_6/ptodata/1/paa/US098_COMB.pep.*
- 23: /cgn2_6/ptodata/1/paa/US099_COMB.pep.*
- 24: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
- 25: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
- 26: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
- 27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	568	99.6	104	18	US-09-472-667-2
2	568	99.6	104	21	US-09-750-240-2
3	545	95.6	1167	18	US-09-472-667-6
4	545	95.6	1167	21	US-09-750-240-6
5	545	95.6	1167	21	US-09-750-240-13
6	545	95.6	1168	18	US-09-472-667-11

7	545	95.6	1168	21	US-09-750-240-11
8	545	95.6	1168	26	US-10-201-000-2
9	472.5	82.9	1165	21	US-09-791-537-121687
10	432	75.8	1165	21	US-09-791-537-12125
11	432	75.8	1180	9	US-08-538-815-12
12	432	75.8	1180	21	US-09-791-537-17912
13	432	75.8	1180	21	US-09-791-537-126174
14	431	75.6	1166	21	US-09-791-537-34515
15	428	75.1	1166	21	US-09-791-537-18463
16	395	69.3	1155	21	US-09-791-537-118669
17	258	45.3	1171	21	US-09-791-537-104384
18	122.5	21.5	1216	27	US-60-248-592-119
19	112	19.6	1099	27	US-60-245-228-339
20	86	15.1	1239	27	US-60-229-518-453
21	86	15.1	1328	27	US-60-212-413-161
22	84.5	14.8	514	1	PCT-US01-08656-9626
23	84	14.7	55	1	PCT-US01-08631-47109
24	83	14.6	160	20	US-09-617-681A-4271
25	82.5	14.5	217	16	US-09-252-991A-28321
26	82.5	14.5	345	16	US-09-252-991A-32377
27	81.5	14.3	217	25	US-10-155-881-11975
28	81.5	14.3	390	20	US-09-675-784A-13125
29	81	14.2	266	25	US-10-104-047-3114
30	81	14.2	370	19	US-09-513-996A-43007
31	81	14.2	370	21	US-09-708-427-54400
32	80.5	14.1	782	1	PCT-US01-49232-54
33	79.5	13.9	146	20	US-09-617-681A-4272
34	79.5	13.9	525	25	US-10-155-881-26729
35	79	13.9	109	20	US-09-617-682A-952
36	79	13.9	111	20	US-09-617-682A-951
37	79	13.9	116	20	US-09-617-682A-950
38	79	13.9	120	16	US-09-252-991A-23748
39	79	13.9	289	21	US-09-791-537-129836
40	79	13.9	454	1	PCT-US02-24842-9
41	79	13.9	454	26	US-10-213-990-9
42	79	13.9	454	27	US-60-309-870-9
43	78.5	13.8	465	8	US-08-447-965-2
44	78.5	13.8	1076	1	PCT-US01-08631-41289
45	78.5	13.8	1076	1	PCT-US01-08656-9311

ALIGNMENTS

RESULT 1
US-09-472-667-2
; Sequence 2, Application US/09472667
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. Kirk
; APPLICANT: Insel, Paul A.
; APPLICANT: Ping, Peipei
; APPLICANT: Post, Steven R.
; APPLICANT: Gao, Meihua
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056722
; CURRENT APPLICATION NUMBER: US/09/472,667
; CURRENT FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: PCT/US99/02702
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 09/021,773
; PRIOR FILING DATE: 1998-02-11
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: PCT/US97/15610
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/058,209

;; PRIOR FILING DATE: 1996-09-05
;; PRIOR APPLICATION NUMBER: PCT/US96/02631
;; PRIOR FILING DATE: 1996-02-27
;; PRIOR APPLICATION NUMBER: US 08/396,207
;; PRIOR FILING DATE: 1995-02-28
;; PRIOR APPLICATION NUMBER: US 08/485,472
;; PRIOR FILING DATE: 1995-06-07
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 104
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: VARIANT
;; LOCATION: (1)...(104)
;; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-472-667-2

Query Match 99.6%; Score 568; DB 18; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.5e-47;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSWFSGLLPKVDERTANGERRGKRRRGTTRAGGCTPRYMCLRDAPPSPTPAGP 60
DB 1 MSWFSGLLPKVDERTANGERRGKRRRGTTRAGGCTPRYMCLRDAPPSPTPAGP 60
QY 61 PRCPWODDAFIRGGPKGKGLGRAVALGFEDTEVTTTTPAGPL 104
DB 61 PRCPWODDAFIRGGPKGKGLGRAVALGFEDTEVTTTTPAGPL 104

RESULT 2

US-09-750-240-2
;; Sequence 2, Application US/09750240
;; GENERAL INFORMATION:
;; APPLICANT: Hammond, H. K.
;; APPLICANT: Insel, P. A.
;; APPLICANT: Ping, P.
;; APPLICANT: Post, S. R.
;; APPLICANT: Gao, M.
;; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART FAILURE
;; FILE REFERENCE: 220002056723
;; CURRENT APPLICATION NUMBER: US/09/750,240
;; CURRENT FILING DATE: 2001-10-12
;; PRIOR APPLICATION NUMBER: US 09/472,667
;; PRIOR FILING DATE: 1999-12-27
;; PRIOR APPLICATION NUMBER: US 09/008,097
;; PRIOR FILING DATE: 1998-01-16
;; PRIOR APPLICATION NUMBER: US 08/924,757
;; PRIOR FILING DATE: 1997-09-05
;; PRIOR APPLICATION NUMBER: US 60/048,933
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: US 08/708,661
;; PRIOR FILING DATE: 1996-09-05
;; NUMBER OF SEQ ID NOS: 13
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 104
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: VARIANT
;; LOCATION: (1)...(104)
;; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-750-240-2

Query Match 99.6%; Score 568; DB 21; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.5e-47;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSWFSGLLPKVDERTANGERRGKRRRGTTRAGGCTPRYMCLRDAPPSPTPAGP 60

DB 1 MSWFSGLLPKVDERTANGERRGKRRRGTTRAGGCTPRYMCLRDAPPSPTPAGP 60
QY 61 PRCPWODDAFIRGGPKGKGLGRAVALGFEDTEVTTTTPAGPL 104
DB 61 PRCPWODDAFIRGGPKGKGLGRAVALGFEDTEVTTTTPAGPL 104

RESULT 3

US-09-472-667-6
;; Sequence 6, Application US/09472667
;; GENERAL INFORMATION:
;; APPLICANT: Hammond, H. Kirk
;; APPLICANT: Insel, Paul A.
;; APPLICANT: Ping, Peipei
;; APPLICANT: Post, Steven R.
;; APPLICANT: Gao, Meihua
;; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART FAILURE
;; TITLE OF INVENTION: FAILURE
;; FILE REFERENCE: 220002056722
;; CURRENT APPLICATION NUMBER: US/09/472,667
;; CURRENT FILING DATE: 1999-12-27
;; PRIOR APPLICATION NUMBER: PCT/US99/02702
;; PRIOR FILING DATE: 1999-02-09
;; PRIOR APPLICATION NUMBER: US 09/008,097
;; PRIOR FILING DATE: 1998-01-16
;; PRIOR APPLICATION NUMBER: US 09/021,773
;; PRIOR FILING DATE: 1998-02-11
;; PRIOR APPLICATION NUMBER: US 08/924,757
;; PRIOR FILING DATE: 1997-09-05
;; PRIOR APPLICATION NUMBER: PCT/US97/15610
;; PRIOR FILING DATE: 1997-09-05
;; PRIOR APPLICATION NUMBER: US 08/708,661
;; PRIOR FILING DATE: 1996-09-05
;; PRIOR APPLICATION NUMBER: US 60/048,933
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/058,209
;; PRIOR FILING DATE: 1996-09-05
;; PRIOR APPLICATION NUMBER: PCT/US96/02631
;; PRIOR FILING DATE: 1996-02-27
;; PRIOR APPLICATION NUMBER: US 08/396,207
;; PRIOR FILING DATE: 1995-02-28
;; PRIOR APPLICATION NUMBER: US 08/485,472
;; PRIOR FILING DATE: 1995-06-07
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 6
;; LENGTH: 1167
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-472-667-6

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Best Local Similarity 97.1%; Pred. No. 3.8e-44;
Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 1 MSWFSGLLPKVDERTANGERRGKRRRGTTRAGGCTPRYMCLRDAPPSPTPAGP 60
QY 61 PRCPWODDAFIRGGPKGKGLGRAVALGFEDTEVTTTTPAG 102
DB 61 PRCPWODDAFIRGGPKGKGLGRAVALGFEDTEVTTTTPAG 102

RESULT 4

US-09-750-240-6
;; Sequence 6, Application US/09750240
;; GENERAL INFORMATION:
;; APPLICANT: Hammond, H. K.
;; APPLICANT: Insel, P. A.
;; APPLICANT: Ping, P.
;; APPLICANT: Post, S. R.

APPLICANT: Gao, M.
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
FILE OF INVENTION: FAILURE
FILE REFERENCE: 220002056723
CURRENT APPLICATION NUMBER: US/09/750,240
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/472,667
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: US 08/924,757
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: US 08/708,661
PRIOR FILING DATE: 1996-09-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 1167
TYPE: PRT
ORGANISM: Homo sapiens
US-09-750-240-6

Query Match 95.6%; Score 545; DB 21; Length 1167;
Best Local Similarity 97.1%; Pred. No. 3.8e-44;
Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 1 MSWFSGLLVKPKVDERKTAWGERNGQKRRRGTRAGGFCCTPRYMSCLRDAPPSPTPAGP 60
|||||
QY 61 PRCPWQDDAFIRRGPKXKGLRAVALGFEDTEVTTTAPG 102
|||||
DB 61 PRCPWQDDAFIRRGPKXKGLRAVALGFEDTEVTTTAPG 102
|||||

RESULT 5
US-09-750-240-13
Sequence 13, Application US/09750240
GENERAL INFORMATION:
APPLICANT: Hammon, H. K.
APPLICANT: Insel, P. A.
APPLICANT: Ping, P. A.
APPLICANT: Post, S. R.
APPLICANT: Gao, M.

TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
FILE OF INVENTION: FAILURE
FILE REFERENCE: 220002056723
CURRENT APPLICATION NUMBER: US/09/750,240
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/472,667
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: US 08/924,757
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: US 08/708,661
PRIOR FILING DATE: 1996-09-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 1167
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Modified AC-VI
US-09-750-240-13

Query Match 95.6%; Score 545; DB 21; Length 1167;
Best Local Similarity 97.1%; Pred. No. 3.8e-44;

Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MSWFSGLLVKPKVDERKTAWGERNGQKRRRGTRAGGFCCTPRYMSCLRDAPPSPTPAGP 60
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DB 1 MSWFSGLLVKPKVDERKTAWGERNGQKRRRGTRAGGFCCTPRYMSCLRDAPPSPTPAGP 60
|||||
QY 61 PRCPWQDDAFIRRGPKXKGLRAVALGFEDTEVTTTAPG 102
|||||
DB 61 PRCPWQDDAFIRRGPKXKGLRAVALGFEDTEVTTTAPG 102
|||||

RESULT 6
US-09-472-667-11
Sequence 11, Application US/09472667
GENERAL INFORMATION:
APPLICANT: Hammon, H. Kirk
APPLICANT: Insel, Paul A.
APPLICANT: Ping, Peipel
APPLICANT: Post, Steven R.
APPLICANT: Gao, Meihua
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
FILE OF INVENTION: FAILURE
FILE REFERENCE: 220002056722
CURRENT APPLICATION NUMBER: US/09/472,667
CURRENT FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: PCT/US99/02702
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: US 09/021,773
PRIOR FILING DATE: 1998-02-11
PRIOR APPLICATION NUMBER: US 08/924,757
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: PCT/US97/15610
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: US 08/708,661
PRIOR FILING DATE: 1996-09-05
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/058,209
PRIOR FILING DATE: 1996-09-05
PRIOR APPLICATION NUMBER: PCT/US96/02631
PRIOR FILING DATE: 1996-02-27
PRIOR APPLICATION NUMBER: US 08/396,207
PRIOR FILING DATE: 1995-02-28
PRIOR APPLICATION NUMBER: US 08/485,472
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 1168
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-667-11

Query Match 95.6%; Score 545; DB 18; Length 1168;
Best Local Similarity 97.1%; Pred. No. 3.8e-44;
Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSWFSGLLVKPKVDERKTAWGERNGQKRRRGTRAGGFCCTPRYMSCLRDAPPSPTPAGP 60
|||||
DB 1 MSWFSGLLVKPKVDERKTAWGERNGQKRRRGTRAGGFCCTPRYMSCLRDAPPSPTPAGP 60
|||||
QY 61 PRCPWQDDAFIRRGPKXKGLRAVALGFEDTEVTTTAPG 102
|||||
DB 61 PRCPWQDDAFIRRGPKXKGLRAVALGFEDTEVTTTAPG 102
|||||

RESULT 7
US-09-750-240-11
Sequence 11, Application US/09750240
GENERAL INFORMATION:
APPLICANT: Hammon, H. K.

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Db      I  MSWFGLLVPKVDGRKKTAWGRNQKRP-RHANRASGFCAPRYMSCLKNABGPPSPTPAAH  59
QY      61  PRCWQDDAETRRGGPKXKGLGRVALGAFEDTEVTTT  PAG  102
          |||||:||||| || :| |||||:|||||:||||| |||
Db      60  TRCQWQDEAFTRRAGPGRGVELGRSVALGDFDTEV-TTPMG  100
          ;

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RESULT 11
US-08-538-815-12
; Sequence 12, Application US/08538815
; GENERAL INFORMATION:
; APPLICANT: Tang, Wei-Jen
; APPLICANT: Gilman, Alfred G.
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL
; CYCLASE AND USES THEREFOR
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/538,815
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSD:450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1180 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-538-815-12

Query Match 75.8%; Score 432; DB 9; Length 1180;
Best Local Similarity 79.4%; Pred. No. 4.6e-33;
Matches 81; Conservative 7; Mismatches 12; Indels 2; Gaps 2;
QY 1 MSWFGLLVPKVDERTKAWGNGOKRRRGTRAGGCTPRYMNSCLRDAPPSPTPAGP 60
DB 15 MSWFGLLVPKVDERTKAWGNGOKRRP-RQATRRAGFCAPRYMSCLKNVPPSPPTPAAR 73
QY 61 PRCPWQDDAFIRRGCPXKXGKLGRLRAVALGFEDTEVTTTTPAG 102
DB 74 TRCPWQDEAFIRRAGPGRGVELGLRLSVALGFDDETEV-TTPMG 114

RESULT 12
US-09-791-537-17912
; Sequence 17912, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN MEMBR
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17912
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Rattus norvegicus

US-09-791-537-17912

Query Match 75.8%; Score 432; DB 21; Length 1180;
Best Local Similarity 79.4%; Pred. No. 4.6e-33;
Matches 81; Conservative 7; Mismatches 12; Indels 2; Gaps 2;
QY 1 MSWFGLLVPKVDERTKAWGNGOKRRRGTRAGGCTPRYMNSCLRDAPPSPTPAGP 60
DB 15 MSWFGLLVPKVDERTKAWGNGOKRRP-RQATRRAGFCAPRYMSCLKNVPPSPPTPAAR 73
QY 61 PRCPWQDDAFIRRGCPXKXGKLGRLRAVALGFEDTEVTTTTPAG 102
DB 74 TRCPWQDEAFIRRAGPGRGVELGLRLSVALGFDDETEV-TTPMG 114

RESULT 13
US-09-791-537-126174
; Sequence 126174, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY M
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 126174
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-791-537-126174

Query Match 75.8%; Score 432; DB 21; Length 1180;
Best Local Similarity 79.4%; Pred. No. 4.6e-33;
Matches 81; Conservative 7; Mismatches 12; Indels 2; Gaps 2;
QY 1 MSWFGLLVPKVDERTKAWGNGOKRRRGTRAGGCTPRYMNSCLRDAPPSPTPAGP 60
DB 15 MSWFGLLVPKVDERTKAWGNGOKRRP-RQATRRAGFCAPRYMSCLKNVPPSPPTPAAR 73
QY 61 PRCPWQDDAFIRRGCPXKXGKLGRLRAVALGFEDTEVTTTTPAG 102
DB 74 TRCPWQDEAFIRRAGPGRGVELGLRLSVALGFDDETEV-TTPMG 114

RESULT 14
US-09-791-537-34515
; Sequence 34515, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY M
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34515
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-34515

Query Match 75.6%; Score 431; DB 21; Length 1166;
Best Local Similarity 79.4%; Pred. No. 5.7e-33;
Matches 81; Conservative 5; Mismatches 14; Indels 2; Gaps 2;
QY 1 MSWFGLLVPKVDERTKAWGNGOKRRRGTRAGGCTPRYMNSCLRDAPPSPTPAGP 60

Db 1 MSWFSGLLVPKVDERTANGERNQGRK-RHANRSGFCAPRYMSCLNNAPSPPTAAH 59
 QY 61 PRCPWQDDAFIRRGKPKGKGLRAVALGFEDTEVTTTTPAG 102
 Db 60 TRCPWQDEAFIRRGKPKGKGLRAVALGFEDTEVTTTTPAG 100

RESULT 15

US-09-791-537-18463
 ; Sequence 18463, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Danzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 18463
 ; LENGTH: 1166
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-09-791-537-18463

Query Match 75.1%; Score 428; DB 21; Length 1166;
 Best Local Similarity 78.4%; Pred. No. 1.1e-32;
 Matches 80; Conservative 8; Mismatches 12; Indels 2; Gaps 2;

QY 1 MSWFSGLLVPKVDERTANGERNQGRKRRRGTTRAGGCTPRYMSCLRDAPSPPTAGP 60
 Db 1 MSWFSGLLVPKVDERTANGERNQGRK-RQATRARGFCAPRYMSCLKNVPPSPPTAAR 59
 QY 61 PRCPWQDDAFIRRGKPKGKGLRAVALGFEDTEVTTTTPAG 102
 Db 60 TRCPWQDEAFIRRGKPKGKGLRAVALGFEDTEVTTTTPAG 100

Search completed: February 19, 2003, 15:42:03
 Job time : 357 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 19, 2003, 15:35:23 ; Search time 30 Seconds
(without alignments)
88.569 Million cell updates/sec

Title: US-09-750-240-2
Perfect score: 570
Sequence: 1 MSWFGLLVPKVDKRTAMG.....RAVALGFEDTEVTTTAPGPL 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues
Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published_Applications_AA.*
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 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US05_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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 - 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	568	99.6	104	10	US-09-750-240-2
2	545	95.6	1167	10	US-09-750-240-6
3	545	95.6	1167	10	US-09-750-240-13
4	545	95.6	1168	9	US-10-201-000-2
5	545	95.6	1168	10	US-09-750-240-11
6	77.5	13.6	213	9	US-09-975-719-27
7	73.5	12.9	1234	10	US-09-854-173A-12
8	72	12.6	232	9	US-10-060-523-9
9	72	12.6	232	9	US-09-935-726-7
10	72	12.6	232	9	US-10-084-488-7
11	72	12.6	232	10	US-09-795-006A-147
12	72	12.6	232	12	US-10-127-551-5
13	71.5	12.5	722	10	US-09-894-998-15
14	70	12.3	156	10	US-09-764-870-402
15	70	12.3	402	10	US-09-933-561-16
16	69	12.1	160	10	US-09-864-761-38608
17	69	12.1	173	10	US-09-867-550-1072
18	67.5	11.8	468	10	US-09-814-777A-2
19	67.5	11.8	468	10	US-09-814-777A-4

20	67	11.8	325	10	US-09-927-112-10	Sequence 10, Appl
21	67	11.8	427	9	US-10-007-132-4	Sequence 4, Appli
22	67	11.8	1207	10	US-09-927-112-2	Sequence 2, Appli
23	66.5	11.7	802	9	US-10-174-590-312	Sequence 312, App
24	66.5	11.7	802	9	US-10-176-758-312	Sequence 312, App
25	66.5	11.7	802	9	US-10-175-737-312	Sequence 312, App
26	66.5	11.7	802	9	US-10-173-706-312	Sequence 312, App
27	66.5	11.7	802	9	US-10-175-738-312	Sequence 312, App
28	66.5	11.7	802	9	US-10-175-752-312	Sequence 312, App
29	66.5	11.7	802	9	US-10-176-482-312	Sequence 312, App
30	66.5	11.7	802	9	US-10-176-757-312	Sequence 312, App
31	66.5	11.7	802	9	US-10-176-913-312	Sequence 312, App
32	66.5	11.7	802	9	US-10-180-553-312	Sequence 312, App
33	66.5	11.7	802	9	US-10-180-557-312	Sequence 312, App
34	66.5	11.7	802	9	US-10-173-700-312	Sequence 312, App
35	66.5	11.7	802	9	US-10-174-572-312	Sequence 312, App
36	66.5	11.7	802	9	US-10-174-579-312	Sequence 312, App
37	66.5	11.7	802	9	US-10-174-582-312	Sequence 312, App
38	66.5	11.7	802	9	US-10-174-588-312	Sequence 312, App
39	66.5	11.7	802	9	US-10-175-739-312	Sequence 312, App
40	66.5	11.7	802	9	US-10-175-740-312	Sequence 312, App
41	66.5	11.7	802	9	US-10-175-743-312	Sequence 312, App
42	66.5	11.7	802	9	US-10-176-488-312	Sequence 312, App
43	66.5	11.7	802	9	US-10-176-492-312	Sequence 312, App
44	66.5	11.7	802	9	US-10-176-747-312	Sequence 312, App
45	66.5	11.7	802	9	US-10-176-750-312	Sequence 312, App

ALIGNMENTS

RESULT 1
US-09-750-240-2
; Sequence 2, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(104)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-750-240-2

Query Match 99.6%; Score 568; DB 10; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.3e-51;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSWFGLLVPKVDKRTAMGKRRRGTRAGGCTPRYNCLRDAPPSPTPAGP 60

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Database Release #1.0 Version 4.3

100

Search completed: February 19, 2003, 15:43:08
Job time : 31 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 19, 2003, 15:32:53 ; Search time 15 Seconds
(without alignments)
203.999 Million cell updates/sec

Title: US-09-750-240-2
Perfect score: 570
Sequence: 1 MSWFGSLVPRVKRTANG.....RAVALGFEDTEVTTPAGPL 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA: *
1: /cgn2.6/ptodata/1/1aa/5A_COMB.pep: *
2: /cgn2.6/ptodata/1/1aa/5B_COMB.pep: *
3: /cgn2.6/ptodata/1/1aa/6A_COMB.pep: *
4: /cgn2.6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2.6/ptodata/1/1aa/PCTUS_COMB.pep: *
6: /cgn2.6/ptodata/1/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	568	99.6	104	US-09-008-097-2	Sequence 2, Appli
2	545	95.6	1167	US-09-008-097-6	Sequence 6, Appli
3	545	95.6	1168	US-09-474-076-2	Sequence 2, Appli
4	472.5	82.9	1165	US-08-240-357-2	Sequence 2, Appli
5	432	75.8	1180	US-08-726-214-12	Sequence 12, Appli
6	78.5	13.8	465	US-08-447-965A-2	Sequence 2, Appli
7	77.5	13.6	213	US-09-199-637A-27	Sequence 27, Appli
8	74	13.0	233	US-08-458-568A-4	Sequence 4, Appli
9	73	12.8	223	US-09-206-676C-1	Sequence 1, Appli
10	72	12.6	231	PCT-US96-09001-10	Sequence 10, Appli
11	72	12.6	232	US-08-999-811-7	Sequence 7, Appli
12	72	12.6	232	US-08-824-996-9	Sequence 9, Appli
13	72	12.6	232	US-08-807-992B-4	Sequence 4, Appli
14	72	12.6	232	US-09-042-105-7	Sequence 7, Appli
15	72	12.6	422	US-09-724-864-45	Sequence 45, Appli
16	71.5	12.5	226	US-09-206-676C-2	Sequence 2, Appli
17	70	12.3	180	US-08-483-533-29	Sequence 29, Appli
18	70	12.3	180	US-09-283-471A-29	Sequence 29, Appli
19	70	12.3	355	US-08-483-533-41	Sequence 41, Appli
20	70	12.3	355	US-09-283-471A-41	Sequence 41, Appli
21	70	12.3	355	PCT-US91-06532-3	Sequence 3, Appli
22	70	12.3	402	US-09-292-097-16	Sequence 16, Appli
23	69.5	12.2	1312	US-09-041-886-19	Sequence 19, Appli
24	69.5	12.2	2205	US-08-093-453B-2	Sequence 2, Appli
25	69	12.1	610	US-08-865-337A-6	Sequence 6, Appli
26	68	11.9	1323	US-08-026-138E-4	Sequence 4, Appli
27	67	11.8	427	US-09-199-737-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-008-097-2
: Sequence 2, Application US/09008097
: Patent No. 6306830
: GENERAL INFORMATION:
: APPLICANT: Hammond, H. Kirk
: APPLICANT: Insel, Paul A.
: APPLICANT: Ping, Peipei
: APPLICANT: Post, Steven R.
: APPLICANT: Gao, Meihua
: TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
: TITLE OF INVENTION: HEART FAILURE
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 PAGE MILL ROAD
: CITY: PALO ALTO
: STATE: CA
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/008,097
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Dylvan, Tyler M
: REGISTRATION NUMBER: 37,612
: REFERENCE/DOCKET NUMBER: 22000-20567.21
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-813-5600
: TELEFAX: 650-494-0792
: TELEX: 706141
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 104 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FRAGMENT TYPE: internal
US-09-008-097-2

28	67	11.8	427	4	US-08-900-230-4	Sequence 4, Appli
29	67	11.8	427	4	US-09-058-333A-4	Sequence 4, Appli
30	66	11.6	732	1	US-08-317-522A-5	Sequence 5, Appli
31	66	11.6	778	1	US-08-439-818A-5	Sequence 5, Appli
32	66	11.6	778	2	US-08-751-965-5	Sequence 5, Appli
33	66	11.6	778	2	US-08-738-975-5	Sequence 5, Appli
34	66	11.6	778	3	US-08-728-626-5	Sequence 5, Appli
35	65.5	11.5	284	2	US-08-808-599A-5	Sequence 5, Appli
36	65.5	11.5	284	3	US-08-589-028-6	Sequence 6, Appli
37	65.5	11.5	284	3	US-08-784-582-6	Sequence 6, Appli
38	65.5	11.5	284	4	US-08-785-271-6	Sequence 6, Appli
39	65.5	11.5	284	4	US-09-031-898-2	Sequence 2, Appli
40	65.5	11.5	659	1	US-08-240-049B-16	Sequence 16, Appli
41	65.5	11.5	659	1	US-08-259-148A-20	Sequence 20, Appli
42	65.5	11.5	659	1	US-08-484-054-20	Sequence 20, Appli
43	65.5	11.5	659	2	US-07-876-941A-20	Sequence 20, Appli
44	65.5	11.5	659	4	US-08-477-292-14	Sequence 14, Appli
45	65.5	11.5	659	4	US-08-477-292-14	Sequence 14, Appli

US-09-474-076-2 ; Sequence 2, Application US/09474076
; Patent No. 6465237

```

: GENERAL INFORMATION:
: APPLICANT: Tomlinson, James E.
: APPLICANT: COR Therapeutics, Inc.
: TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL

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; FILE REFERENCE: 44101 0000 001 000
; CURRENT APPLICATION NUMBER: US/09/474,076
; CURRENT FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694

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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1168
; TYPE: PRT
; ORGANISM: human type VI adenylyl cyclase
US-09-474-076-2

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Query Match	95.68;	Score 545;	DB 4;	Length 1168;
Best Local Similarity	97.1%;	Pred. No. 1.7e-52;		
Matches 99;	Conservative	0;	Mismatches 3;	Indels 0;
			Gaps	0;

QY	1	MSWFGLLVPKVDERTKWTAWGERNQKRSRRRGTRAGGCTPRYMSCLRDAEPPSPTPAGP	60
Db	1	MSWFGLLVPKVDERTKWTAWGERNQKRSRRRGTRAGGCTPRYMSCLRDAEPPSPTPAGP	60
QY	61	PRCPWDDAFIRRGPGXGKELGLRAVALGFEDTEVTTT	102
Db	61	PRCPWDDAFIRRGPGXGKELGLRAVALGFEDTEVTTT	102

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RESULT 4
US-08-240-357-2
; Sequence 2, Application US/08240357
; Patent No. 5578481
; GENERAL INFORMATION:
; APPLICANT: Ishikawa, Yoshihiro
; TITLE OF INVENTION: Cloning and Characterization of a
; TITLE OF INVENTION: Cardiac Adenylyl Cyclase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,357
; FILING DATE: 10-MAY-1994

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; SOFTWARE: PatentLin Release #1.0, version #1.2.
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; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/240,357
;   FILING DATE: 10-MAY-1994

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CLASSIFICATION: 455
ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Alan M.
REGISTRATION NUMBER: 30.637

REFERENCE/DOCKET NUMBER: 31,705-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3244

```

QY   61  PRCPWQDAFIRRGPGPKXGKELGRVALGFEDTETVTTTAG 102
      |||||:||||| || : | |||||:|||||:||||| ||| |
Db    74  TRCPWQDEAFIRRAGPGRGVGLRLSRVALGFDDTEV-TTPMG 114

RESULT 6
US-08-447-965A-2
; Sequence 2, Application US/08447965A
; Patent No. 5776692
; GENERAL INFORMATION:
; APPLICANT: El-zaatari, Fouad A.K.
; APPLICANT: Graham, David Y.
; APPLICANT: Naser, Saleh
; TITLE OF INVENTION: Mycobacterial Genus-Specific DNA Probe
; TITLE OF INVENTION: and its Expressed Product
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 801 Pennsylvania Ave. N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,965A
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Davis, Peter J.
; REGISTRATION NUMBER: 36,119
; REFERENCE/DOCKET NUMBER: 311.019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-662-4669
; TELEFAX: 202-662-4643
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 465 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-447-965A-2

Query Match          13.8%   Score 78.5; DB 1; Length 465
Best Local Similarity 37.5%; Pred. No. 0.56;
Matches 30; Conservative 4; Mismatches 35; Indels

QY   13  DERKTAWGERNGKRRRRTTRAGGCTPRYMYSCLURDAEPPS-----PTTPAGPPP
      |: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    99  DQDQGADARANRPAPHARRRTRA--IAMPASAAS--TSAAPPSHRAALSAAAGPPP
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QY   68  DAFTIRRGPGPKXGKELGRAV 87
      | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   153  PAAGRROGERRRVGLGAAV 172

RESULT 7
US-09-199-637A-27
; Sequence 27, Application US/09199637A
; Patent No. 6355411
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick
; APPLICANT: Goodman, Howard M.
; APPLICANT: Rahme, Laurence G.
; APPLICANT: Mahajan-Miklos, Shalina
; APPLICANT: Tan, Man-Wah
; APPLICANT: Cao, Hui
; APPLICANT: Drenkard, Elliana

```

```

; APPLICANT: Tsongalis, John
; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; FILE REFERENCE: 00786/361002
; CURRENT APPLICATION NUMBER: US/09/199,637A
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,517
; PRIOR FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-27

Query Match      13.6%; Score 77.5; DB 4; Length 213;
Best Local Similarity 32.6%; Pred. No. 0.3;
Matches 29; Conservative 8; Mismatches 29; Indels 23; Gaps 6;

Qy 8 LVPKYDERKTAWGER-NGQKRSRR------GTRAGGCTPRYMSCL-----RDABPP 53
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 104 LTPEGARTRTRTERPNRLAKSASRPKLLPASATNIRG-----RYMASIWQMLVRDAD-- 157

Qy 54 SPTPAGPPRCQDDAFIRRGPKXKGL 82
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Db 158 LPEPVGPKMKPW---AFTCRSLLNGSKV 183

RESULT 8
US-08-458-568A-4
; Sequence 4, Application US/08458568A
; Patent No. 5821339
; GENERAL INFORMATION:
; APPLICANT: Schaffer, Priscilla A.
; APPLICANT: Yeh, Lily
; TITLE OF INVENTION: Compositions and Methods for Treatment of Herpesvirus
; TITLE OF INVENTION: Infections
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,568A
; FILING DATE: 02-JUNE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/065,146
; FILING DATE: 05-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn R.
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: DFCI-0029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-568A-4
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Query Match      13.0%; Score 74; DB 2; Length 233;
Best Local Similarity 26.2%; Pred. No. 0.81;
Matches 32; Conservative 3; Mismatches 41; Indels 46; Gaps 3;

Qy 28 SRRRGTRAGGCTPRYMSCLRDAPPSPTPAGPPR-----
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Db 88 TRRRRRGRGRRKREGGWEGSAPPPGTPGGGGRGAAAVGRASGADSGGLSGQSSS 147
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 63 -----CPWQDDAFIRRGPKXKGLGLRAVA-----LGFE---DTEVTTTPA 101
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 148 SSSSDADSGTWSHWRSSSEQEGGPPAGGGGAAAGALLTAGSELGVEVTWDCAVGTAPV 207
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 102 GP 103
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Db 208 GP 209

RESULT 9
US-09-206-676C-1
; Sequence 1, Application US/09206676C
; Patent No. 6383738
; GENERAL INFORMATION:
; APPLICANT: BRUNI, RENATO
; APPLICANT: ROIZMAN, BERNARD
; TITLE OF INVENTION: HERPES SIMPLEX VIRUS ORF P IS A REPRESSOR OF VIRAL
; TITLE OF INVENTION: PROTEIN SYNTHESIS
; FILE REFERENCE: ARCD:306
; CURRENT APPLICATION NUMBER: US/09/206,676C
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 223
; TYPE: PRT
; ORGANISM: HERPES VIRUS, TYPE 1
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (97)
; OTHER INFORMATION: Xaa - Any Set Containing N
; NAME/KEY: UNSURE
; LOCATION: (176)
; OTHER INFORMATION: Xaa - Any Set Containing N
US-09-206-676C-1

Query Match      12.8%; Score 73; DB 4; Length 223;
Best Local Similarity 23.3%; Pred. No. 1;
Matches 37; Conservative 5; Mismatches 47; Indels 70; Gaps 5;

Qy 15 RKTAWGE-----RNGQKR-----SRRRGTRAGGCTPRYMSCLRDA 50
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Db 39 RTRTWGEXRTRAGVAGSGAPSPPARRRRRRARCASVTRRRRRARRGRRKREGGWEXA 98
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 51 EPPSPTPAGPPR-----
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 99 PPGPAPGGDGRGAAAVGRASGSGGLSGQSSSSSDADSGTWSHWRSSSEQEGG 158
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Qy 75 GPXKXKGLGLRAVA-----LGFE---DTEVTTTPAGP 103
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 159 GPPAGGGGAAAGALLTXGSELGVEVTWDCAVGTAPVGP 197

RESULT 10
PCT-US96-09001-10
; Sequence 10, Application PC/TUS9609001
; GENERAL INFORMATION:
; APPLICANT: HU, ET AL.
; TITLE OF INVENTION: Human Vascular EndothelialGrowth Factor 2
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
```


GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 19, 2003, 15:23:18 ; Search time 36 Seconds
(without alignments)
384,946 Million cell updates/sec

Title: US-09-750-240-2

Perfect score: 570

Sequence: 1 MSWFSGLLPVKVDKRTAMG.....RAVALGFEDTEVTTTAPAGPL 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	568	99.6	104	AAE04308	Human partial card
2	568	99.6	709	AAW53345	Human adenylycycl
3	545	95.6	1167	AAE04310	Human cardiac aden
4	545	95.6	1167	AAE04312	Human modified car
5	545	95.6	1168	AAW30599	Human type VI aden
6	545	95.6	1168	AAE04311	Human cardiac aden
7	472.5	82.9	1165	AAE04309	Cardiac adenylyl c
8	432	75.8	1165	ABB57257	Mouse ischaemic co
9	432	75.8	1180	AAH02010	Type VI adenylyl c
10	87	15.3	319	AAW18658	Fragmented human N

11	84	14.7	55	22	ABG16750	Novel human diagno
12	81	14.2	370	21	AAG35230	zea mays protein f
13	80.5	14.1	782	23	ABP60967	Novel human protei
14	78.5	13.8	465	19	AAW60723	36K antigen of Myc
15	78.5	13.8	1076	22	ABG10930	Novel human diagno
16	78.5	13.8	2348	22	ABG10929	Novel human diagno
17	78	13.7	142	22	ABG27722	Novel human diagno
18	77.5	13.6	213	20	AAV29113	Amino acid sequenc
19	77.5	13.6	356	21	AAG35231	zea mays protein f
20	76	13.3	338	13	AAE21107	HSV-1 (MGH-10) ICP
21	75	13.2	104	22	AAE95652	Human protein sequ
22	74.5	13.1	104	22	ABG13930	Novel human diagno
23	74	13.0	233	16	AAE64327	HSV L/St Orf1. He
24	73.5	12.9	125	22	AAO01472	Human polypeptide
25	73.5	12.9	142	22	AAO12919	Human polypeptide
26	73.5	12.9	282	22	AAE03414	Human gene 10 enco
27	73.5	12.9	536	21	AAE84592	Amino acid sequenn
28	73.5	12.9	1202	22	AAW78807	Human protein SEQ
29	73.5	12.9	1239	21	AAE42729	Human ORF ORF2493
30	73.5	12.9	1240	22	AAU30861	Novel human secret
31	73.5	12.9	1334	22	AAW79791	Human protein SEQ
32	73.5	12.9	1416	22	AAU30862	Novel human secret
33	73	12.8	512	23	AAE19558	Herpes simplex vir
34	73	12.8	774	23	AAE14512	GST-Herpes simplex
35	73	12.8	830	22	ABG08145	Novel human diagno
36	72.5	12.7	110	22	AAW79915	Human protein SEQ
37	72.5	12.7	151	22	AAW79915	Human protein SEQ
38	72.5	12.7	168	23	ABG64813	Human albumin fusi
39	72.5	12.7	168	23	AAU96179	Human secreted pro
40	72.5	12.7	414	22	AAU32999	Novel human secret
41	72.5	12.7	459	22	AAU20370	Human secreted pro
42	72.5	12.7	940	22	AAW40068	Human polypeptide
43	72	12.6	232	16	AAE91078	Human vascular end
44	72	12.6	232	17	AAE94004	VEGF206
45	72	12.6	232	19	AAW62527	Amino acid sequenc

ALIGNMENTS

RESULT 1

AAE04308

ID AAE04308 standard; Protein; 104 AA.

XX AAE04308;

AC AAE04308;

XX 04-SEP-2001 (first entry)

DT 04-SEP-2001 (first entry)

XX Human partial cardiac adenylycyclase VI (ACVI) isoform #1.

DE Human; cardiant; beta-adrenergic signalling protein; beta-ASP;

XX myocardiun; gene therapy; beta-adrenergic receptor; beta-AR;

KW adenylylycyclase; adenylylate cyclase; cAMP synthetase;

KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;

KW cardiac adenylycyclase VI; ACVI isoform; beta-ASP transgene.

XX Homo sapiens.

XX Homo sapiens.

XX Key Location/Qualifiers

PH Key Location/Qualifiers

FT Misc-difference 77

FT /label= Unknown

FT /note= "Encoded by NGC"

XX WO200148164-A2.

XX 05-JUL-2001.

XX 26-DEC-2000; 2000WO-US35411.

XX 27-DEC-1999; 99US-0472667.

XX (REGC) UNIV CALIFORNIA.

XX

```

PI Hammond HK, Gao M;
XX WPI; 2001-418260/44.
DR N-PSDB; AAD08561.
XX Novel polynucleotide encoding a modified adenylyl cyclase polypeptide
PT useful for enhancing cardiac function in mammalian hearts, and for
PT treating heart disease, especially congestive heart failure -
XX Example 5; Page 115; 153pp; English.
XX The present invention relates to methods and compositions for enhancing
CC cardiac function in mammalian hearts by inserting transgenes encoding
CC beta-adrenergic signalling proteins (beta-ASP) which increase
CC beta-adrenergic responsiveness within the myocardium using in vivo
CC gene therapy. The beta-ASPs of the invention include beta-adrenergic
CC receptors (beta-AR), adenylyl cyclases (also referred as adenylyl cyclase,
CC adenylylate cyclase and cAMP synthetase) and G-protein receptor kinase
CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
CC in mammalian hearts and for treating heart disease, especially
CC congestive heart failure. The present sequence is a human
CC partial cardiac adenylyl cyclase VI (ACVI) isoform which is used for
CC generating a third beta-ASP transgene, used in the exemplification
CC of the invention.
XX Sequence 104 AA;
SQ Query Match 99.6%; Score 568; DB 22; Length 104;
Best Local Similarity 100.0%; Pred. No. 6.2e-55;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSWFSGLLVKPKVDERTKATWGERNGQKRSRRGCTPRYMSCLRDAPPSPTPAGP 60
Db 1 MSWFSGLLVKPKVDERTKATWGERNGQKRSRRGCTPRYMSCLRDAPPSPTPAGP 60
Qy 61 PRCPWQDDAFIRRGPGPKXGKELGLRAVALGFEDTEVTTTPAGPL 104
Db 61 PRCPWQDDAFIRRGPGPKXGKELGLRAVALGFEDTEVTTTPAGPL 104
RESULT 2
AAW53345
ID AAW53345 standard; Protein; 709 AA.
XX AC AAW53345;
XX DT 17-JUL-1998 (first entry)
XX DE Human adenylyl cyclase isoform VI.
XX KW Human; adenylyl cyclase VI; AC-VI; beta-adrenergic signalling protein;
KW transgene; gene therapy; congestive heart failure; cardiac function;
KW adenovirus.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 77 /label= unknown
FT FT /note= "encoded by NGC"
FT Misc-difference 105 /label= unknown
FT FT /note= "encoded by AAN where N indicates a gap of 0.5 kb"
FT FT
PN WO9810085-A2.
XX 12-MAR-1998.
XX 05-SEP-1997; 97WO-US15610.
XX 16-JUN-1997; 97US-0048933.
XX 05-SEP-1996; 96US-0708661.
XX

```

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PA (COLL-) COLLATERAL THERAPEUTICS.
PA (REGC ) UNIV CALIFORNIA.
PI Gao M, Hammond HK, Insel PA, Ping P, Post SR;
XX WPI; 1998-193633/17.
DR N-PSDB; AAV23246.
XX Vectors containing transgene(s) encoding beta-adrenergic signalling
PT proteins - useful for gene therapy of congestive heart failure
XX Claim 62; Fig 12B; 114pp; English.
XX The present sequence represents human adenylyl cyclase isoform VI (AC-VI)
CC from the present invention. The present invention describes a
CC recombinant replication-defective viral particle (I) comprising a gene
CC encoding a beta-adrenergic signalling protein (beta-ASP) operably
CC linked to a promoter. Also described are: (1) a recombinant pro-viral
CC plasmid (Ia) comprising a gene encoding a beta-ASP, as above, operably
CC linked to a promoter and further comprising a replication-defective
CC viral genome; (2) a (mammalian) cell transfected with (I) or (Ia); (3)
CC an isolated polynucleotide comprising a sequence encoding a human
CC adenylyl cyclase isoform VI (AC-VI), or a variant having AC activity;
CC (4) a human AC-VI encoded by (3); (5) an isolated polynucleotide
CC sequence which hybridises at high stringency to (3); and (6) a vector
CC comprising the polynucleotide of (3). (I) can be used to form a
CC filtered adenovirus particle preparation. (I) is used to enhance
CC cardiac function in mammals.
XX Sequence 709 AA;
SQ Query Match 99.6%; Score 568; DB 19; Length 709;
Best Local Similarity 100.0%; Pred. No. 5.3e-54;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSWFSGLLVKPKVDERTKATWGERNGQKRSRRGCTPRYMSCLRDAPPSPTPAGP 60
Db 1 MSWFSGLLVKPKVDERTKATWGERNGQKRSRRGCTPRYMSCLRDAPPSPTPAGP 60
Qy 61 PRCPWQDDAFIRRGPGPKXGKELGLRAVALGFEDTEVTTTPAGPL 104
Db 61 PRCPWQDDAFIRRGPGPKXGKELGLRAVALGFEDTEVTTTPAGPL 104
RESULT 3
AAE04310
ID AAE04310 standard; Protein; 1167 AA.
XX AC AAE04310;
XX DT 04-SEP-2001 (first entry)
XX DE Human cardiac adenylyl cyclase VI (ACVI) isoform #1.
XX KW Human; cardiac; beta-adrenergic signalling protein; beta-ASP;
KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;
KW adenylyl cyclase; adenylylate cyclase; cAMP synthetase;
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;
KW cardiac adenylyl cyclase VI; ACVI isoform; beta-ASP transgene.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 77 /label= unknown
FT FT /note= "encoded by NGC"
FT Misc-difference 105 /label= unknown
FT FT /note= "encoded by AAN where N indicates a gap of 0.5 kb"
FT FT
PN WO200148164-A2.
XX 05-JUL-2001.
XX 26-DEC-2000; 2000WO-US35411.
XX 27-DEC-1999; 99US-0472667.
XX (REGC ) UNIV CALIFORNIA.
XX Hammond HK, Gao M;
PI

```

XX WPI; 2001-418260/44.
 DR N-PSDB; AAD08563.
 XX
 PT Novel polynucleotide encoding a modified adenylylcyclase polypeptide
 PT useful for enhancing cardiac function in mammalian hearts, and for
 PT treating heart disease, especially congestive heart failure -
 XX
 PS Example 5; Page 130-133; 153pp; English.
 XX
 CC The present invention relates to methods and compositions for enhancing
 CC cardiac function in mammalian hearts by inserting transgenes encoding
 CC beta-adrenergic signalling proteins (beta-ASP) which increase
 CC beta-adrenergic responsiveness within the myocardium using in vivo
 CC gene therapy. The beta-ASPs of the invention include beta-adrenergic
 CC receptors (beta-AR), adenylylcyclases (also referred as adenylylcyclase,
 CC adenylylate cyclase and CAMP synthetase) and G-protein receptor kinase
 CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
 CC in mammalian hearts and for treating heart disease, especially
 CC congestive heart failure. The present sequence is a human
 CC cardiac adenylylcyclase VI (ACVI) isoform which is used for generating
 CC a third beta-ASP transgene, used in the exemplification
 CC of the invention.
 XX
 SQ Sequence 1167 AA;
 Query Match 95.6%; Score 545; DB 22; Length 1167;
 Best Local Similarity 97.1%; Pred. No. 3.1e-51;
 Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MSWFSGLLPKVDERTANGERNQKRRRRGTRAGGCTTPRYMSCLRDAEPSPPTPAG 60
 Db 1 MSWFSGLLPKVDERTANGERNQKRRRRGTRAGGCTTPRYMSCLRDAEPSPPTPAG 60
 QY 61 PRCPWDDAFIRRGPGKGKGLRAVALGFEDTEVTTT 102
 Db 61 PRCPWDDAFIRRGPGKGKGLRAVALGFEDTEVTTT 102
 RESULT 4
 AAE04312
 ID AAE04312 standard; Protein; 1167 AA.
 AC AAE04312;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human modified cardiac adenylylcyclase VI (ACVI) isoform.
 XX
 KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;
 KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;
 KW adenylylcyclase; adenylylate cyclase; CAMP synthetase;
 KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;
 KW cardiac adenylylcyclase VI; ACVI isoform; beta-ASP transgene.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200148164-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US35411.
 XX
 PR 27-DEC-1999; 99US-0472667.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Hammond HK, Gao M;
 XX
 DR WPI; 2001-418260/44.
 DR N-PSDB; AAD08568.
 XX

PT Novel polynucleotide encoding a modified adenylylcyclase polypeptide
 PT useful for enhancing cardiac function in mammalian hearts, and for
 PT treating heart disease, especially congestive heart failure -
 XX
 PS Claim 3; Page 150-153; 153pp; English.
 XX
 CC The present invention relates to methods and compositions for enhancing
 CC cardiac function in mammalian hearts by inserting transgenes encoding
 CC beta-adrenergic signalling proteins (beta-ASP) which increase
 CC beta-adrenergic responsiveness within the myocardium using in vivo
 CC gene therapy. The beta-ASPs of the invention include beta-adrenergic
 CC receptors (beta-AR), adenylylcyclases (also referred as adenylylcyclase,
 CC adenylylate cyclase and CAMP synthetase) and G-protein receptor kinase
 CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
 CC in mammalian hearts and for treating heart disease, especially
 CC congestive heart failure. The present sequence is a human
 CC modified cardiac adenylylcyclase VI (ACVI) isoform which is used for
 CC generating a beta-ASP transgene, used in the exemplification of the
 CC invention.
 XX
 SQ Sequence 1167 AA;
 Query Match 95.6%; Score 545; DB 22; Length 1167;
 Best Local Similarity 97.1%; Pred. No. 3.1e-51;
 Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MSWFSGLLPKVDERTANGERNQKRRRRGTRAGGCTTPRYMSCLRDAEPSPPTPAG 60
 Db 1 MSWFSGLLPKVDERTANGERNQKRRRRGTRAGGCTTPRYMSCLRDAEPSPPTPAG 60
 QY 61 PRCPWDDAFIRRGPGKGKGLRAVALGFEDTEVTTT 102
 Db 61 PRCPWDDAFIRRGPGKGKGLRAVALGFEDTEVTTT 102
 RESULT 5
 AAW30599
 ID AAW30599 standard; Protein; 1168 AA.
 AC AAW30599;
 XX
 DT 21-MAY-1999 (first entry)
 XX
 DE Human type VI adenylyl cyclase.
 XX
 KW Adenylyl cyclase type VI; human; hAC6; therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO9901547-A1.
 XX
 PD 14-JAN-1999.
 XX
 PF 01-JUL-1998; 98WO-US13694.
 XX
 PR 01-JUL-1997; 97US-0886550.
 PR 01-JUL-1997; 97US-0070904.
 XX
 PA (CORP-) COR THERAPEUTICS INC.
 XX
 PI Tomlinson JA;
 XX
 DR WPI; 1999-106049/09.
 DR N-PSDB; AAX00461.
 XX
 PT Newly isolated and purified human type VI adenylyl cyclase (hAC6)
 PT polypeptide - useful for identifying potential therapeutic agents
 PT that modulate hAC6 activity, and for the diagnosis of
 PT hAC6-associated diseases and disorders
 XX
 PS Claim 1; Fig 1A-G; 42pp; English.
 XX
 CC This is the amino acid sequence of human type VI adenylyl cyclase

CC (hac6), as deduced from an isolated cDNA clone sequence (see
 CC AAX00461). hac6 is expressed mainly in the heart and brain. It has
 CC a similar putative structure to other adenylyl cyclase isoforms
 CC but, like type V, is distinguishable in that it has a larger
 CC N-terminus and a relatively shorter C-terminus as it lacks the C2b
 CC region. The invention relates to the hac6 gene, methods for the
 CC recombinant production of purified hac6 and the proteins made by
 CC these methods, antibodies against hac6, vectors, probes and host
 CC cells (especially HBK-293) transformed by genes encoding
 CC polypeptides having hac6 activity, along with diagnostic and
 CC therapeutic uses for these various reagents. hac6 can be used as a
 CC tool to screen for agonists and antagonists that stimulate/inhibit
 CC hac6. Such compounds have therapeutic utility in treating diseases
 CC caused by aberrant activity of this enzyme, and diseases whose
 CC symptoms can be ameliorated by stimulating or inhibiting the
 CC activity of hac6.
 XX
 SQ Sequence 1168 AA;
 Query Match 95.6%; Score 545; DB 20; Length 1168;
 Best Local Similarity 97.1%; Pred. No. 3.1e-51;
 Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MSWFGLLVPKVDERTKATWGERNGQKRRRGTRAGGCTPRYMSCLRDAPPSPPTAGP 60
 DB 1 MSWFGLLVPKVDERTKATWGERNGQKRRRGTRAGGCTPRYMSCLRDAPPSPPTAGP 60
 QY 61 PRCPQDDAFIRRGPGKXGKGLGRAVALGFEDTEVTTTTPAG 102
 DB 61 PRCPQDDAFIRRGPGKXGKGLGRAVALGFEDTEVTTTTPAG 102
 RESULT 6
 ID AAE04311 standard; Protein; 1168 AA.
 AC AAE04311;
 DT 04-SEP-2001 (first entry)
 DE Human cardiac adenylyl cyclase VI (ACVI) isoform #2.
 KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;
 KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;
 KW adenylyl cyclase; adenylylate cyclase; CAMP synthetase;
 KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;
 KW cardiac adenylyl cyclase VI; ACVI isoform; beta-ASP transgene.
 OS Homo sapiens.
 XX WO200148164-A2.
 XX 05-JUL-2001.
 XX 26-DEC-2000; 2000WO-US35411.
 XX 27-DEC-1999; 99US-0472667.
 XX (REGC) UNIV CALIFORNIA.
 XX Hammond HK, Gao M;
 XX WPI; 2001-418260/44.
 XX N-PSDB; AAD08567.
 PT Novel polynucleotide encoding a modified adenylyl cyclase polypeptide
 PT useful for enhancing cardiac function in mammalian hearts, and for
 PT treating heart disease, especially congestive heart failure -
 XX
 PS Claim 5; Page 140-143; 153pp; English.
 CC The present invention relates to methods and compositions for enhancing
 CC cardiac function in mammalian hearts by inserting transgenes encoding

CC beta-adrenergic signalling proteins (beta-ASP) which increase
 CC beta-adrenergic responsiveness within the myocardium using in vivo
 CC gene therapy. The beta-ASPs of the invention include beta-adrenergic
 CC receptors (beta-AR), adenylyl cyclases (also referred as adenylyl cyclase,
 CC adenylylate cyclase and CAMP synthetase) and G-protein receptor kinase
 CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
 CC in mammalian hearts and for treating heart disease, especially
 CC congestive heart failure. The present sequence is a human
 CC cardiac adenylyl cyclase VI (ACVI) isoform which is used for generating
 CC a fourth beta-ASP transgene, used in the exemplification
 CC of the invention.
 XX
 SQ Sequence 1168 AA;
 Query Match 95.6%; Score 545; DB 22; Length 1168;
 Best Local Similarity 97.1%; Pred. No. 3.1e-51;
 Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MSWFGLLVPKVDERTKATWGERNGQKRRRGTRAGGCTPRYMSCLRDAPPSPPTAGP 60
 DB 1 MSWFGLLVPKVDERTKATWGERNGQKRRRGTRAGGCTPRYMSCLRDAPPSPPTAGP 60
 QY 61 PRCPQDDAFIRRGPGKXGKGLGRAVALGFEDTEVTTTTPAG 102
 DB 61 PRCPQDDAFIRRGPGKXGKGLGRAVALGFEDTEVTTTTPAG 102
 RESULT 7
 ID AAR37309 standard; Protein; 1165 AA.
 AC AAR37309;
 DT 14-SEP-1993 (first entry)
 DE Cardiac adenylyl cyclase.
 KW Regulation; cardiac function; heart; heart failure.
 OS Canis familiaris.
 XX EP543137-A.
 XX 26-MAY-1993.
 XX 12-OCT-1992; 92EP-0117374.
 XX 18-NOV-1991; 91US-0793961.
 XX (AMCY) AMERICAN CYANAMID CO.
 XX Ishikawa Y;
 XX WPI; 1993-168873/21.
 XX N-PSDB; AAQ42525.
 XX Purified DNA encoding cardiac adenylyl cyclase - useful to screen
 XX for cpds. which stimulate activity of the cyclase
 XX Claim 11; Fig 2; 34pp; English.
 XX A canine heart cDNA library was constructed in lambda gt10 and was
 XX screened with a 970 bp AatI-HincII fragment from type I adenylyl
 XX cyclase cDNA probe (encodes the first cytoplasmic domain of adenylyl
 XX cyclase, which has significant homology to other previously known
 XX types of adenylyl cyclase). One positive clone, of 5.4 kb was obtd.
 XX Positive colonies were subcloned into puc18 and further subcloned
 XX and sequenced bidirectionally. The 5.4 kb clone was used to
 XX rescreen the library and on overlapping clone contg. the 5' end of
 XX the gene was isolated. Together the two clones cover the complete
 XX canine cardiac adenylyl cyclase gene. The gene is suspected of
 XX being involved in the regulation of cardiac function and it is thought
 XX that decreased activity of adenylyl cyclase in the heart may be a

Sequence	1165 AA;
SQ	

Query Match	75.8%	Score 432;	DB 21;	Length 1180;
Best Local Similarity	79.4%;	Pred. No. 9e-39;		
Matches 81: Conservative	7;	Mismatches 12;	Indels 2;	

Query Match	75.8%	Score 432;	DB 21;	Length 1180;
Best Local Similarity	79.4%	Pred. NO. 9e-39;		
Matches 81;	Conservative	7;	Mismatches 12;	Gaps 2;
			Indels	

CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 55 AA;

Query Match 14.7%; Score 84; DB 22; Length 55;

Best Local Similarity 46.5%; Pred. No. 0.065;

Matches 20; Conservative 3; Mismatches 12; Indels 8; Gaps 1;

QY 22 RNQKSRRRGCTAGGCTPRYMSCLRDAPPSPPTAGPPRCP 64

|||||: ||||| |

Db 21 RHGQHTPPQGTGAPGAPP-----GPPSPPTAGPVRRPP 55

RESULT 12

AAG35230

ID AAG35230 standard; Protein; 370 AA.

XX AC AAG35230;

XX DT 18-OCT-2000 (first entry)

XX DE Zea mays protein fragment SEQ ID NO: 43007.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.

XX OS Zea mays subsp. mays.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0123548.

XX PR 23-MAR-1999; 99US-0125788.

XX PR 25-MAR-1999; 99US-0126264.

XX PR 29-MAR-1999; 99US-0126785.

XX PR 01-APR-1999; 99US-0127462.

XX PR 06-APR-1999; 99US-0128234.

XX PR 08-APR-1999; 99US-0128714.

XX PR 16-APR-1999; 99US-0129845.

XX PR 19-APR-1999; 99US-0130077.

XX PR 21-APR-1999; 99US-0130449.

XX PR 23-APR-1999; 99US-0130510.

XX PR 28-APR-1999; 99US-0131449.

XX PR 30-APR-1999; 99US-0132048.

XX PR 04-MAY-1999; 99US-0132484.

XX PR 05-MAY-1999; 99US-0132485.

XX PR 06-MAY-1999; 99US-0132486.

XX PR 07-MAY-1999; 99US-0132487.

XX PR 11-MAY-1999; 99US-0132863.

XX PR 14-MAY-1999; 99US-0134256.

XX PR 14-MAY-1999; 99US-0134219.

XX PR 14-MAY-1999; 99US-0134221.

XX PR 18-MAY-1999; 99US-0134370.

XX PR 18-MAY-1999; 99US-0134768.

XX PR 19-MAY-1999; 99US-0134941.

XX PR 20-MAY-1999; 99US-0135124.

XX PR 21-MAY-1999; 99US-0135353.

XX PR 24-MAY-1999; 99US-0135629.

XX PR 25-MAY-1999; 99US-0136021.

XX PR 27-MAY-1999; 99US-0136392.

XX PR 28-MAY-1999; 99US-0136782.

XX PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.

transduction deficiency, neurological diseases, stroke, angiogenesis,
ovulation disorders, diseases in the spinal cord, thyroid gland, heart,
trachea, thymus, lymph node and muscular system, obesity, anorexia,
growth abnormalities, and alleviation of precocious puberty. The
sequences given in records AB086130-AB086184 represent novel human cDNA's
of the invention.

QY 13 DERKIAWGERNGQAKSKRRGIRAGGFCIFRIMSCLRDAEPPS-----PTPAGPPFRCPWQD 07

DU 33 DQDQGADANRNFAPFHARRKIRK--IAMP5AAS--ISAAPF5HRAAL5AAAGPPGCGW--IS

QY 68 DAFIRGGPXXKGKELGLRAV 87

Abstract: This paper discusses the role of the state in the development of the private sector in the context of the transition from a centrally planned to a market economy. The paper argues that the state should play a role in the development of the private sector, but that the role should be limited to the provision of a legal and institutional framework, and the provision of information and advice to private firms. The paper also discusses the role of the state in the development of the private sector in the context of the transition from a centrally planned to a market economy. The paper argues that the state should play a role in the development of the private sector, but that the role should be limited to the provision of a legal and institutional framework, and the provision of information and advice to private firms.

THE UNIVERSITY OF MICHIGAN LIBRARY

RESULT 15

ID ABG10930 standard; Protein;

AC ABG10930;

XX
10-11

DE
Nov

[illegible][illegible]

OS Homo sapiens.

XX PN WO200175067-A2.

AA	
PD	11-OCT-2001.
XX	
PF	30-MAR-2001; 2001WO-US08631.

31-MAR-2000; 2000US-0540217.

XX
FR 23-AUG-2000; 2000

PA	(HISE-7) HISEQ INC.
XX	
XX	Drmanao RT, Liu C, Tang YT;
PI	
XX	
XX	WPI: 2001-639362/73.
DR	N-PSDB; AAS75117.
DR	
XX	
XX	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity -

XX
DR
WPT: 2001-639362/73

DR N-PSDB; AAS/511/.
XX

PT new isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity - PT

PT responsible for genetic diversity -

PS Claim 20: SEQ ID No 41289: 103pp: English.

XX The invention relates to isolated polynucleotide (T) and

WPI: 1998-398024/34.

DR P-PSDB; AAV36085.

1000

GenCore version 5.1.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 20:53:24 ; Search time 4480.99 Seconds
(without alignments)
11768.450 Million cell updates/sec

Title: US-09-750-240-3
Perfect score: 1812
Sequence: 1 gttacgtgtgtctggcat.....gcagcttctctgaggtgttc 1812

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg_hum.*
- 31: em.htg_inv.*
- 32: em.htg_other.*
- 33: em.htg_mus.*
- 34: em.htg_pln.*
- 35: em.htg_rod.*
- 36: em.htg_mam.*
- 37: em.htg_vrt.*
- 38: em.sy.*
- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1812	100.0	1812	6	AR174472	AR174472 Sequence
2	1812	100.0	1812	6	AX189759	AX189759 Sequence
3	1808.4	99.8	3549	6	AR174473	AR174473 Sequence
4	1808.4	99.8	3549	6	AX189761	AX189761 Sequence
5	1763.4	97.3	3552	6	AX189766	AX189766 Sequence
6	1763	97.3	6463	9	AF250226	AF250226 Homo sapi
7	1657.8	91.5	3582	6	AX189768	AX189768 Sequence
8	1604.2	88.5	5877	9	AB007882	AB007882 Homo sapi
9	1527.8	84.3	4046	4	DOGADENCYC	M94968 Canis fami
10	1519.8	83.9	4046	6	I29958	I29958 Sequence 1
11	1449.4	80.0	3465	10	MUSADNLNLCYC	M96653 Mus musculu
12	1437.2	79.3	4131	6	AR106659	AR106659 Sequence
13	1437.2	79.3	4131	10	RATADCYB	M96160 Rattus norv
14	1431.8	79.0	5841	6	AX305965	AX305965 Sequence
15	1431.8	79.0	5841	10	MUSADCYC	M93422 Mouse adeny
16	1427.6	78.8	6036	10	RATADC	L01115 Rattus norv
17	906.2	50.0	4995	4	OCMRADCYV	Z29371 O.cuniculus
18	886.6	48.9	4545	4	DOGADNDCYC	M88649 Canis fami
19	858.2	47.4	3924	6	AR106658	AR106658 Sequence
20	858.2	47.4	4847	10	RATADCYA	M96159 Rattus norv
21	811	44.8	2743	9	AF497517	AF497517 Homo sapi
22	799	44.1	3137	6	AX418303	AX418303 Sequence
23	798	44.0	2554	9	AK093840	AK093840 Homo sapi
24	780	43.0	4236	5	GGA293817	AJ293817 Gallus ga
25	667.2	36.8	2429	4	DOGADCYC	M97886 Canis fami
26	436	24.1	3978	4	BOVADC	M25579 Bovine aden
27	436	24.1	3978	6	AR106654	AR106654 Sequence
28	415.2	22.9	2857	10	AF053980	AF053980 Mus muscu
29	404	22.3	3811	6	AX418306	AX418306 Sequence
30	393.2	21.7	1652	6	AR106662	AR106662 Sequence
31	362.2	20.0	7546	3	DRORAC	M81887 Drosophila
32	340	18.8	6193	4	BTAC11MR	Z49806 B.taurus mR
33	339	18.7	3563	9	AB011083	AB011083 Homo sapi
34	339	18.7	4080	9	AK027857	AK027857 Homo sapi
35	339	18.7	4142	9	AF033861	AF033861 Homo sapi
36	338.2	18.7	6005	9	HSADENCYR	Z35309 H.sapiens m
37	335.6	18.5	4533	6	AR106656	AR106656 Sequence
38	335.6	18.5	4533	10	RATADCY3	M55075 R.norvegicu
39	333.2	18.4	3674	10	AF458089	AF458089 Mus muscu
40	320.6	17.7	4601	6	AR106661	AR106661 Sequence
41	320.6	17.7	4601	10	RATACV111	L26986 Rat adenily
42	320.6	17.7	4901	10	MMU85021	U85021 Mus musculu
43	318.2	17.6	2496	9	AK093706	AK093706 Homo sapi
44	316.6	17.5	3243	6	AX463632	AX463632 Sequence
45	316.6	17.5	6196	6	AX463638	AX463638 Sequence

ALIGNMENTS

RESULT 1	AR174472	AR174472	Sequence 3 from patent US 6306830.	1812 bp	DNA	linear	PAT 17-DEC-2001
LOCUS	AR174472	Sequence 3 from patent US 6306830.	1812 bp	DNA	linear	PAT 17-DEC-2001	
DEFINITION	AR174472	Sequence 3 from patent US 6306830.	1812 bp	DNA	linear	PAT 17-DEC-2001	
ACCESSION	AR174472	Sequence 3 from patent US 6306830.	1812 bp	DNA	linear	PAT 17-DEC-2001	
VERSION	AR174472.1	GI:17914792	GI:17914792				
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE	1 (bases 1 to 1812)						
AUTHORS	Hammond,H.Kirk., Insel,P.A., Ping,P., Post,S.R. and Gao,M.						
TITLE	Gene therapy for congestive heart failure						
JOURNAL	Patent: US 6306830-A 3 23-OCT-2001;						
FEATURES	Location/Qualifiers						

8

AUTHORS Hammond,H.K. and Gao,M.
TITLE Gene therapy for congestive heart failure
JOURNAL Patent: WO 0148164-A 3 05-JUL-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
FEATURES Location/Qualifiers

source

1. .1812
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 361 a 539 c 507 g 405 t

ORIGIN

Query Match 100.0%; Score 1812; DB 6; Length 1812;
Best local Similarity 100.0%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GTTAACTGGTGGGATCCTGGCGGAGTGCAGGTGGGGCGCTTTTCGCAGCAGAC 60
QY 61 CCGCGAGCCCTCTCGGGGCTCTGGTGGCCCTGTGTCTTTGTATACATCGCATACAG 120
DB 61 CCGCGAGCCCTCTCGGGGCTCTGGTGGCCCTGTGTCTTTGTATACATCGCATACAG 120
QY 121 CTCTCCCATCCGATCGGGGCTGGCGTCTCAGCGGCTGGGCTCTCCACCTTGCAT 180
DB 121 CTCTCCCATCCGATCGGGGCTGGCGTCTCAGCGGCTGGGCTCTCCACCTTGCAT 180
QY 181 TTGATCTGGCTGGCAACTTAAACCGTGGTGCATGCCCTTCCCTGGAAGCAGCTCGGTGCC 240
DB 181 TTGATCTGGCTGGCAACTTAAACCGTGGTGCATGCCCTTCCCTGGAAGCAGCTCGGTGCC 240
QY 241 AATGTGTGCTGTCTCTGCACCAACGTCTATTAGCATCTGCACACATATCCAGCAGAG 300
DB 241 AATGTGTGCTGTCTCTGCACCAACGTCTATTAGCATCTGCACACATATCCAGCAGAG 300
QY 301 GTGTCTCAGCCGAGGCTTTTCAGAGACCCGCGAGTTACATCCAGGCGCGCTCCACCTG 360
DB 301 GTGTCTCAGCCGAGGCTTTTCAGAGACCCGCGAGTTACATCCAGGCGCGCTCCACCTG 360
QY 361 CAGCATGAGATCGCAGCAGGCGGTGCTGTGCGGTATTGCGCCACAGCAGTTGCC 420
DB 361 CAGCATGAGATCGCAGCAGGCGGTGCTGTGCGGTATTGCGCCACAGCAGTTGCC 420
QY 421 ATGGAGATGAAGAAGACATCAACACAAAAAAGAACATGTTCCAAAGATCTACATA 480
DB 421 ATGGAGATGAAGAAGACATCAACACAAAAAAGAACATGTTCCAAAGATCTACATA 480
QY 481 CAGAGCATGACATGTCAGCATCCTGTTTGCACACATTGAGGCTTCACAGCCTGGCA 540
DB 481 CAGAGCATGACATGTCAGCATCCTGTTTGCACACATTGAGGCTTCACAGCCTGGCA 540
QY 541 TCCAGTGCACTGCGCAGGAGCTGGTCATGACCTGAATGAGCTTTTGGCCGCTTTGAC 600
DB 541 TCCAGTGCACTGCGCAGGAGCTGGTCATGACCTGAATGAGCTTTTGGCCGCTTTGAC 600
QY 601 AAGCTGGCTGGGAGATCACTGCTGAGGATCAAGATCTTTGGGGAGCTGTTACTACTGT 660
DB 601 AAGCTGGCTGGGAGATCACTGCTGAGGATCAAGATCTTTGGGGAGCTGTTACTACTGT 660
QY 661 GTGTCAGGGCTGCGGAGGCGCGGCGACCATGCCACTGCTGTGGAGATGGGGTA 720
DB 661 GTGTCAGGGCTGCGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGTA 720
QY 721 GACATGATTGAGGCCATCTCGCTGCTAGTGCAGGTGACAGGTGTAATGTCAACATCGC 780
DB 721 GACATGATTGAGGCCATCTCGCTGCTAGTGCAGGTGACAGGTGTAATGTCAACATCGC 780
QY 781 GTGGGATCCACAGCGGCGGCTGCATCGCGCGCTTCCTTTGGCTTTCGCGAAATGGCAGTTC 840
DB 781 GTGGGATCCACAGCGGCGGCTGCATCGCGCGCTTCCTTTGGCTTTCGCGAAATGGCAGTTC 840
QY 841 GATGTGGTCCATGATGTGACCTTGGCCAAACACATGGAAGCAGGAGCGGGCTGGC 900
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DB 841 GATGTGGTCCCAATGATGTGACCTTGCCCAACACACATGGAAGCAGGAGCGGGCTGGC 900
QY 901 CGCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGAGTACGAGTGGAGCA 960
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DB 901 CGCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGAGTACGAGTGGAGCA 960
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QY 961 GGCCTGGTGCAAGCGCAACGCTACCTCAAGGAGCAGCACATGTGAGACTTTCTCTCATC 1020
DB 961 GGCCTGGTGCAAGCGCAACGCTACCTCAAGGAGCAGCACATGTGAGACTTTCTCTCATC 1020
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QY 1021 CTGGGCCGCCAGACAGAACGAGAGAGAAAGGCATGCTGGCCAAAGCTGCAGCGGACT 1080
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DB 1021 CTGGGCCGCCAGACAGAACGAGAGAGAAAGGCATGCTGGCCAAAGCTGCAGCGGACT 1080
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QY 1081 CGGGCCAACTCCATGGAAGGCTGATGCCGATGGGTTCCTGATCGTGCCTTCTCCCGG 1140
DB 1081 CGGGCCAACTCCATGGAAGGCTGATGCCGATGGGTTCCTGATCGTGCCTTCTCCCGG 1140
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QY 1141 ACCAAGGACTCCAAAGGCTTCCGCGAGATGGGCATTGATGATTCAGCAAAAGACAACCGG 1200
DB 1141 ACCAAGGACTCCAAAGGCTTCCGCGAGATGGGCATTGATGATTCAGCAAAAGACAACCGG 1200
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QY 1201 GGCACCCAAAGATGCCCTGAACCCCTGAGATGAGGTGGATGAGTTCCTCAGCCGTGCCATC 1260
DB 1201 GGCACCCAAAGATGCCCTGAACCCCTGAGATGAGGTGGATGAGTTCCTCAGCCGTGCCATC 1260
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QY 1321 CAGAGAGGATTTTGAAGAAGTACTTCCGGAAGGTGATGATGATTCAGCAAAAGACAACCGG 1380
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QY 1381 GTTCCCTGTGCCCTGTTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCA 1440
DB 1381 GTTCCCTGTGCCCTGTTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCA 1440
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QY 1441 CACTCCACCTGTGCTGGGATTTATGCCAGCATCTTCCCTGCTGCTGCTAATCACCCTG 1500
DB 1441 CACTCCACCTGTGCTGGGATTTATGCCAGCATCTTCCCTGCTGCTGCTAATCACCCTG 1500
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QY 1501 CTGATCTGTGCTGTACTCTGTGGTTCCTGTGTTCCCTAAGGCGCTGCAACGCTGTGCC 1560
DB 1501 CTGATCTGTGCTGTACTCTGTGGTTCCTGTGTTCCCTAAGGCGCTGCAACGCTGTGCC 1560
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QY 1561 CGCAGCATTTGCTCCGCTCAGCGGCACATAGCACCGAGTTGGCATCTTTTCCGCTCTGCTT 1620
DB 1561 CGCAGCATTTGCTCCGCTCAGCGGCACATAGCACCGAGTTGGCATCTTTTCCGCTCTGCTT 1620
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QY 1621 GTGTTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
DB 1621 GTGTTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
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QY 1681 GCAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
DB 1681 GCAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
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QY 1741 AATTACTCTCTGGGCTGGATGCTCCCTGTGTGAGGGCAGCATGCCACCTGCAAGCTTT 1800
DB 1741 AATTACTCTCTGGGCTGGATGCTCCCTGTGTGAGGGCAGCATGCCACCTGCAAGCTTT 1800
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QY 1801 CCTGAGGTGTTTC 1812
DB 1801 CCTGAGGTGTTTC 1812
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RESULT 3
LOCUS AR174473 3549 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 5 from patent US 6306830.
ACCESSION AR174473
VERSION AR174473.1 GI:17914793

KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 3549)
AUTHORS Hammond,H.Kirk., Insel,P.A., Ping,P., Post,S.R. and Gao,M.
TITLE Gene therapy for congestive heart failure
JOURNAL Patent: US 6306830-A 5 23-OCT-2001;
FEATURES Location/Qualifiers
source 1..3549
/organism="unknown"
BASE COUNT 699 a 1025 c 1061 g 764 t
ORIGIN
Query Match 99.8%; Score 1808.4; DB 6; Length 3549;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 TAACGTGGTCTGGGCATCCTGCGCGCAGTGCAGGTGCGGGGCGCTTTCGCAGCAGACCC 62
DB 636 TAACGTGGTCTGGGCATCCTGCGCGCAGTGCAGGTGCGGGGCGCTTTCGCAGCAGACCC 695
QY 63 GCGCAGCCCTCTGCGGGGCTCTGGTGCCTGTGTTCTTTGTATACATGCATACAGCCT 122
DB 696 GCGCAGCCCTCTGCGGGGCTCTGGTGCCTGTGTTCTTTGTATACATGCATACAGCCT 755
QY 123 CTTCCCATCCGATCGGGGCTGCCCTCCTCAGCGGCCCTGGGCTCTCCACCTTGCATTT 182
DB 756 CCTCCCATCCGATCGGGGCTGCCCTCCTCAGCGGCCCTGGGCTCTCCACCTTGCATTT 815
QY 183 GATCTTGGCTGGCACTTAACCGTGGTGATGCTTCTTGAAGCAGCTCGGTGCCAA 242
DB 816 GATCTTGGCTGGCACTTAACCGTGGTGATGCTTCTTGAAGCAGCTCGGTGCCAA 875
QY 243 TGTGCTGCTTCTCTGCACCAACGTCATTAGCATCTGCACACTATCCACGAGGT 302
DB 876 TGTGCTGCTTCTCTGCACCAACGTCATTAGCATCTGCACACTATCCACGAGGT 935
QY 303 GTCTCAGCCCGAGGCTTTTCAGAGAGCCGCGAGTTACATCCAGGCCGCGCTCCACCTGCA 362
DB 936 GTCTCAGCCCGAGGCTTTTCAGAGAGCCGCGAGTTACATCCAGGCCGCGCTCCACCTGCA 995
QY 363 GCATGAGATCGGCACGAGGCGCTGCTGCTCGGTATTTGCCCCGACGAGCTTGCCTAT 422
DB 996 GCATGAGATCGGCACGAGGCGCTGCTGCTCGGTATTTGCCCCGACGAGCTTGCCTAT 1055
QY 423 GGAGATGAAGAAGACATCAACACAAAAAAGAGACATGTTCCACAAGATCTACATACA 482
DB 1056 GGAGATGAAGAAGACATCAACACAAAAAAGAGACATGTTCCACAAGATCTACATACA 1115
QY 483 GAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTTAGGGGCTTCACGAGCCTGGCATC 542
DB 1116 GAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTTAGGGGCTTCACGAGCCTGGCATC 1175
QY 543 CCAGTCCATCGGCAGGAGCTGTCATGACCTGTAATGAGCTTTTTCGCCGGTTTGACAA 602
DB 1176 CCAGTCCATCGGCAGGAGCTGTCATGACCTGTAATGAGCTTTTTCGCCGGTTTGACAA 1235
QY 603 GCTGGCTCGGAGAACTACTGCTGAGGATCAAGATCTTGGGGGACTGTACTACTGTGT 662
DB 1236 GCTGGCTCGGAGAACTACTGCTGAGGATCAAGATCTTGGGGGACTGTACTACTGTGT 1295
QY 663 GTCAGGGCTCGCGAGGCGCGGCCGCCACCATGCCACTGCTGTGTGGAGATGGGGGTAGA 722
DB 1296 GTCAGGGCTCGCGAGGCGCGGCCGCCACCATGCCACTGCTGTGTGGAGATGGGGGTAGA 1355
QY 723 CATGATTGAGGCATCTCGCTGGTACGTGAGGTGACAGGTGAAATGTGAACATGCGCGT 782
DB 1356 CATGATTGAGGCATCTCGCTGGTACGTGAGGTGACAGGTGAAATGTGAACATGCGCGT 1415
QY 783 GGGCATCCACAGGGCGGCTGCACCTGCGGCGTCTTGGCTTCCGGAATGCGAGTTCCA 842
DB 1416 GGGCATCCACAGGGCGGCTGCACCTGCGGCGTCTTGGCTTCCGGAATGCGAGTTCCA 1475

RESULT 4

AX189761

LOCUS

3549 bp

DNA

linear

PAT 08-AUG-2001

DEFINITION	Sequence 5 from Patent WO0148164.	
ACCESSION	AX189761	
VERSION	AX189761.1	GI:15143135
KEYWORDS	human.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 3549)	
TITLE	Hammond,H.K. and Gao,M.	
JOURNAL	Gene therapy for congestive heart failure	
FEATURES	Patent: WO 0148164-A 5 05-JUL-2001.	
source	THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)	
BASE COUNT	Location/Qualifiers	
ORIGIN	1. 3549	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	699 a 1025 c 1061 g 764 t	
Query Match	99.8%;	Score 1808.4;
Best Local Similarity	99.9%;	Pred. No. 0;
Matches 1809;	Conservative 0;	Mismatches 1;
	Indels 0;	Gaps 0;
QY	3	TAACTGTGCTGGGCATCTCGGGCAGTCGAGTCGGGGCGCTTTCGCAGACAGCC 62
DB	636	TAACTGTGCTGGGCATCTCGGGCAGTCGAGTCGGGGCGCTTTCGCAGACAGCC 695
QY	63	CGCAGAGCCCTCGGGCCCTCGTGCCTCTGTTCTTCTGTTATACATCGCATACAGCT 122
DB	696	CGCAGAGCCCTCGGGCCCTCGTGCCTCTGTTCTTCTGTTATACATCGCATACAGCT 755
QY	123	CCTCCCATCGCATCGGGCTGCGCTCCTCAGCGGCTTGGGCCCTCCACCTTGCATTT 182
DB	756	CCTCCCATCGCATCGGGCTGCGCTCCTCAGCGGCTTGGGCCCTCCACCTTGCATTT 815
QY	183	GATCTGGCTGGCAACTTAACCGTGTGATGTCCTCTGGAAGCAGCTCGGTGCCAA 242
DB	816	GATCTGGCTGGCAACTTAACCGTGTGATGTCCTCTGGAAGCAGCTCGGTGCCAA 875
QY	243	TGTCGCTGTTCTCTGCACCAAGCTCATTAGCATCTGCACACACTATCCAGCAGGT 302
DB	876	TGTCGCTGTTCTCTGCACCAAGCTCATTAGCATCTGCACACACTATCCAGCAGGT 935
QY	303	GTCTCAGCGCCAGGCTTTTCAGGAGACCGCAGTTTACATCCAGGCCCGCTCCACCTGCA 362
DB	936	GTCTCAGCGCCAGGCTTTTCAGGAGACCGCAGTTTACATCCAGGCCCGCTCCACCTGCA 995
QY	363	GCATGAGAAATCGCAGGAGCGCTGCTGCTGTCGGTATTGCCCCAGCAGTTGCCAT 422
DB	996	GCATGAGAAATCGCAGGAGCGCTGCTGCTGTCGGTATTGCCCCAGCAGTTGCCAT 1055
QY	423	GGAGTGAAGAAGACATCAACAAAAAAGAACACATGTTCCACAGATCTACATACA 482
DB	1056	GGAGTGAAGAAGACATCAACAAAAAAGAACACATGTTCCACAGATCTACATACA 1115
QY	483	GAAGCATGACAAATGTCAGCATCTCTTTTCAGACAAATGAGGCTTCACAGCCTGGCATC 542
DB	1116	GAAGCATGACAAATGTCAGCATCTCTTTTCAGACAAATGAGGCTTCACAGCCTGGCATC 1175
QY	543	CCAGTGCATCGCAGGAGCTGGTATGACCCCTGAATGAGCTCTTTGGCCCGTTTGACAA 602
DB	1176	CCAGTGCATCGCAGGAGCTGGTATGACCCCTGAATGAGCTCTTTGGCCCGTTTGACAA 1235
QY	603	GCTGCTCGGAGAAATCACTGCTGAGGATCAAGATCTTTGGGGGACTGTTTACTACTGTGT 662
DB	1236	GCTGCTCGGAGAAATCACTGCTGAGGATCAAGATCTTTGGGGGACTGTTTACTACTGTGT 1295
QY	663	GTCAGGGCTCGGGAGGCCCGCCGACCTGCCCCACTGCTGTGCGAGATGGGGTAGA 722
DB	1296	GTCAGGGCTCGGGAGGCCCGCCGACCTGCCCCACTGCTGTGCGAGATGGGGTAGA 1355
QY	723	CATGATTTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGT 782

Qy 1740 CAATTACTCTCTGGGCTGGATGCTCCCTCTGTGTGAGGGCAACCATGCCACCTGCAGCTT 1799
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Db 2376 CAATTACTCTCTGGGCTGGATGCTCCCTCTGTGTGAGGGCAACCATGCCACCTGCAGCTT 2435

Qy 1800 TCCTGAGGTGTC 1812
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Db 2436 TCCTGAGTACTTC 2448

RESULT 6
AF250226 6463 bp mRNA linear PRI 15-SEP-2000
LOCUS
DEFINITION Homo sapiens adenylyl cyclase type VI mRNA, complete cds.
ACCESSION AF250226
VERSION AF250226.1 GI:9049782
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6463)
Wicker, R., Catalan, A.G., Caillieux, A., Starenki, D., Stengel, D.,
Sarasin, A. and Suarez, H.G.
Cloning and expression of human adenylyl cyclase type VI in normal
thyroid tissues
Biochim. Biophys. Acta 1493 (1-2), 279-283 (2000)
JOURNAL
MEDLINE 20435313
PUBMED 10978539
REFERENCE 2 (bases 1 to 6463)
Wicker, R., Gascon Catalan, A., Caillieux, A.-F., Starenki, D.,
Stengel, D., Sarasin, A. and Suarez, H.G.
Direct Submission
TITLE Submitted (28-MAR-2000) Lab Etude des Relations - Instabilite
genetique et Cancer UPR 2169, Institut de Recherches sur le Cancer
CNRS IFR 1221, 7 rue Guy Moquet, Villejuif 94801, France

FEATURES
source
1. 6463
/organism="Homo sapiens"
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/chromosome="12"
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complement(19..447)
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695..4201
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/db_xref="GI:9049783"
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SCLRDAPDPSPTAGPPRCQDDAFIRGGPGKGKGLGRVALGFEDEVTTTAGG
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GVDIMEAISLVREVTGVNVMNRYIHSGRVHCVGLGRKQWFDWNSDVTLANHMEAG
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DEFLSRAIDRSIDOLRKQHVRELLTFQREDLEKKYSRKVDPRFGAYACALLVFCF
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PPATIFDNVLLGLGASSNETFDGLCPAAGRVALKYMTPIVILLVVALYLAHQ
QVSTARLQPLQATGKEEMEELQAVNRLHLNLPKDVAAHFLAPERRNDELYY
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BASE COUNT 1264 a 1795 c 1871 g 1533 t
ORIGIN
Query Match 97.3%; Score 1763; DB 9; Length 6463;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 20; Indels 3; Gaps 1;
Qy 5 ACCTGGTCTGGGCATCCTGGCGCAGTGCAGGTGCGGGGGCGCTTTCGCACGACGACCGC 64
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Db 1332 ACCTGGTCTGGGCATCCTGGCGCAGTGCAGGTGCGGGGGCGCTCTCGCAGCAGACCGC 1391
Qy 65 GCAGCCCTCTCGCGGCTCTGTGSCCTGTGTCTTTGTATACATCGCATACAGCTCC 124
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Db 1392 GCAGCCCTCTCGCGGCTCTGTGSCCTGTGTCTTTGTCTACATCGCTACAGCTCC 1451
Qy 125 TCCCATCCGATCGGGCTGCGCTCTCAGCGGCTTGGGCTCTCCACCTTGCAATTGA 184
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Db 1452 TCCCATCCGATCGGGCTGCGCTCTCAGCGGCTTGGGCTCTCCACCTTGCAATTGA 1511
Qy 185 TCTTGGCTGGCAACTTAAACCGTGTGATGCTTCCCTCTGGAAGCAGCTCGTGCCAAATG 244
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Db 1512 TCTTGGCTGGCAACTTAAACCGTGTGATGCTTCCCTCTGGAAGCAGCTCGTGCCAAATG 1571
Qy 245 TGCTGTCTTCTCTGTCACCAACCTCATTAAGCATCTGCACACATATCCAGCAGAGTGT 304
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Db 1572 TGCTGTCTTCTCTGTCACCAACCTCATTAAGCATCTGCACACATATCCAGCAGAGTGT 1631
Qy 305 CTCAGCGCCAGGCTTTCAGGAGACCCGCGATTTACATCCAGGCGCGGCTCCACCTGCAGC 364
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Db 1632 CTCAGCGCCAGGCTTTCAGGAGACCCGCGGTTTACATCCAGGCGCGGCTCCACCTGCAGC 1691
Qy 365 ATGAGATCGGCACGAGGCGCTGTGCTGCTGGTATTCGCCACGACCTTCCCATGG 424
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Qy	1680	TGCAGCCGGATGCTGAATTTAACCCTGCTGACATCACTGCTGCCACCTGCGAGCAGCT	1739
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DEFINITION Homo sapiens KIAA0422 mRNA, partial cds.
ACCESSION AB007882
VERSION AB007882.2 GI:20521044
KEYWORDS KIAA0422.

SOURCE Homo sapiens male brain cDNA to mRNA, clone_lib:pBluescriptII SK
plus clone:hh01205s1.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Ishikawa,K., Nagase,T., Nakajima,D., Seki,N., Ohira,M.,
Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
TITLE Prediction of the coding sequences of unidentified human genes.
VIII. 78 new cDNA clones from brain which code for large proteins
in vitro
JOURNAL DNA Res. 4 (5), 307-313 (1997)
MEDLINE 98116655
PUBMED 9455477
REFERENCE 2 (bases 1 to 5877)
AUTHORS Ohara,O.
TITLE Direct Submission
JOURNAL Submitted (06-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology, Yana 1532-3, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel: +81-438-52-3913,
Fax: +81-438-52-3914)
COMMENT On May 9, 2002 this sequence version replaced gi:2887418.
Sequence updated (05-Jan-1998).
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hh01205)."
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Best Local Similarity 98.7%; Pred. No. 0;
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Qy	542	CCCAGTCACTGCGCAGGAGCTGGTCATGACCCCTGAATGAGCTCTTTGCCCGTTTGACA	601
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Qy	602	AGCTGGCTGGGAGATCACTGCCTGAGGATCAAGATCTTGGGGGACTGTTTACTACTGTG	661
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Db	1434	TGTCAGGGCTGCCCGAGGCGCGGCGACCATGCCCTGCTGTGTGGAGATGGGGGTAG	1493
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DEFINITION		Canis familiaris		adenyl cyclase type VI		4046 bp mRNA sequence.				
ACCESSION		M94968								
VERSION		M94968.1		GI:163896						
KEYWORDS		adenyl cyclase type VI.								
SOURCE		Canis familiaris		cardiac muscle cDNA		to mRNA.				
ORGANISM		Canis familiaris								
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom								
AUTHORS		Katsushika,S., Chen,L., Kawabe,J., Nilakantan,R., Hainon,N.J.,								
TITLE		Homcy,C.J., and Ishikawa,Y.								
		Cloning and characterization of a sixth adenyl cyclase isoform								
		types V and VI constitute a subgroup within the mammalian adeny								
		cyclase family								
JOURNAL		Proc. Natl. Acad. Sci. U.S.A.		89 (18), 8774-8778		(1992)				
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LOCUS 129958
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ACCESSION 129958
VERSION 129958.1 GI:1820749
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4046)
AUTHORS Ishikawa,Y.
TITLE Cloning and characterization of a cardiac adenylyl cyclase
JOURNAL Patent: US 5578481-A 1 26-NOV-1996;
FEATURES Location/Qualifiers
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Best Local Similarity 90.7%; Pred. No. 0;
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LOCUS
DEFINITION
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JOURNAL
FEATURES
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BASE COUNT
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Query Match
Best Local Similarity
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Search completed: February 23, 2003, 02:25:16
Job time : 4522.99 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 20:52:08 ; Search time 334.621 Seconds
(without alignments)
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Title: US-09-750-240-3

Perfect score: 1812

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1812	100.0	1812	22	AA08562 Human partial card
2	1812	100.0	2127	19	AAV23246 Human adenylylcycl
3	1808.4	99.8	3549	22	AA08563 Human cardiac aden
4	1763.4	97.3	3552	22	AA08567 Human cardiac aden
5	1763	97.3	4942	20	AA00461 Human type VI aden
6	1657.8	91.5	3582	22	AA08568 Human modified car
7	1527.8	84.3	4046	14	AAQ42525 Cardiac adenylyl c
8	1437.2	79.3	4131	21	AAAS3923 Type VI adenylyl c
9	1431.8	79.0	5841	24	AB199680 Mouse ischaemic co

10	895	49.4	4523	20	AA000462	Human type V adeny
11	884.6	48.8	4356	16	AA095540	Cardiac adenylyl c
12	883.4	48.8	4356	14	AA037543	Cardiac adenylyl c
13	858.2	47.4	3924	21	AAAS3922	Type V adenylyl cy
14	799	44.1	3137	24	AA028058	Human adenylyl and
15	445.8	24.6	4827	23	AB107501	Drosophila melanog
16	436	24.1	3978	21	AAAS3918	Adenylyl cyclase t
17	404	22.3	3811	24	AA028061	Human adenylyl and
18	393.2	21.7	1652	21	AAAS3926	Adenylyl cyclase C
19	362.2	20.0	7005	23	AB115355	Drosophila melanog
20	339	18.7	4080	22	AAH16647	Human cDNA sequenc
21	337.2	18.6	3505	24	AA034078	Human secreted pro
22	335.6	18.5	4533	21	AAAS3920	Type III adenylyl
23	320.6	17.7	4601	21	AAAS3925	Type VIII adenylyl
24	319.4	17.6	2601	21	AA099124	Human pancreatic c
25	311.2	17.2	5199	21	AAAS3924	Type VII adenylyl
26	301.2	16.6	4011	22	AA066820	Human adenylyl cy
27	301.2	16.6	6470	24	AA031191	Human NS cDNA sequ
28	298	16.4	4355	24	AB139754	Rat adenylyl cycla
29	286	15.8	4008	17	AA014528	Adenylyl cyclase t
30	286	15.8	4008	21	AAAS3919	Human adenylyl cy
31	284	15.7	3518	22	AA026694	Human adenylyl cy
32	280.6	15.5	5873	24	AA031190	Human polynucleoti
33	273.6	15.1	320	24	AB190026	Drosophila melanog
34	267.6	14.8	5201	23	AB129627	Type IV adenylyl c
35	256.2	14.1	3357	21	AAAS3921	Human adenylyl and
36	242.2	13.4	3769	24	AA028057	Human adenylyl and
37	241	13.3	5046	23	AB102755	Drosophila melanog
38	240.2	13.3	3312	24	ABN89298	Human adenylyl cy
39	234.4	12.9	6363	23	AB116645	Drosophila melanog
40	230.8	12.7	3239	22	AA033100	Human secreted pro
41	216.8	12.0	4473	17	AA035209	Murine adenylyl c
42	209.4	11.6	4985	20	AA00463	Human type IX aden
43	189	10.4	627	22	AB142228	Human nervous syst
44	188.2	10.4	6597	23	AB114977	Drosophila melanog
45	172	9.5	1041	23	ABV25672	Human prostate exp

ALIGNMENTS

RESULT 1

AA08562

ID AA08562 standard; cDNA; 1812 BP.

XX AC AA08562;

XX DT 04-SEP-2001 (first entry)

XX XX Human partial cardiac adenylylase VI (ACVI) isoform #2 cDNA.

XX DE Human; cardiant; beta-adrenergic signalling protein; beta-ASP;

XX KW myocardiium; gene therapy; beta-adrenergic receptor; beta-AR;

XX KW adenylylase; adenylylase; adenylylase; adenylylase; adenylylase;

XX KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;

XX KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 1..1812

XX FT /*tag= a

XX FT /product= "Human partial cardiac ACVI isoform #2"

XX FT /note= "CDS does not include start and stop codon"

XX FT /EC_number= "4.6.1.1"

XX FT

XX WO200148164-A2.

XX PD 05-JUL-2001.

XX XX 26-DEC-2000; 2000WO-US35411.

XX PF Cardiac adenylyl c

XX XX 27-DEC-1999; 99US-0472667.

XX PR

XX (REG) UNIV CALIFORNIA.
XX PA Hammond HK, Gao M;
XX PI WPI: 2001-418260/44.
XX DR P-PSDB; AAE04309.
XX
PT Novel polynucleotide encoding a modified adenylyl cyclase polypeptide
PT useful for enhancing cardiac function in mammalian hearts, and for
PT treating heart disease, especially congestive heart failure -
XX PS Example 5; Page 115-119; 153pp; English.
XX
CC The present invention relates to methods and compositions for enhancing
CC cardiac function in mammalian hearts by inserting transgenes encoding
CC beta-adrenergic signalling proteins (beta-ASP) which increase
CC beta-adrenergic responsiveness within the myocardium using in vivo
CC gene therapy. The beta-ASPs of the invention include beta-adrenergic
CC receptors (beta-AR), adenylyl cyclases (also referred as adenylylase,
CC adenylylase and cAMP synthetase) and G-protein receptor kinase
CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
CC in mammalian hearts and for treating heart disease, especially
CC congestive heart failure. The present cDNA sequence encodes human
CC partial cardiac adenylylase VI (ACVI) isoform which is used for
CC generating a third beta-ASP transgene, used in the exemplification
CC of the invention.
XX
XX Sequence 1812 BP; 361 A; 539 C; 507 G; 405 T; 0 other;
SQ
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GTTAAAGTGGTGGGCATCTGGCGGAGTCAGTCAGGTGGGGGCGCTTTCGACGACAG 60
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DB 121 CTCTCTCCCATCCGATGGGGTGGCGTCTCTAGCGGCTGGGGCTCTCCACCTTGCAT 180
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DB 181 TTGATCTTGGCTTGGCAACTTAAACCTGGTGTGCTCTCTCTGGAAGCAGCTCGGTGCC 240
QY 241 AATGTGCTGCTTCTCTGCACCAACGTCATTAGCATCTGCACACATATCCAGCAGAG 300
DB 241 AATGTGCTGCTTCTCTGCACCAACGTCATTAGCATCTGCACACATATCCAGCAGAG 300
QY 301 GTGTCTCAGCGCAGGCTTTTACAGAGACCGCAGTTACATCCAGGCGCGCTCCACCTG 360
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DB 1021 CTGGGCGCAGCCAGCAAAAGAGAGAAAGGATGCTGGCCAAAGTGCAGCGGACT 1080
QY 1081 CGGGCCAACTCCATGAAGGGCTGATGCCGATGGTTCCTGATGCTGCTCTCCCG 1140
DB 1081 CGGGCCAACTCCATGAAGGGCTGATGCCGATGGTTCCTGATGCTGCTCTCCCG 1140
QY 1141 ACCAAGGACTTCCAAAGCCCTTCCGCCAGATGGGCAATTTGATTTCCAGCAAAACACCG 1200
DB 1141 ACCAAGGACTTCCAAAGCCCTTCCGCCAGATGGGCAATTTGATTTCCAGCAAAACACCG 1200
QY 1201 GGCACCCAGATGCCCTGAACCTGAGGATGAGGTGGATGAGTTCTGAGCCGTGCCATC 1260
DB 1201 GGCACCCAGATGCCCTGAACCTGAGGATGAGGTGGATGAGTTCTGAGCCGTGCCATC 1260
QY 1261 GATGCCCGCAGCATTTGATCAGCTGCGGAAGGACCATGTGCGCGGTTTTCCTCAGCTTC 1320
DB 1261 GATGCCCGCAGCATTTGATCAGCTGCGGAAGGACCATGTGCGCGGTTTTCCTCAGCTTC 1320
QY 1321 CAGAGAGAGATTTTGAGAGAGATTAATCCCGAAGTGGATCCCGCTTCGGAGGCTTAC 1380
DB 1321 CAGAGAGAGATTTTGAGAGAGATTAATCCCGAAGTGGATCCCGCTTCGGAGGCTTAC 1380
QY 1381 GTTGCCTGTGCCCTGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1440
DB 1381 GTTGCCTGTGCCCTGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1440
QY 1441 CACTCCACCTGATGCTTGGGATTTATGCGAGCATCTCTCTCTCTCTCTCTCTCTCTCTCT 1500
DB 1441 CACTCCACCTGATGCTTGGGATTTATGCGAGCATCTCTCTCTCTCTCTCTCTCTCTCTCT 1500
QY 1501 CTGATCTGTGCTGTACT 1560
DB 1501 CTGATCTGTGCTGTACT 1560
QY 1561 CGGAGCATTTGTCGGCTCAGGGGACATAGACCGGAGTTGGGATCTTTCCGCTCTCTCTCTCT 1620
DB 1561 CGGAGCATTTGTCGGCTCAGGGGACATAGACCGGAGTTGGGATCTTTCCGCTCTCTCTCTCT 1620
QY 1621 GTGTTTACTTCTGCCATTCGCAACATGTTACCTGTAAACACACACCCCATACGAGCTGT 1680
DB 1621 GTGTTTACTTCTGCCATTCGCAACATGTTACCTGTAAACACACACCCCATACGAGCTGT 1680

QY 1681 GCAGCCGGATGTAATTTAAACACCTGCTGACATCACTGCCTGCCACCTGCAGAGCTC 1740
Db 1681 GCAGCCGGATGTAATTTAAACACCTGCTGACATCACTGCCTGCCACCTGCAGAGCTC 1740
QY 1741 AATTACTCTCGGCCCTGGATGCTCCCTGTGTGAGGGCACCATGACCTGAGCTTT 1800
Db 1741 AATTACTCTCGGCCCTGGATGCTCCCTGTGTGAGGGCACCATGACCTGAGCTTT 1800
QY 1801 CCTGAGGTGTC 1812
Db 1801 CCTGAGGTGTC 1812
RESULT 2
AAV23246
ID AAV23246 standard; cDNA; 2127 BP.
XX
AC AAV23246;
XX
DT 17-JUL-1998 (first entry)
XX Human adenylyl cyclase isoform VI encoding cDNA.
DE
XX
KW Human; adenylyl cyclase VI; AC-VI; beta-adrenergic signalling protein;
KW transgene; gene therapy; congestive heart failure; cardiac function;
KW adenovirus; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2127
FT FT /*tag= a
FT FT /product= "adenylyl cyclase isoform VI"
FT FT /transl_except= (pos:229..231,aa:Xaa)
FT FT /transl_except= (pos:315..317,aa:Xaa)
FT FT /note= "no stop codon given; xaa = unknown"
FT FT misc_difference 315
FT FT /*tag= b
FT FT /note= "n indicates a gap of about 0.5 kb"
XX
PN WO9810085-A2.
XX
PD 12-MAR-1998.
XX
XX 05-SEP-1997; 97WO-US15610.
XX
XX 16-JUN-1997; 97US-0048933.
PR 05-SEP-1996; 96US-0708661.
XX
PA (COLL-) COLLATERAL THERAPEUTICS.
PA (REGC) UNIV CALIFORNIA.
XX
XX Gao M, Hammond HK, Insel PA, Ping P, Post SR;
PI
XX WPI; 1998-193633/17.
DR P-PSDB; AAW53345.
XX
XX Vectors containing transgene(s) encoding beta-adrenergic signalling
PT proteins - useful for gene therapy of congestive heart failure
XX
XX Claim 60; Fig 12A; 114pp; English.
XX
XX The present sequence encodes human adenylyl cyclase isoform VI (AC-VI)
CC from the present invention. The present invention describes a
CC recombinant replication-defective viral particle (I) comprising a gene
CC encoding a beta-adrenergic signalling protein (beta-ASP) operably
CC linked to a promoter. Also described are: (1) a recombinant pro-viral
CC plasmid (Ia) comprising a gene encoding a beta-ASP, as above, operably
CC linked to a promoter and further comprising a replication-defective
CC viral genome; (2) a (mammalian) cell transfected with (I) or (Ia); (3)
CC an isolated polynucleotide comprising a sequence encoding a human
CC adenylyl cyclase isoform VI (AC-VI), or a variant having AC activity;
CC (4) a human AC-VI encoded by (3); (5) an isolated polynucleotide

CC sequence which hybridises at high stringency to (3); and (6) a vector
CC comprising the polynucleotide of (3). (I) can be used to form a
CC filtered adenovirus particle preparation. (I) is used to enhance
CC cardiac function in mammals.
XX
SQ Sequence 2127 BP; 421 A; 637 C; 615 G; 452 T; 2 other;
Query Match 100.0%; Score 1812; DB 19; Length 2127;
Best Local Similarity 100.0%; Pred No. 0;
Matches 1812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTAACTGTGTGGCATCTCTGGCGGAGTGCAGGTTCGGGGCGCTTTTCGCAGACAG 60
Db 316 GTTAACTGTGTGGCATCTCTGGCGGAGTGCAGGTTCGGGGCGCTTTTCGCAGACAG 375
QY 61 CCGGGCAGCCCTCTGCGGGCTCTGTGCTCTGTGCTCTTTGTATATACATGCATACAG 120
Db 376 CCGGGCAGCCCTCTGCGGGCTCTGTGCTCTGTGCTCTTTGTATATACATGCATACAG 435
QY 121 CTCTCCCATCCGCATGCGGGCTGCGGTCTCTAGCGGCTTCCCTCTCCACCTTGCAT 180
Db 436 CTCTCCCATCCGCATGCGGGCTGCGGTCTCTAGCGGCTTCCCTCTCCACCTTGCAT 495
QY 181 TTGATCTTGGCTGGCAACTTAACCGTGGTATGCCCTTCCCTCTGGAAGCAGCTCGGTGCC 240
Db 496 TTGATCTTGGCTGGCAACTTAACCGTGGTATGCCCTTCCCTCTGGAAGCAGCTCGGTGCC 555
QY 241 AATGTGCTGTGTCTCTGCACCAAGTCAATTAGCATCTGCACACATATCCAGCAGAG 300
Db 556 AATGTGCTGTGTCTCTGCACCAAGTCAATTAGCATCTGCACACATATCCAGCAGAG 615
QY 301 GTGTCTCAGGCCAGGCTTTTCAGGAGACCGCGAGTTTACATCCAGGGCCGCTCCACCTG 360
Db 616 GTGTCTCAGGCCAGGCTTTTCAGGAGACCGCGAGTTTACATCCAGGGCCGCTCCACCTG 675
QY 361 CAGCATGAGAATCGGCGAGGAGCGGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 420
Db 676 CAGCATGAGAATCGGCGAGGAGCGGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 735
QY 421 ATGGAGATGAAGAAGACATCAACACAAAAAAGACATGTTCCCAACATCTACATA 480
Db 736 ATGGAGATGAAGAAGACATCAACACAAAAAAGACATGTTCCCAACATCTACATA 795
QY 481 CAGAAGCATGACATGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 540
Db 796 CAGAAGCATGACATGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 855
QY 541 TCCAGTGCATGCGCAGGAGCTGGTCAATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 600
Db 856 TCCAGTGCATGCGCAGGAGCTGGTCAATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 915
QY 601 AAGCTGGCTGGGAGATCACTGCTGAGGATCAAGATCTTTGGGGAGCTGTACTACTGT 660
Db 916 AAGCTGGCTGGGAGATCACTGCTGAGGATCAAGATCTTTGGGGAGCTGTACTACTGT 975
QY 661 GTGTGAGGCTGCGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
Db 976 GTGTGAGGCTGCGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1035
QY 721 GACATGATGAGGCGCATCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 1036 GACATGATGAGGCGCATCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1095
QY 781 GTGGGCATCCACAGCGGCGGCTGCATGCGGCGGCTTCTGCTGCTGCGGAAATGCGAGTTC 840
Db 1096 GTGGGCATCCACAGCGGCGGCTGCATGCGGCGGCTTCTGCTGCTGCGGAAATGCGAGTTC 1155
QY 841 GATGTGTGCTCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 1156 GATGTGTGCTCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1215
QY 901 CGCATCCACATCACTCGGCGCAACACTGCAGTACCTGCAACGGGGAGCTACGAAGTGGAGCCA 960
XX

Db	1216	CGCATCCACATCACTCGGGCAACACTGCAAGTACCTGAAACGGGGAGCTACGAAGTGGAGCCA	1271
Qy	961	GGCCGTGGTGGCAAGGCCAACCGTACCTCAAGGAGCAGCACATTGAGACTTTTCCCTCATC	1020
Db	1276	GGCCGTGGTGGCAAGCGCAACCGTACCTCAAGGAGCAGCACATTGAGACTTTTCCCTCATC	1335
Qy	1021	CTGGGGCCCAAGCCAGCAAAACGGAAAGAGAGAAAGCATGCTGGCCAAAGCTGCAGCGGACT	1080
Db	1336	CTGGGGCCCAAGCCAGCAAAACGGAAAGAGAGAAAGCATGCTGGCCAAAGCTGCAGCGGACT	1395
Qy	1081	CGGGCCAACTCCATGGAAGGGCTGATGCCCGCATGGTTCTCTGATCGTGGCTTCTCCCGG	1140
Db	1396	CGGGCCAACTCCATGGAAGGGCTGATGCCCGCATGGTTCTCTGATCGTGGCTTCTCCCGG	1455
Qy	1141	ACCAAGGACTCCAAGGCCTTCGCGCAGATGGGCATTGATGATTCACGCAAGACAAACCGG	1200
Db	1456	ACCAAGGACTCCAAGGCCTTCGCGCAGATGGGCATTGATGATTCACGCAAGACAAACCGG	1515
Qy	1201	GGCACCCCAAGATCCCTGAAACCTCAGGATGAGGTGGATGAGTTCCCTGAGCCGTGCCATC	1260
Db	1516	GGCACCCCAAGATCCCTGAAACCTCAGGATGAGGTGGATGAGTTCCCTGAGCCGTGCCATC	1575
Qy	1261	GATGCCCGCAGCATTTGATCAGCTGCGGAAGGACATGTGCGCGGTTTTTGGCTCACCTTC	1320
Db	1576	GATGCCCGCAGCATTTGATCAGCTGCGGAAGGACATGTGCGCGGTTTTTGGCTCACCTTC	1635
Qy	1321	CAGAGAGAGATTTTGAGAAGAAAGTACTCCCGGAAGGTGGATCCCGCTTCGGAGCGCTAC	1380
Db	1636	CAGAGAGAGATTTTGAGAAGAAAGTACTCCCGGAAGGTGGATCCCGCTTCGGAGCGCTAC	1695
Qy	1381	GTTGCCGTGCGCCTGTGTGTTCTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCA	1440
Db	1696	GTTGCCGTGCGCCTGTGTGTTCTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCA	1755
Qy	1441	CACTCCACCTGATGCTGGGATTTATGCCAGCATTTCCCTGCTGCTGCTTAATCACCGTG	1500
Db	1756	CACTCCACCTGATGCTGGGATTTATGCCAGCATTTCCCTGCTGCTGCTTAATCACCGTG	1815
Qy	1501	CTGATCTGTGCTGTACTCCTGTGTTCTCTGTTCCTTAAGGCCCTGCAACGCTGTGTC	1560
Db	1816	CTGATCTGTGCTGTACTCCTGTGTTCTCTGTTCCTTAAGGCCCTGCAACGCTGTGTC	1875
Qy	1561	CGCAGCATTTGCGCTGCAGGGCACATAGCACCGCAGTTGGCATCTTTTCGGTCCGTGTT	1620
Db	1876	CGCAGCATTTGCGCTGCAGGGCACATAGCACCGCAGTTGGCATCTTTTCGGTCCGTGTT	1935
Qy	1621	GTGTTTACTTCTGCCATTTGCCACATGTTACACTGCTGACATCACTGGCTGCCACATACGGAGCTG	1680
Db	1936	GTGTTTACTTCTGCCATTTGCCACATGTTACACTGCTGACATCACTGGCTGCCACATACGGAGCTG	1995
Qy	1681	GCAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGGCTGCCACATACGGAGCTG	1740
Db	1996	GCAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGGCTGCCACATACGGAGCTG	2055
Qy	1741	AATTACTTCTTGGGCGCTGGATGCTCCCTGTGTGAGGCAACCATGCCACCTGCAGCTTT	1800
Db	2056	AATTACTTCTTGGGCGCTGGATGCTCCCTGTGTGAGGCAACCATGCCACCTGCAGCTTT	2115
Qy	1801	CTGAGGTGTTTC	1812
Db	2116	CTGAGGTGTTTC	2127
RESULT 3			
AAD08563			
ID	AAD08563 standard; DNA; 3549 BP.		
XX	AAD08563;		
XX	AAD08563;		
XX	04-SEP-2001 (first entry)		
XX	Human cardiac adenylcyclase VI (ACVI) isoform #1 DNA.		
XX			

PT Novel polynucleotide encoding a modified adenylyl cyclase polypeptide
PT useful for enhancing cardiac function in mammalian hearts, and for
PT treating heart disease, especially congestive heart failure -
XX
PS Claim 6; Page 134-140; 153pp; English.

XX The present invention relates to methods and compositions for enhancing
CC cardiac function in mammalian hearts by inserting transgenes encoding
CC beta-adrenergic signalling proteins (beta-ASP) which increase
CC beta-adrenergic responsiveness within the myocardium using in vivo
CC gene therapy. The beta-ASPs of the invention include beta-adrenergic
CC receptors (beta-Ak), adenylyl cyclases (also referred as adenylylase,
CC adenylyl cyclase and cAMP synthetase) and G-protein receptor kinase
CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
CC in mammalian hearts and for treating heart disease, especially
CC congestive heart failure. The present DNA sequence encodes human
CC cardiac adenylyl cyclase VI (ACVI) isoform which is used for generating
CC a fourth beta-ASP transgene, used in the exemplification
CC of the invention.

XX Sequence 3552 BP; 686 A; 1037 C; 1068 G; 761 T; 0 other;

Query Match 97.3%; Score 1763.4; DB 22; Length 3552;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 21; Indels 3; Gaps 1;

QY 3 TAACGTGGTGGCATCTCGCGCAGTGCAGGTGCGGGCGCTTTCGCAGCAGACC 62
DB TTTACGTGGTGGCATCTCGCGCAGTGCAGGTGCGGGCGCTTTCGCAGCAGACC 695
QY 63 GCGCAGCCCTCTGGGGCTCTGGTGGCCCTGTGTTTGTATACATCGATACACGCT 122
DB GCGCAGCCCTCTGGGGCTCTGGTGGCCCTGTGTTTGTATACATCGATACACGCT 755
QY 123 CTTCCCATCCGATCGCGGCTGCGTCTCAGCGGCTGGGCTTCCACCTTGCATTT 182
DB CTTCCCATCCGATCGCGGCTGCGTCTCAGCGGCTGGGCTTCCACCTTGCATTT 815
QY 183 GATCTGGCTGGCACTTAACCGTGGTGGTATGCTTCTCGGAAGCAGCTCGGTGCCAA 242
DB GATCTGGCTGGCACTTAACCGTGGTGGTATGCTTCTCGGAAGCAGCTCGGTGCCAA 875
QY 243 TGTGCTGCTTTCCTCTGCACCAAGTCAATTAGCATCTGCACACATATCCAGCAGGT 302
DB TGTGCTGCTTTCCTCTGCACCAAGTCAATTAGCATCTGCACACATATCCAGCAGGT 935
QY 303 GTCTCAGCCAGGCTTTTCAGAGACCGCAGTTACATCCAGGCCGGCTCCACCTGCA 362
DB GTCTCAGCCAGGCTTTTCAGAGACCGCAGTTACATCCAGGCCGGCTCCACCTGCA 995
QY 363 GCATGAGATCGGCAGAGGCGGCTGCTGCTGGTATTTGCCCGCAGCAGCTTGCCAT 422
DB GCATGAGATCGGCAGAGGCGGCTGCTGCTGGTATTTGCCCGCAGCAGCTTGCCAT 1055
QY 423 GGAGATGAAGAGACATCAACACAAAAAAGACATGATGTTCCCAAGATCTACAT 1115
DB GGAGATGAAGAGACATCAACACAAAAAAGACATGATGTTCCCAAGATCTACAT 1115
QY 480 ACAGAGCATGACATGTCAGCATCTGTTTCAGACATTTAGGGCTTCCAGGCTGGC 539
DB ACAGAGCATGACATGTCAGCATCTGTTTCAGACATTTAGGGCTTCCAGGCTGGC 1175
QY 540 ATCCAGTGCATGGCGAGGAGCTGTCATGACCCCTGAATGAGCTCTTTGCCCGTTTCA 599
DB ATCCAGTGCATGGCGAGGAGCTGTCATGACCCCTGAATGAGCTCTTTGCCCGTTTCA 1235
QY 600 CAAGCTGGCTGGGAGATCATGCTGAGATCAAGATCTTTGGGGAGCTGTTACTAC 659
DB CAAGCTGGCTGGGAGATCATGCTGAGATCAAGATCTTTGGGGAGCTGTTACTAC 1295
QY 660 TGTGTACGGGCTGCGGAGGCGCGGCGCACCATGCCACTGCTGTGTGAGATGGGGT 719
DB TGTGTACGGGCTGCGGAGGCGCGGCGCACCATGCCACTGCTGTGTGAGATGGGGT 1355

Qy	1560	CCGAGCAGATTGTCGGCTCACGGGCACATAGCACCAGATTGGCATCTTTTCGGTCCCTGCT	1619
Db	2214	CCGAGCAGATTGTCGGCTCACGGGCACATAGCACCAGATTGGCATCTTTTCGGTCCCTGCT	2273
Qy	1620	TGCTGTTTACTCTTGCCATTCGCCAACATGTTTACCTGTAAACCACACCCCATACGAGCTG	1679
Db	2274	TGCTGTTTACTCTTGCCATTCGCCAACATGTTTACCTGTAAACCACACCCCATACGAGCTG	2333
Qy	1680	TGCAGCCCGGATGCTGAATTTAAACACCTGCTGACATCACTGCCTGCCACTTGCAGCAGCT	1739
Db	2334	TGCAGCCCGGATGCTGAATTTAAACACCTGCTGACATCACTGCCTGCCACTTGCAGCAGCT	2399
Qy	1740	CAATTACTCTCTGGGCTGGATGCTCCCTCTGTGTAGGGCACCATGCCCACCTGCAGCTT	1799
Db	2394	CAATTACTCTCTGGGCTGGATGCTCCCTCTGTGTAGGGCACCATGCCCACCTGCAGCTT	2453
Qy	1800	TCCTGAGGTGTC 1812	
Db	2454	TCCGAGTACTTC 2466	
RESULT 7			
ID	AAQ42525		
XX	AAQ42525 standard; DNA; 4046 BP.		
AC	AAQ42525;		
DT	14-SEP-1993 (first entry)		
XX	Cardiac adenyl cyclase gene.		
DE	Regulation; cardiac function; heart; heart failure; ss.		
KW	Canis familiaris.		
OS			
XX	Key	Location/Qualifiers	
FT	CDS	131..3627	
FT		/tag= a	
XX	EP543137-A.		
PN			
XX	26-MAY-1993.		
PD			
XX	12-OCT-1992; 92EP-0117374.		
PF			
XX	18-NOV-1991; 91US-0793961.		
PR			
XX	(AMCY) AMERICAN CYANAMID CO.		
PA			
XX	Ishikawa Y;		
PI			
XX	WPT; 1993-168873/21.		
DR	P-PSDB; AAR37309.		
DR			
XX	Purified DNA encoding cardiac adenyl cyclase - useful to, screen		
PT	for cpds. which stimulate activity of the cyclase		
PT	Claim 1; Fig 2; 34pp; English.		
PS			
XX	A canine heart cDNA library was constructed in lambda gt10 and was		
CC	screened with a 970 bp AatI-HincII fragment from type I adenyl		
CC	cyclase cDNA probe (encodes the first cytoplasmic domain of adenyl		
CC	cyclase, which has significant homology to other previously known		
CC	types of adenyl cyclase). One positive clone, of 5.4 kb was obtd.		
CC	Positive colonies were subcloned into pUC18 and further subcloned		
CC	and sequenced bidirectionally. The 5.4 kb clone was used to		
CC	rescreen the library and on averlapping clone contg. the 5' end of		
CC	the gene was isolated. Together the two clones cover the complete		
CC	canine cardiac adenyl cyclase gene. The gene is suspected of		
CC	being involved in the regulation of cardiac function and it is thought		
CC	that decreased activity of adenyl cyclase in the heart may be a		
CC	major factor in the development of heart failure. Thus, the adenyl		

CC cyclase gene is useful to screen cpds. which stimulate the activity
XX of the cyclase.
SQ Sequence 4046 BP; 743 A; 1206 C; 1254 G; 843 T; 0 other;

Query Match 84.3%; Score 1527.8; DB 14; Length 4046;
Best Local Similarity 91.0%; Pred. No. 0;
Matches 1648; Conservative 0; Mismatches 157; Indels 6; Gaps 2;

QY	5	ACCTGCTGCTGGCAGTCCCTGGCGGCAGTGCAGTGGGGCGCTTTTCGACGACAGACCCGC	64
DB	762	ACGTGGTGTGGGCATCTCGGACGCGTTACAGTTGGGGTGCCCTGGGACGCAACCCGCC	821
QY	65	GCAGCCCTCTCGGGGCTCTGCTGGCCCTGTGTTCTTGTATACATCGATACACGCTCC	124
DB	822	GCAGCCCTCTGTGGGCTCTGTGGCCCTGTGTTCTTGTCTACATCACCTACACGCTCC	881
QY	125	TCCCATTCGCATGCGGGCTGCGCTCTCAGCGGCTTGGGCTCTCACCTTGCAATTTGA	184
DB	882	TACCATTCGCATGCGGGCAGCTGCTTTCAGTGGCTTGGGCTGTCCACCTGCATTTGA	941
QY	185	TCTTGGCTGGCAACTTAACCGTGGTGCCTTCTCTGGAAGCAGCTCGGTGCGCAATG	244
DB	942	TCTTGGCTGGCAACTCAACCGGCTGGAGGCTTCTCTTGGAAAGCAGCTCGGTGCGCAACA	1001
QY	245	TGCTGCTGTTCTCTGCACCAAGTCAATAGCATCTGCACACACTATCCAGCAGAGGTGT	304
DB	1002	TGCTGCTGTTCTCTGCACCAAGTCAATAGCATCTGCACACACTATCCAGCAGTGGTCT	1061
QY	305	CTCAGGCCGAGGCTTTTCAGGAGACCGGAGTTACATCCAGGCGGGCTCCACCTCGAGC	364
DB	1062	CTCAGGCCGAGGCTTTTCAGGAGACCGGAGTTACATTCAGGCGGGCTGCACCTGCCAG	1121
QY	365	ATCAGAAATGGCAGCAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	424
DB	1122	ATGAGAACCGGAGCAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1181
QY	425	AGATGAAGAAGACATCAACACAAAAAAGAGAC---ATGTTCCACAAAGATCTACATAC	481
DB	1182	AGATGAAGAAGATATCAACACAAAAAAGAGACATGATTTCCACAAAGATCTACATCC	1241
QY	482	AGAACATGACATGTGACATGCTGTTTCGACAGATTTGAGGCTTTCACAGGCTGGCAT	541
DB	1242	AGAAGCATGACATGTGACATGCTGTTTCGACAGATTTGAAAGGCTTTCACAGGCTGGCGT	1301
QY	542	CCCACTGCACTGGCAGGAGCTGGTCAATGACCTGAATGAGCTCTTTGCGCGGTTTGACA	601
DB	1302	CCCACTGCACTGGCAGGAGCTGGTCAATGACCTGAACAGCTCTTTGCGCGGTTTGACA	1361
QY	602	AGCTGCTGGGAGATCACTGCTGAGGATCAAGATCTTTAGGGGACTGTTACTACTGTG	661
DB	1362	AGCTGCTGGGAGATCACTGCTGAGGATCAAGATCTTTAGGGGACTGTTACTACTGTG	1421
QY	662	TGTCAGGCTGCGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	721
DB	1422	TGTCAGGCTGCGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	1481
QY	722	ACATGATGAGGCGCATCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	781
DB	1482	ACATGATGAGGCGCATCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1541
QY	782	TGGGCATCCACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	841
DB	1542	TGGGCATCCACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	1601
QY	842	ATGCTGTGGTCCCATGATGTGACCTTGGCCACACCATGGAAGCAGGAGCGGCTGGCC	901
DB	1602	ACGTGTGGTCCCATGATGTGACCTTGGCCACACCATGGAAGCAGGAGCGGCTGGCC	1658
QY	902	GCATCCACATCACTCGGCGCAACACTGACGTACCTGAACGGGACTACGAAGTGGAGCCAG	961
DB	1659	GCATCCACATCACTCGGCGCAACACTGACGTACCTGAACGGGACTACGAAGTGGAGCCAG	1718

Type VI adenyl cyclase coding sequence.

Adenyl cyclase; type I; type II; recombinant; enzyme; cAMP;
cyclic AMP; adenosine monophosphate; screening; stimulation;

RESULT 8
AAAS3923
ID AAAS3923 standard; cDNA; 4131 BP.

XX AAAS3923;

XX AAAS3923;
DT 03-JAN-2001 (first entry)

XX Type VI adenyl cyclase coding sequence.

XX Adenyl cyclase; type I; type II; recombinant; enzyme; cAMP;
KW cyclic AMP; adenosine monophosphate; screening; stimulation;

KW inhibition; treatment; cholera; pituitary tumour; heart failure;
 KW ischaemia; endocrine disorder; cell necrosis;
 KW pseudohypoparathyroidism; endocrine deficiency; human; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 14..3556
 FT /*tag= a
 FT /product= Type VI adenyl cyclase
 XX
 PN US6107076-A.
 XX
 XX 22-AUG-2000.
 XX
 XX 04-OCT-1996; 96US-0726214.
 XX
 XX 04-OCT-1995; 95US-0005498.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX Gilman AG, Tang W;
 XX
 DR WPI; 2000-578539/54.
 DR P-PSDB; AAB02010.
 XX
 XX Novel soluble mammalian polypeptide composition comprising adenyl
 PT cyclase activity for screening stimulators and inhibitors of adenyl
 PT cyclase, is activated by Gsalpha
 XX
 PS Disclosure; Columns 75-78; 73pp; English.
 XX
 CC A recombinant Adenyl cyclase is described which lacks membrane
 CC bound domains. Separation and purification of the recombinant
 CC enzyme is much easier compared with wild type enzymes and the
 CC recombinant enzyme is more stable than the wild type enzyme which
 CC allows easier screening of compounds that stimulate and inhibit
 CC Adenyl cyclase activity. The recombinant adenyl cyclase comprises
 CC a chimera of adenyl cyclase C.1 and C.2 domains linked covalently.
 CC The domains may be linked by a linker peptide. The recombinant
 CC adenyl cyclase is useful for screening inhibitors and stimulators
 CC of adenyl cyclase activity. Inhibitors of the enzyme are useful for
 CC treating cholera, pituitary tumors, heart failure, ischaemia,
 CC endocrine disorders and cell necrosis. Stimulators of adenyl
 CC cyclase are useful for treating pseudohypoparathyroidism and other
 CC endocrine deficiencies.
 XX
 SQ Sequence 4131 BP; 835 A; 1190 C; 1182 G; 924 T; 0 other;

Query Match 79.3%; Score 1437.2; DB 21; Length 4131;
 Best Local Similarity 87.5%; Pred. No. 0;
 Matches 1584; Conservative 0; Mismatches 223; Indels 3; Gaps 1;

Qy 5 ACGTGGTCTGGGATCCTGGCGGAGTGACAGTTCGGGGGCGCTTCGACGACAGCCGC 64
 Db 687 ATGTGGTCTGGGATCCTAGCAGCGGTGCAAGTCGGGGTGCCTCGACGCCAACCCAC 746
 Qy 65 GCAGCCCTCGCGGCTCTGGTGGCCCTGTGTTGTATATACATCCATACAGCTCC 124
 Db 747 GCAGCCCTCAGCAGGCGCTTGGTGGCCCGGTGTTCTCGTCTATACCTACACACTTC 806
 Qy 125 TCCCATCCGATCGGGCTCCCTCGCTCAGCGGCTGGGCTCTCCACCTTGCATTGA 184
 Db 807 TTCCCATCTGATCGGAGCGCGGTGCTCAGTGGCTGGGTCTTCCACCTGCATTGA 866
 Qy 185 TCTTGGCTGCACACTTAACGCTGGTGAIGCTTCTCTTGGAGCAGCTCGGTGCCAATG 244
 Db 867 TTTTGGCTGGCATCTCAACAATGGTGACCCCTTCCCTTTTGGAGCAGCTCGTGTCTAACG 926
 Qy 245 TGCTGCTTCTCTGACACCACTGATAGCATCTGCACACATATCCACGAGGTGT 304
 Db 927 TGGTGTCTTCTGTGCAACCAATGCCATCGTGTCTGCACGACTACCCCGCTGAAGTGT 986

Qy 305 CTCAGCCCGAGCCCTTTCAGGAGACCCCGAGTTACATCCAGCCCGGCTCCACCTGCAGC 364
 Db 987 CTCAGCGCAAGCCTTTTCAGGAGACCCCGTGTACATCCAGCCCGGCTGCACCTTGCAGC 1046
 Qy 365 ATGAGAATCGCAGCAGGAGCGGCTGCTGTGCGTATTTGCCAGACACGCTTGCATGG 424
 Db 1047 ATGAGAATCGACAGCAGGAGCGGCTGCTGTGCGGTGTTGCCCGAGCATGTTGCCATGG 1106
 Qy 425 AGATGAAGAAGACATCAACACAAAAAAGAGAC--ATGTTCCACAAAGATCTACATAC 481
 Db 1107 AATGAAGAAGATATCAACACAAAAAAGAGACATGTTCCACAAAGATTTACATCC 1166
 Qy 482 AGAAGCATGACATGTCAGCATCTCTTTTCAGACATTTAGGGGTTTACCAGCCTGGCAT 541
 Db 1167 AGAAGCATGACATGTCAGCATCTCTTTTCAGACATCGAGGGCTTTCACAGCCTGGCT 1226
 Qy 542 CCCAGTGCATGCGCAGGAGCTGGTCAATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACA 601
 Db 1227 CCCAGTGCATGCGCAGGAGCTGGTCAATGAGCTTGAATGAGCTCTTTGCCCGGTTTGACA 1286
 Qy 602 AGCTGGCTGGGAGAAATCACTGCCTGAGGATCAAGATCTTGGGGAGCTGTACTACTGTG 661
 Db 1287 AGCTGGCTGGGAGAAATCACTGTCTGAGGATCAAGATCTTAGGAGACTGTTACTACTGTG 1346
 Qy 662 TGTCAAGGCTGCCGAGGCGCGGCGGACCATGCCACTGCTGTGTGAGATGGGGTAG 721
 Db 1347 TGTCCGGGCTGCCGAGGCGCGGCGGAGACCATGCCACTGCTGTGTGAGATGGGGTAG 1406
 Qy 722 ACATGATTGAGGCAATCTCGCTGTGTGAGGTGACAGGTGTGAATGTGAACATTCGCG 781
 Db 1407 ACATGATCGAGGCCATCTCGCTGGTGGTAAAGGTAAAGGTGTAATGTGAACATTCGCG 1466
 Qy 782 TGGGCATCCACAGCGGCGCTGCACCTGCGGCTCTTGGCTTGGGAAATGCGAGTTCG 841
 Db 1467 TGGGCATCCACAGCGGCGGTGTACACTGCGGTGCTTGGTTCGCGAAATGCGAGTTG 1526
 Qy 842 ATGTGTGTCCAATGATGTGACCTTGGCCAAACCATCATGGAAGCAGGAGCGGGCTGGCC 901
 Db 1527 ATGTGTGTCCAACGATGTGACCTTGGCCAAACCATCATGAGCGGGGCGCGGGGCGC 1586
 Qy 902 GCATCCACATCACTCGGCGCAACATGCACTGACCTGGAAGCGGAGCTACGAAGTGGAGCCAG 961
 Db 1587 GCATCCACATCACTCGGCGCAACATGCACTGACCTGGAAGCGGAGCTATGAGTGGAGCCAG 1646
 Qy 962 GCGGTGTGGCAAGCGCAACCGCTACCTCAAGGAGCAGACATTCAGACTTCTCTCATCC 1021
 Db 1647 GCGGTGTGGGTGAGCGCAACCGCTACCTCAAGGAGCAGTGCATTCAGACTTCTCTCATAC 1706
 Qy 1022 TGGGCGCGAGCCAGAAAGCGGAAAGAGAGATGCTGCGCAAGCTGCAGCGGAGCTC 1081
 Db 1707 TAGGAGCGAGCCAGAAAGCGGAAAGAGAGAGAGGCGCATGCTGCTCAAGCTGCAGCGGAGCG 1766
 Qy 1082 GGGCCAACTCCATGGAAGGCTGATGCGCGCATGGGTTCCTGATGCTGCTTCTCCCGGA 1141
 Db 1767 GGGCCAACTCCATGGAAGGACTGATGCGCGCTGGGTTCCTGACCGTCTCTTCTCCCGGA 1826
 Qy 1142 CCAAGGACTCCAAAGCGCTTCCCGCAGATGGGCTTGTGATTCACAGAAAGACAAACCGG 1201
 Db 1827 CCAAGGACTCTAAGGCATTCGACAGATGGGCTGCTGACTCTAGCAAGAGAGAACCGG 1886
 Qy 1202 GCACCCAAAGTCCCTGAACCTCGAGGATGAGGTGAGTTCCTGAGCGCTGCATCG 1261
 Db 1887 GTGCCCCAAGATGCTCTGAACCTCGAGGATGAGGTGAGGAGTTCCTGGGCGGAGCCATCG 1946
 Qy 1262 ATGCCCGCAGCATTTGATCAGCTGGGAAAGAGCAGTGTGGCGGGTTTTTGTCTACCTTCC 1321
 Db 1947 ATGCCCGAAGCATCGACCGAGCTGGCTAAGAGCAGTGTGGCGGGTTCTGTCTACCTTCC 2006
 Qy 1322 AGAGAGGATTTTTCAGAAAGTACTCCCGGAAGGTGATCCCGCTTCGGAGCCTACG 1381
 Db 2007 AGAGGAGGATCTCGAAGAAGATATTCCAGGAAGTAGACCTCGTTTCGGAGCCTACG 2066
 Qy 1382 TTGCTGTGCGCTGTGTTGCTTCTGCTTCTATCTGCTTCATCCAGCTTCTAAATTTTCCAC 1441

[illegible]

RESULT 9	
ABI199680	
ID	ABI199680 standard; cDNA; 5841 BP.
XX	
AC	ABI199680;
XX	
AC	
XX	
DT	07-MAR-2002 (first entry)
XX	
DE	Mouse ischaemic condition related cDNA sequence SEQ ID NO:716.
XX	
KW	Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW	vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX	
OS	Mus musculus.
XX	
WO	WO200188188-A2.
XX	
PN	
PD	22-NOV-2001.
XX	
PF	18-MAY-2001; 2001WO-JP04192.
XX	
PR	18-MAY-2000; 2000JP-0145977.
XX	
PA	(UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX	
PI	Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX	
DR	WPI; 2002-034733/04.
DR	P-PSDB; ABB57257.
XX	
PT	Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT	expression levels of particular genes defined in the specification or
PT	by determining the expression profile of a gene group comprising these
PT	genes -
XX	
PS	Claim 2; Page 1771-1780; 2690pp; English.
XX	
CC	The present invention describes a method for examining ischaemic
CC	conditions, comprising measuring the expression levels of particular
CC	genes (I) in a test sample or determining the expression profile of a
CC	gene group in the sample comprising genes selected from (I). The method

AC	AAX00462;	AC
XX		
DT	25-MAY-1999 (first entry)	
XX		
DE	Human type V adenylyl cyclase coding sequence.	
XX		
KW	Type V adenylyl cyclase; human; hAC5; heart disease; brain;	
KW	therapy; diagnosis; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9901546-A1.	
PD	14-JAN-1999.	
XX		
PF	01-JUL-1998; 98WO-US13540.	
XX		
PR	01-JUL-1997; 97US-0886362.	
PR	01-JUL-1997; 97US-0070901.	
XX		
PA	(CORT-) COR THERAPEUTICS INC.	
XX		
PI	Tomlinson JA;	
XX		
DR	WPI: 1999-106048/09.	
DR	P-PSDB; AAW30600.	
XX		
PT	Newly isolated and purified human type V adenylyl cyclase (hAC5)	
PT	polypeptide - useful for identifying potential therapeutic agents	
PT	that modulate hAC5 activity, and for the diagnosis of	
PT	hAC5-associated diseases and disorders	
XX		
PS	Claim 3; Fig 1a-h; 4Opp; English.	
XX		
CC	This sequence encodes the human type V adenylyl cyclase (hAC5) of the	
CC	invention. hAC5 has a similar putative structure to other adenylyl	
CC	cyclase isoforms but, like type VI, is distinguishable in that it has	
CC	larger N-terminus and a relatively shorter C-terminus as it lacks the	
CC	c2b region. The hAC5 polypeptides are useful in assays that screen for	
CC	potential therapeutic agents, which modulate hAC5 activity. These	
CC	polypeptides are also useful in assays for the diagnosis of diseases a	
CC	disorders. Agonists of hAC5 are useful control agents in such assays,	
CC	they may have useful effects in vivo for treating disease. Antibodies	
CC	acting as (ant)agonists have diagnostic and therapeutic effects, and a	
CC	useful in immunoassays for hAC5. (Ant)agonists are particularly useful	
CC	treating diseases caused by abnormal hAC5 activity (e.g. In the heart	
CC	brain), and in diseases, which are alleviated by modulating hAC5	
CC	activity. The oligonucleotides are useful in methods that inhibit or	
CC	regulate hAC5 expression in vivo and in vitro. The cloning of the huma	
CC	isotype of AC5 enables the development of tissue-specific and selectiv	
CC	pharmacological agents for use in treating particular human diseases	
CC	associated with hAC5.	
XX		
SQ	Sequence 4523 BP; 840 A; 1419 C; 1428 G; 836 T; 0 other;	
	Query Match 49.4%; Score 895; DB 20; Length 4523;	
	Best Local Similarity 69.8%; Pred. No. 5.7e-229;	
	Matches 1277; Conservative 0; Mismatches 525; Indels 27; Gaps	
QY	5 ACCTGGTGTCTGGGCATCTCTGGCGGAGTGCAGGTCTGGGGGCGCTTTTCGCACGACACCCG 64	
Db	1046 ATCGGCTCATCGCGGTGGTGTCTGGCGTCCAGGTGGTGGCCCTGCTGCTGGCGGAGCCAC 1105	
QY	65 GCAGCCCCCTCGCGGCCCTCTGGTGCCTCTGTTCTTTGTATACATCATACACGCTCC 124	
Db	1106 GCAGCGCCTCTGAGGCGCATCTGGTGACCGTGTCTTCATCTACACCATCTACACGCTGC 1165	
QY	125 TCCCCATCCGCATCGGGCTGCGGTCCCTCAGCGGCGCTGGCCCTCTCCACCTTGATTTGA 184	
Db	1166 TGCCCGTGGCAFTGCGGGCGGCGAGTGC TCAGCGGGGTGCTCTCTGTCCGCCCTCCACCTGG 1235	
QY	185 TCTTTGGCTGGCAACTTAACCGGTGGTGTATGCCCTTCTCTGGAAGCAGCGCTCGGTGCCAATG 244	

[illegible]

QY 842 ATGTGTGGTCCATATGATGTACCTGGCCAAACACATGGAAGCAGGACCGGCTGGCC 901
Db 1261 ACGTGTGGTCTACGATGTACACATGCGCCAAACACATGGAAGCTGCGCGCAGGCG 1320
QY 902 GCATCCACATCACTCGGGCAACACTCCAGTACCTGAACGGGAGCTACGAGTGGAGCCAG 961
Db 1321 GCATCCACATCACTCAAGGGCCACTCACTTACCTGAACGGGAGCTATGAGGTGGAGCCAG 1380
QY 962 GCGGTGGTGGCAACGCAACGCTACTCAAGGAGCAGCACATTTGAGACTTTCCTCATCC 1021
Db 1381 GCTGTGGTGGAGCGCAATGCTACTCAAGGAGCAGCACATCGAGACTTTCCTCATCC 1440
QY 1022 TGGGCGCCAGCCAGAAACGGAAGAGAGGAAGGCGATGTGGCCAAAGCTGCACGCGACTC 1081
Db 1441 TGGCGTGTACCCAGAGCGAAGAGAGAGAGGAGCCATGATCGCCAAAGATGAACCGCCAGA 1500
QY 1082 GGGCCAACTCCATGGAGGGCTGATCGCGGATGGGTTCTGTATCGTGCCTTCTCC --- 1137
Db 1501 GAACCAACTCCATTTGGACACAATCCGCTCTACTTGGGGAGCTGAGCGCCCTTCTTACAACC 1560
QY 1138 -----CGGACCAAGGACTCCAAAGGCTTCCGCCAGATGGGCATTGATGATTCAGCA 1189
Db 1561 ACTTGGGTGCAACACAGGTGTCCAAGAAATGAAGAGATGGCTTTGAGGCCCA--- 1617
QY 1190 AAGACAACCGGGCCACCCAGATGCCCTGAACCTGAGGATGAGGTGGATGATTCCTGA 1249
Db 1618 ---AGGACAAGATGATCCAGGAAGTGCCAAACCTGAGGATGAAGTGGAGCTTCTG 1674
QY 1250 GCGGTGCCATCGATGCCCGACGATGATCAGCTCGGAGGACCATGTCGCCGGTTT 1309
Db 1675 GTGAGCCATCGATGCCAGGATGATGACAGCTCGGATCCGAACACGTCGGAAGATTCC 1734
QY 1310 TGCTACCTTCCAGAGAGGAGTTTGAAGAAGTACTCCCGGAAGTGGATCCCGCT 1369
Db 1735 TCTTGACCTTTAGGAGCGCGACTTAGAAGAAGTACTCCAAAGCAGGTGGATGACCGAT 1794
QY 1370 TCGGAGCCTACGTTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1429
Db 1795 TTGGTGGCTATGTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1854
QY 1430 TAATTTTCCCACTCCACCTGTATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGC 1489
Db 1855 CCATTTGCTCCCACTCCCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1914
QY 1490 TAATCAGCTGTGATCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1549
Db 1915 CTTGTGTGTGTTATATCTGTGATCTACGCTGTGTGAAGCTTCTCCCTACTCCCTGCG 1974
QY 1550 AAGCTGTGCTCCCGCAGCATGTCGCTCAGGGGCACATAGCAGCCGAGTTGGATCTTTT 1609
Db 1975 AGACACTCTCCAGGAAGATAGTGCATCCAAAGAAGAACAGCACACCTGTGGGGTGTTC 2034
QY 1610 CGTCTCTGT 1669
Db 2035 CCATCAGCTGT 2094
QY 1670 TAGGAGCTGTGAGCGCCGATGCTGAATTTAACACCTGCTGACATCACTGCTGCCAC 1729
Db 2095 TGT 2154
QY 1730 TGCAGCAG-----CTCATTTACTTCTTGGGCTGATGCTGCCCTGTGTGAGGGACCA 1783
Db 2155 TGAATGAGTGTGGCTTTCACTACAGCTGTGGGACGAGGAGGCTTCTGTGGCAGGCC 2214
QY 1784 TGGCCACCTGCGAGCTTCTCTGAGGTGTC 1812
Db 2215 AGTCCAACTGCAACTTCCAGAGTACTTC 2243

RESULT 14
AAD28058
ID AAD28058 standard; cDNA; 3137 BP.
.XX

AC AAD28058;
XX 22-APR-2002 (first entry)
XX Human adenyl and guanylyl cyclase (ADGUC)-2 cDNA.
XX
XX Human; adenyl and guanylyl cyclase; ADGUC-2; cardiovascular disorder;
KW angina pectoris; myocardial infarction; vision disorder; keratitis;
KW iritis; cataract; neurological disorder; epilepsy; Alzheimer's disease;
KW Pick's disease; stroke; mental disorder; mood and anxiety disorder;
KW reproductive disorder; infertility; endometriosis; impotence; asthma;
KW smooth muscle disorder; migraine; bacterial infection; gene therapy;
KW transgenic animal; vaccine; enzyme; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT 1..2514
FT CDS /*tag= a
FT /product= "Human ADGUC-2 protein"
XX
XX WO200202757-A2.
XX
XX 10-JAN-2002.
XX
XX 26-JUN-2001; 2001WO-US20491.
XX
XX 29-JUN-2000; 2000US-215476P.
XX
XX 04-AUG-2000; 2000US-223545P.
XX
XX 31-AUG-2000; 2000US-229876P.
XX
XX 22-SEP-2000; 2000US-234838P.
XX
XX 29-SEP-2000; 2000US-236483P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Gandhi AR, Tribouley C, Ding L, Lu DAM, Lee EA, Yue H, Yang J;
PI Baughn MR, Thornton M, Yao MG, Walla NK, Tang YT, Elliott VS;
PI Lu Y;
XX
XX WPI; 2002-154740/20.
XX
XX P-PSDB; AAE17130.
XX
XX Novel human adenyl and guanylyl cyclases and polynucleotides encoding
PT the cyclases, useful for treating, diagnosing or preventing
PT cardiovascular, neurological, vision, reproduction and smooth muscle
PT disorders
XX
XX Claim 5; Page 112-113; 116pp; English.
XX
XX The invention relates to human adenyl and guanylyl cyclases (ADGUC)
CC preferably ADGUC1-ADGUC5 and nucleic acid molecules encoding such
CC polypeptides. ADGUC sequences are useful in the diagnosis, prevention
CC and treatment of cardiovascular disorders (e.g. angina pectoris,
CC myocardial infarction, ischaemic heart disease, hypertension and
CC atherosclerosis), vision disorders (e.g. keratoconjunctivitis sicca,
CC keratitis, iritis, cataract), neurological disorders (e.g. epilepsy,
CC Alzheimer's disease, Pick's disease, Huntington's disease, dementia,
CC Parkinson's disease, Creutzfeldt-Jakob disease, stroke, schizophrenia,
CC mental disorders including mood and anxiety and prion diseases including
CC kuru), reproductive disorders (e.g. infertility, endometriosis,
CC impotence, uterine fibroid and gynaecomastia), smooth muscle disorders
CC (e.g. arrhythmias, asthma and migraine) and bacterial infections.
CC ADGUC polynucleotides are useful for creating knock-in humanised animals
CC or transgenic animals to model human diseases. They are useful in
CC somatic or germline gene therapy. ADGUC polynucleotides are also useful
CC for detecting differences in the chromosomal location due to
CC translocation, inversion, etc. among normal, carrier or affected
CC individuals. ADGUC polypeptides are useful in a number of drug screening
CC techniques and in vaccines. The present sequence is human ADGUC-2 cDNA.
XX
XX Sequence 3137 BP; 553 A; 973 C; 1044 G; 567 T; 0 other;

Query Match 44.1%; Score 799; DB 24; Length 3137;

Best Local Similarity 73.5%; Pred. No. 2.4e-203;
Matches 1069; Conservative 0; Mismatches 365; Indels 21; Gaps 3;

QY	5	ACGTGGTGGCTGGGCATCCTGGCGGACGTGCGAGTGGGGGCGCTTTCGACGACGACCGC	64
Db	1064	ATGCGCTCATCGCGTGGTGGTGGCGGCTCAGGTGGGGCTGCTGCTGGCGGAGCCAC	1123
QY	65	GCAGCCCTCTGGCGGCTCTGGTGGCCCTGTGTCTTTGTATACATGCATACACGCTCC	124
Db	1124	GCAGCGCTCTGAGGGCATCTGGTGGACCGGTGTTCTTCACTACACCATCTACACGCTGC	1183
QY	125	TCCCATTCGGATCGGGCTGGCGTCTCAGCGGCTTGGGCTCTCCACCTTGCAATTGA	184
Db	1184	TGCCGTGGCATCGGGGCGGACGTGCTCAGCGGGTGTCTCTGTCGGCCCTCCACCTGG	1243
QY	185	TCTTGGCTGSCAACTTAAACCGTGGTGTGCTTCTCTGGAACGACGTGGTCCCAATG	244
Db	1244	CCATCGCCCTGGCACCACGCCACGACCAAGTTCCTGCTGGAACGACGTGTCTCCAAATG	1303
QY	245	TGCTGTGTTCTCTGCACCAACGCTCATTAAGCACTCTGCACACACTATCCAGCAGAGTGT	304
Db	1304	TTCTCAATTTCTCTGCACCAACATCTGTGGGTGTCTGCACCCACTATCCGGCTCAGGTCT	1363
QY	305	CTCAGCGCGAGGCTTTCAGGAGACCGCGAGTTCATCTCAGGCGCGGCTCCACCTGAGC	364
Db	1364	CCCAGACACAGGCTTTCAGGAGACCGGAGAGTGCATCCAGGCGCGCTCCACCTCGCAGC	1423
QY	365	ATGAGATCGGACGACGAGCGGCTGCTGTCTGGTATTGCCCCAGCAGCTTGCCTATGG	424
Db	1424	GGGAGACGACGACGAGAGCGGCTCTGTCTGTCTCTCTCTCCCGCTCATGTTGCCATGG	1483
QY	425	AGATGAAGAGAGCATCAACACAAAAGAAAGA---CATGTTCCCAAGATCTACATAC	481
Db	1484	AGATGAAGCAGACATCAACGCCAAGCAGGAGGATATGATGTTCCATAAGATTTCATACC	1543
QY	482	AGAAGCATGACATGTGAGCATCTGTTTCAGACATGTAGGGCTTCACAGCGCTGGCAT	541
Db	1544	AGAAACATGACAGCTGAGCATCTGTTTGTGACATCGAGGGCTTCACCAGCGCTGGCGT	1603
QY	542	CCCAGTGCATCGCAGGAGTGTGTCATGACCCGTAATGAGCTCTTTGCCCGTTTGACA	601
Db	1604	CCCASTGCATGACAGGAAGTGTGATGACCCCTCAGAGCTCTTCCCGCTTTGACA	1663
QY	602	AGCTGGCTGGGGAATCACTGCTCAGGATCAAGATCTTTGGGGAGTGTACTACTGTG	661
Db	1664	AGCTGGCGGAGAGAATCACTGTTTACGTATTAAGATCTTTGGGGATTGTTATTACTGCG	1723
QY	662	TGTCAGGCTGCCGGAGGCGGCGCCAGCCATGCCACTGCTGTGTGGAGTGGGGTAG	721
Db	1724	TCTCGGGGCTGCCGTAAGCAGAGGCTGACCCAGCCCACTGCTGTGTGGAGTGGGCATGG	1783
QY	722	ACATGATTGAGGCCATCTCGCTGCTGCTAGGTGACAGGTGTGAATCTGAACATGCGCG	781
Db	1784	ACATGATCGAGGCCATCTCTGTGTGTCGGGAGGTGACAGGGGTGAAGTGAACATGCGTG	1843
QY	782	TGGCATCCACAGCGGCGGTGCACTCGCGCTCTTGGCTTCGGAAATGGCAGTTGC	841
Db	1844	TGGCAATTCACAGCGGCGGAGTACACTCGCGTGTCTTGGTCTCAGGAAGTGGCAGTTGC	1903
QY	842	ATGTGTGTCATGATGTGACCTTGGCAACACATGGAAGCAGGAAGCGGCTGGCC	901
Db	1904	ACGTCTGGTCTAACGATGTACAGTACACTGACCTACCTGAAATGGGACTACGAGGTGAGCCAG	1963
QY	902	GCATCCACATCACTCGGCGACACTGCGAGTACCTGAACGGGACTACGAGTGGAGCCAG	961
Db	1964	GCATCCACATCACCAGAGTACACTCAACTACCTGAAATGGGACTACGAGGTGAGCCAG	2023
QY	962	GCCGTGTGGCAAGCAACGCTACCTCAAGGAGCAGCACATGAGACTTTCCTCATCC	1021
Db	2024	GCTGTGGGGGCGGCAACGCCCTACCTCAGGAGCAGCATGTATCGAGACCTTCTCATCC	2083
QY	1022	TGGCGCGCAGCCAGAAACGGAAAGAGGAGGATGCTGCGCAAGCTCGAGCGGACTC	1081

Db	2084	TGCGCTGCACCCGAGAACGCGAAAGAGAGAGGAGCCATGATCCCAAGATGAACCGCCAGA	2143
QY	1082	GGGCAAACTCCATGAAAGGGCTGATGCGCGATGGGTTCCTCTGATCGTCCCTTCTCC----	1137
Db	2144	GAACCAACTCCATCGGCACACACCCACCACTGGGGGCTGAGCGCCCTTCTACAAACC	2203
QY	1138	-----CGAACCAAGGACTCCAAAGCCCTTCCGCCAGATGGGATGGGATGATGATTCCAGCA	1189
Db	2204	ACCTGGGTGGCAACACAGGTGTCCAAGGAGATGAAGCGGATGGGCTTTGAACACCCCA---	2260
QY	1190	AAGACACCGGGGACCAACAGATGCCCTGACCCCTGAGGATGAGGTGAGTTCCTGA	1249
Db	2261	---AGSACAAGAACGCCAGGAGAGTGCGAACCCCTGAGGATGAAGTGGATGAGTTCCTGG	2317
QY	1250	GCCGTGCATCATGTCGCCGAGCATTTGATCAGCTGCCGAGGACATGTGCGCCGGTTTT	1309
Db	2318	GCCGTGCCATTGACGCCAGGAGCATTTGATAGCTTCGGTCTGAGCAGCTCCGCAAGTCC	2377
QY	1310	TGCTCAGCTTCCAGAGAGAGGATTTTGAGAAGAAGTACTCCCGGAAGTGGATCCCGCT	1369
Db	2378	TCCTGACCTTCAGGGAGCCTGACTTAGAAGAAGTACTCCCAAGCAGGTAGACGACCGAT	2437
QY	1370	TCGAGGCTACGTTGCCCTGTGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTC	1429
Db	2438	TTGTGCTCTATGTGGCGTATGCCCTCGCTCGTCTTCTCTTCATCTGCTTTGTCAGATCA	2497
QY	1430	TAATTTTCCCACT 1444	
Db	2498	CCATCGTGCCCACT 2512	
RESULT 15			
ABL07501	ID ABL07501 standard; cDNA; 4827 BP.		
XX	AC	ABL07501;	
XX	DT	26-MAR-2002 (first entry)	
XX	DE	Drosophila melanogaster expressed polynucleotide SEQ ID NO 16985.	
XX	KW	Drosophila; developmental biology; cell signalling; insecticide;	
XX	OS	Drosophila melanogaster.	
XX	PN	WO200171042-A2.	
XX	PD	27-SEP-2001.	
XX	PF	23-MAR-2001; 2001WO-US09231.	
XX	PR	23-MAR-2000; 2000US-191637P.	
XX	PR	11-JUL-2000; 2000US-0614150.	
XX	PA	(PEKE) PE CORP NY.	
XX	PI	Venter JC, Adams M, Li PWD, Myers EW;	
XX	DR	WPI; 2001-656860/75.	
XX	DR	P-PSDB; ABB63398.	
XX	PT	New isolated nucleic acid detection reagent for detecting 1000 or more	
XX	PT	genes from Drosophila and for elucidating cell signalling and cell-cell	
XX	PS	interactions -	
XX	PS	Claim 1; SEQ ID NO 16985; 21pp + Sequence Listing; English.	
XX	CC	The invention relates to an isolated nucleic acid detection reagent	
XX	CC	capable of detecting 1000 or more genes from Drosophila. The invention is	
XX	CC	useful in developmental biology and in elucidating cell signalling and	
XX	CC	cell-cell interactions in higher eukaryotes for the development of	
XX	CC	insecticides, therapeutics and pharmaceutical drugs. The invention	

CC discloses genomic DNA sequences (ABLI16176-ABLI30511), expressed DNA
CC sequences (ABLI1840-ABLI16175) and the encoded proteins
CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 4827 BP; 1115 A; 1377 C; 1340 G; 995 T; 0 other;

Query Match 24.6%; Score 445.8; DB 23; Length 4827;
Best Local Similarity 57.7%; Pred. No. 1.2e-108;
Matches 913; Conservative 0; Mismatches 607; Indels 63; Gaps 4;

QY 5 ACCTGTGCTGGCAGTCCTGGCGGAGTGCAGGTGGGGGGCGCTTTCGAGCAGACCCCGC 64
DB 1187 ACCTGATTCGGGCACCTTCCTGGCCATCGAAGTGCCGCTTAGCTATGCCATGCAACCCA 1246
QY 65 GCAGCCCCCTCTGGGGGCTCTGGTGCCCTGTGTTTGTATACATCGCATACACGCTCC 124
DB 1247 GCAAAATCCTTCAACGGCAGCGCTGCTGCATTGTGCTCATCATAGCTACACGATGC 1306
QY 125 TCCCCATCCGCATGCGGGCTGC-----CGTCTCAGCGGCTGGGCTCT 169
DB 1307 TGGCCCTTCGCTTGGGGAGGCTCTGATCGGGGAATCTCTGAGCGCTGCTCCATCTGT 1366
QY 170 CCACCTTGGCATTTGATCTTTGGCCTGGCAACTTAACCGTGGTGATGCTTCCCTTGGAAAGC 229
DB 1367 ACACCTGCCTGAGGCTCAACGGATSCAGGATCAGCGGTTCGAGATGATCCACTGGGAGG 1426
QY 230 AGCTCGGTGCCAATGTGCTGTCTTCCCTCTGCACCAACGTCATTTAGCATCTGCACACT 289
DB 1427 AGCTCTCTGCACTTTGGTGGGCTCTCTCTGGCCCAATCTCACTGGCGCTACACCACT 1486
QY 290 ATCCACGACAGGTGCTCAGCGCCAGCGCTTTCAGAGACCCGCGAGTTACATCCAGGCC 349
DB 1487 GGCAGGAGAGAGGCCCCAGGAGGCGTTTCATCAGAGACGAGCGAGTGCATCGAGGCCA 1546
QY 350 GGCTCCACCTGCAGCATGAGATTCGCGACGAGCGGCTGTGCTGTGGGTATTTCCGCC 409
DB 1547 GGCTGAGGACGACGCGGAAACCAACACAGCAGAACGCTTGTGCTGTGGTCTCGCG 1606
QY 410 AGCACGTTGCCATGCCAGTGCAGTGCAGGAGAGCTGCATCAACAAAAAGAGACAT---GTTCC 466
DB 1607 GTCATGTGGCCATGGAGATGAAGGAGCATATTGCGGGGCCACGACGTGACACCCAGTTCC 1666
QY 467 ACAAGATCTACATACAGAGCATGACAATGTACAGTCTGTGTCAGACATTTGACAGACTTGAGGGCT 526
DB 1667 ATAAGATATACATCCAACGGCAGGAGATGTCAGCATCTCTTTTGGGACATCTGCGGT 1726
QY 527 TCACCAAGCTGGCATCCCGAGTGCAGTGCAGGAGAGCTGTGATGACCCCTGAATGAGCTCT 586
DB 1727 TCACCAAGCTCTCGGATCAGTGCAGCGCGGAGGAATGGTGGCTCTGCTGAACGAGCTCT 1786
QY 587 TTGCGCGGTTTGACAGCTGGCTGGCGGAGAACTACCTGCTGAGGATCAAGATCTTGGGG 646
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DB 1847 ATTGCTACTACTGCTCTCGGACTCCCGAACCCTCGGATCAGCCCCATTTGTCGG 1906
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Job time : 377.621 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 22:08:18 ; Search time 59,7082 Seconds
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9306.902 Million cell updates/sec

Title: US-09-750-240-3

Perfect score: 1812

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1808.4	99.8	3549	4	US-09-008-097-5
3	1763	97.3	4942	1	US-09-474-076-1
4	1519.8	83.9	4046	1	US-07-793-961A-1
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6	1437.2	79.3	4131	3	US-08-726-214-11
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8	858.2	47.4	3924	3	US-08-726-214-9
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12	320.6	17.7	4601	3	US-08-726-214-15
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29	64.4	3.6	2013	2	US-08-997-080-176	Sequence 176, App
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44	39.2	2.2	2734	3	US-09-135-021-79	Sequence 79, Appl
45	39.2	2.2	2821	4	US-09-135-010A-115	Sequence 115, Appl

ALIGNMENTS

RESULT 1
US-09-008-097-3
: Sequence 3, Application US/09008097
: Patent No. 6306830
: GENERAL INFORMATION:
: APPLICANT: Hammond, H. Kirk
: APPLICANT: Insel, Paul A.
: APPLICANT: Ping, Peipei
: APPLICANT: Post, Steven R.
: APPLICANT: Gao, Meihua
: TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
: TITLE OF INVENTION: HEART FAILURE
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 PAGE MILL ROAD
: CITY: PALO ALTO
: STATE: CA
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/008,097
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Dylan, Tyler M
: REGISTRATION NUMBER: 37,612
: REFERENCE/DOCKET NUMBER: 22000-20567.21
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-813-5600
: TELEFAX: 650-494-0792
: TELEX: 706141
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1812 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Coding Sequence
: LOCATION: 1...1812
: OTHER INFORMATION:

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RESULT 2
US-09-008-097-5
: Sequence 5, Application US/09008097
: Patent No. 6306830
:
: GENERAL INFORMATION:
:
: APPLICANT: Hammond, H. Kirk
: APPLICANT: Insel, Paul A.
: APPLICANT: Ping, Peipei
: APPLICANT: Post, Steven R.
: APPLICANT: Gao, Meihua
:
: TITLE OF INVENTION: GENE THERAPY
:
: NUMBER OF SEQUENCES: 9
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER

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STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,097
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dylan, Tyler M
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 22000-20567.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3549 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...3501
OTHER INFORMATION:
US-09-008-097-5

Query Match 99.8%; Score 1808.4; DB 4; Length 3549;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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; Sequence 1, Application US/09474076
; Patent No. 6455237
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/09/474,076
; CURRENT FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-09-474-076-1

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QY 1142 CCAAGGACTCCAAGGCTTCCGCCAGATGGGATTCGATGATTCAGCAAGACAAACCGGG 1201
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QY 1202 GCACCCAGATGCCCTGAACCTCAGGATGAGTGATGATTCCTGAGCCGTCGCATCG 1261
DB 1959 GTGCCCCAAGATGCCCTGAACCCGAGGATGAGTGATGATTCCTGAGCCGTCGCATCG 2018
QY 1262 ATGCCCGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1321
DB 2019 ATGCCCGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2078
QY 1322 AGAGAGGAGATTTTGAGAGAGTACTCCCGGAAGGTGGATCCCGCTTCGGAGCGCTACG 1381
DB 2079 AGAGAGGAGATTTTGAGAGAGTACTCCCGGAAGGTGGATCCCGCTTCGGAGCGCTACG 2138
QY 1382 TTGCGCTGCGCTGTTGGTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTT 1441
DB 2139 TTGCGCTGCGCTGTTGGTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTT 2198
QY 1442 ACTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCT 1501
DB 2199 ACTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCT 2258
QY 1502 TGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1561
DB 2259 TGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2318
QY 1562 GAGGATTTCCGCTCAGCGGACATAGCAGCGAGTGGCATCTTTCGCTGCTGCTGCTGCT 1621
DB 2319 GAGGATTTCCGCTCAGCGGACATAGCAGCGAGTGGCATCTTTCGCTGCTGCTGCTGCT 2378
QY 1622 TGTTCACCTCTGCCATCGCCAAACATGTTACACCTGTAAACACACACCCCATACGAGCTGTG 1681
DB 2379 TGTTCACCTCTGCCATCGCCAAACATGTTACACCTGTAAACACACACCCCATACGAGCTGTG 2438
QY 1682 CAGCCCGGATGCTGAATTTAACACCTGTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCT 1741
DB 2439 CAGCCCGGATGCTGAATTTAACACCTGTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCT 2498
QY 1742 ATTACTCTCGGCCCTGGATGCTCCCTGTGTGAGGGCACCATTGCCACCTCGAGCTTTC 1801
DB 2499 ATTACTCTCGGCCCTGGATGCTCCCTGTGTGAGGGCACCATTGCCACCTCGAGCTTTC 2558
QY 1802 CTGAGGTGTT 1812
DB 2559 CTGAGGTACTTC 2569
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RESULT 5
US-08-240-357-1
; Sequence 1, Application US/08240357
; Patent No. 5578481
; GENERAL INFORMATION:
; APPLICANT: Ishikawa, Yoshihiro
; TITLE OF INVENTION: Cloning and Characterization of a
; TITLE OF INVENTION: Cardiac Adenyl cyclase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
```

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; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,357
; FILING DATE: 10-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,705-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4046 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 131..3625
; US-08-240-357-1
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Query Match 83.9%; Score 1519.8; DB 1; Length 4046;
Best Local Similarity 90.7%; Pred. No. 0;
Matches 1643; Conservative 0; Mismatches 162; Indels 6; Gaps 2;

QY 5 ACGTGTGTGTGGGATCTTGGGCGGAGTGCAGTCTGGGGGGCGCTTTCGAGCAGAGACCCCG 64
DB 762 ACGTGTGTGTGGGATCTTGGGCGGAGTGCAGTCTGGGGGGCGCTTTCGAGCAGAGACCCCG 821
QY 65 GCAGCCCCCTCTGGGCGGCTCTGGTGGCCCTGTCTTGTATACATCGCATACACCGCTCC 124
DB 822 GCAGCCCCCTCTGGGCGGCTCTGGTGGCCCTGTCTTGTATACATCGCATACACCGCTCC 881
QY 125 TCCCCATCCGCGATCGCGGCTCTCTCAGCGGCTCTGGGCGCTCTCCACCTTGCATTTGA 184
DB 882 TACCATCCGCGATCGCGGCGGAGTGTCTTCTAGTGGCCCTGGGCGCTCTCCACCTTGCATTTGA 941
QY 185 TCTTGGCCCTGGCAACTTAACCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 244
DB 942 TCTTGGCCCTGGCAACTTAACCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1001
QY 245 TGTGCTGTCTCTCTCGACCAAGCTCATTTAGCATCTGCACACACTATCCAGCAGAGGTGT 304
DB 1002 TGTGCTGTCTCTCTCGACCAAGCTCATTTAGCATCTGCACACACTATCCAGCAGGTGT 1061
QY 305 CTCAGCGCCAGGCTTTTCAGGAGACCCGAGTTTACATCCAGGCGCGGCTCCACCTGCAGC 364
DB 1062 CTCAGCGCCAGGCTTTTCAGGAGACCCGAGTTTACATCCAGGCGCGGCTCCACCTGCAGC 1121
QY 365 ATGAGAATCGGAGCAGGAGCGGCTCTGCTGTGTGGTATTTGGCCCCCAGCAGTGTGCCATG 424
DB 1122 ATGAGAATCGGAGCAGGAGCGGCTCTGCTGTGTGGTATTTGGCCCCCAGCAGTGTGCCATG 1181
QY 425 AGATGAAGAAGACATCAACACAAAAAAGAGAC---ATGTTCCACAGATCTACATAC 481
DB 1182 AGATGAAGAAGATATCAACACAAAAAAGAGACATGATGTTTCCACAGATCTACATAC 1241
QY 482 AGAAGCATGACATGTCAGCATCTCTTTTCAGACATTTGAGGGCTTTCACGAGCTGGCAT 541
DB 1242 AGAAGCATGACATGTCAGCATCTCTTTTCAGACATTTGAGGGCTTTCACGAGCTGGCAT 1301
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QY	542	CCAGTGCAC	TCCGGCAGGAGCTGTGATGACCCCTGAATGAGACTCTTTGGCCGGTTTGACA	601	
Db	1302	CCCAAGTGCAC	CCGCGAGGAGCTGTGTCATGACCCCTGAACGAGACTCTTGCCCGGTTTGACA	1361	
QY	602	AGCTGGCTCG	CAGAGATCAC	TGSCCTGAGSATCAAGATCTTGGGGAGACTGTTACTACHTGC	661
Db	1362	AGCTGGCTCG	GAAATCAC	TGCCCTGAGATCAAGATCTTAGGGGAGCTGTTACTACHTGC	1421
QY	662	TGTCAGGGCTCG	CGGAGGCCGGCGGCGACCACTGCCC	ACTGCTGTGTGGAGATGGGGGTAG	721
Db	1422	TGTCAGGGCTCG	CGGAGGCCGGCGGCGAGACCACTGCCC	ACTGCTGTGTGGAGATGGGGGTG	1481
QY	722	ACATGATTGAG	GCCATCTCGCTGTGTGATCGTGAAGTGACAGTGTCGAA	TGTGAACATGCGCG	781
Db	1482	ACATGATCAG	GCCATCTCGCTGTGTGCGTGAGGTGACAGTGTCGAA	CTGCAACGTGAACATCGCG	1541
QY	782	TGGGCATCAC	AGCGGCGCGTGCACTCGGGCGTCTTGGCTT	CGGGAATGCGCAGTTGC	841
Db	1542	TGGGCATCAC	AGCGGCGGTGTGCACTGTGTGTCTTGGCTT	CGGGAATGCGCAGTTGC	1601
QY	842	ATGTGTGTTC	CAATGATGTGACCCCTGGCCAAACCACTGAACAGCAGGAAGCCGGCTGGCC	901	
Db	1602	ACGTGTGTTC	CAATGACGTGACTCTGGCCACCACTATGAGAGCGCG	---CCGGGCGCGCC	1658
QY	902	GCATCACATCA	CTCGGCACACTGCAGTACCTGAAACGGGGACTACGAAGTGGAGCCAG	961	
Db	1659	GCATCACATCA	CCCGGCGCACGTGCACTACCTGAACGGGGACTACGAGTGGAGCCG	1718	
QY	962	GCGTGGTGGC	AAGCGCAACGGGTACTCTAAGGAGCAGCACTTGAGACATTTCTCTATCC	1021	
Db	1719	GCGCGGTTGG	CAGCGGAAACGGGTACTCTAAGAGAGCAGACATCGAGACCTTCTCTATCC	1778	
QY	1022	TGGGCGCCAG	CAGAAACGGAAGAGGAAAGGCATGCTGGCCAAAGCTGACGGGCACTC	1081	
Db	1779	TGGGACCCAG	CAGAAACGGAAGAGAGAGGCCATGCTGGCCAGCTGCAGCGGAGCC	1838	
QY	1082	GGGCCAACTCC	ATGGAAGGGCTGTATGCCCGCATGGGTTCCTGATCTGTCCTTCTCCCGGA	1141	
Db	1839	GGGCCAACTCC	ATGGAAGGGCTGTATGCCACGCTGGGTGGCGACCGCGCTTCTTCCCGGA	1898	
QY	1142	CAAGAGACTTC	CAAGGGCTTCCGCCAGATGGGCAATGTATGATTCAGACAAAGACAACCGGG	1201	
Db	1899	CAAGAGACTTC	CAAGGGCTTCCGCCAGATGGGCATTTGATGATTCAGACAAAGACAACCGGG	1958	
QY	1202	GCACCCAGATGC	CTGAAACCTGAGGATGAGGTGGATGAGTCTCTGAGCGGTGCCATCG	1261	
Db	1959	GTCCCCAAGATGC	CTGAACCCCGAGATGAGGTGCATGAGTCTCTGGGCGGTGGCATCG	2018	
QY	1262	ATGCCCGCAG	CATGTATCAGCTGCGGAAGCACCATGTGCGCGGTTTTTGTCTACCTTCC	1321	
Db	2019	ATGCCCGCAG	CATGATCAGTACGGAAGGACCATGTGCGCGGCTTCTGCTCACCTTCC	2078	
QY	1322	AGAGAGAGATTT	TGAGAAGAAGTACTCCCGAAGGTGGATCCCGGCTTGGAGCCCTACG	1381	
Db	2079	AGAGAGAGATCT	TGAAAAGAAGTACTCAAGGAAGGTGGACCCCGGCTTCGGAGCCCTACG	2138	
QY	1382	TTGCCCTG	CGCCTGTGTGCTTCTGCTTCATCTGCTTCATCCAGCTCTCTAATTTTCCAC	1441	
Db	2139	TGGCCTGTG	CGCTGTGTGCTTCTGCTTCATCTGCTTTATCCAGCTCGTCTTCCAC	2198	
QY	1442	ACTCCACCCTG	ATGCTGGGATTTATGCGACATCTTCCCTGCTGCTGCTAATCACCGTGC	1501	
Db	2199	ACTCAACCGT	GTATGCGGATCTACGCCAGTATCTTTTGTGCTGTTGCTGATCACCGTGC	2258	
QY	1502	TGATCTGCTGT	GTACTCTCTGTGTCTTCTGTTCCCTTAAGGGCCCTGCAAGCTCTGTCCC	1561	
Db	2259	TGACCTGTG	CGCGTACTCTCTGTGCTCTCTTCTCCCAAGGCCCTCGACGTCTTTCCC	2318	
QY	1562	GCAGCATTTG	CGCTCACGGGCACATAGCACCGAGTTGGCATCTTTTTCGTCTCTGCTG	1621	
Db	2319	GCAGCATTTG	CGCCTCTCGGGCACAGCAGCTGTGGTTGGCATTTTTCAGTCTTTCTAG	2378	
QY	1622	TGTTTACTTCT	GCAATTGGCAATGTTTACCTGTGAACACACACCCCATACGAGAGCTGTG	1681	

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Db 2379 TGTTCACCTCTGCGCAATGGCCAAACATGTTCCACCTGTAAACACACACCCCACTCGGACCTGTG 2438
QY 1682 CAGCCGGGATGCTGAATTTAAACACCTGCTGCATCAGCTGCCTGCCACCTGCAGCAGCTCA 1741
Db 2439 CAGCCGGGATGCTGAATGTAAACACCCGCTGCATCAGCTGCCTGCCACCTGCAGCAGCTCA 2498
QY 1742 ATTACTCTCTGGGCCCTGGATGCTCCCGCTGTGTGAGGGGACCAATGCCACCTGCAGCTTTC 1801
Db 2499 ATTACTCTCTGGGCCCTGGATGCTCCCGCTGTGTGAGGGGACCGCACCCCACTTTGCAGCTTCC 2558
QY 1802 CTGAGGTGTTCT 1812
Db 2559 CTGAGTACTTC 2569

RESULT 6
US-08-726-214-11
: Sequence 11, Application US/08726214
: Patent No. 6107076
: GENERAL INFORMATION:
: APPLICANT: Tang, Wei-Jen
: APPLICANT: Gilman, Alfred G.
: TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
: TITLE OF INVENTION: AND USES THEREFOR
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P. O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: United States of America
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/726,214
: FILING DATE: Concurrently Herewith
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/005,498
: FILING DATE: 04-OCT-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Highlander, Steven L.
: REGISTRATION NUMBER: 37,642
: REFERENCE/DOCKET NUMBER: UTSD:450
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (512) 418-3000
: TELEFAX: (512) 474-7577
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4131 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-726-214-11

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	Query Match	79.3%;	Score 1437.2;	DB 3;	Length 4131;
	Best Local Similarity	87.5%;	Pred. No. 0;		
	Matches 1584;	Conservative 0;	Mismatches 223;	Indels - 3;	Gaps 1;
Qy	5	ACGTGGTCTCGGGCATCCTGCGGCAGTCAGTGCTGGGGGGCGCTTCCGACGACGACC GC 64			
Dd	687	ATGTGGTTCTGGGCATCTAGCAGCGGTGCAGTGGGGGTGCCCTGCACGCCAACCCAC 746			
Qy	65	GCAGCCCTCTCGGGGCTCTGGTGCCTCTGCTCTTGTATACATCGCATACAGCTCC 124			
Dd	747	GCAGCCCCCTCAGCAGGCGCTTGGTGCCCGGTCTTCGCTACATCACTCACACATTC 806			
Qy	125	TCCCACATCCGATGCGGGCTCGCGCTCTCAGCGGCTGGGGCTCTCCACCTTGCAATTGA 184			

Db	1887	GTGCCCAAGATGCTCTGTAACCCCTGAGGATGAGGTGGACGAGTGTCTTGGCGCCGACGCATCG	194
Qy	1262	ATGCCCGCAGCATTTGATCAGCTGCGGAAGGACCATGTGCGCGGGTTTTTGTCTACCTTCC	1321
Db	1947	ATGCCGGAAGCATCGACACGCTGCGTAAAGGACCATGTGCGCGGGTTCCTGCTCACCTTCC	2006
Qy	1322	AGAGAGAGGATTTTGAGAAGAAGTACTCCCGGAAGGTGGANTCCCGCTTTCGGAGCCCTACG	1381
Db	2007	AGAGGGAGGATCTCGAGAAGAAGTATTCACGGAAGATAGACCCCTGTTTCGGAGCCCTACG	2066
Qy	1382	TTGCCTGTGCCCTGTTTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAAATTTTCCAC	1441
Db	2067	TCGCCGTGCCCCCTCTGGTTTCTGCTTCATCTGTTTTCATCCAGTTCCTCGTATTCCAC	2126
Qy	1442	ACTCCACCCTGATGCTTTGGGATTTATGCGAGCATCTTCCTGCTGCTGCTTAATACCGTGC	1501
Db	2127	ACTCCGCCCTGATACTCGGGATTTATGCGGGATTTATGCGGGATCTTCTCTTTTGTGCTGCTACCGTGC	2186
Qy	1502	TGATCTGTGCTGTACTCTCTGTTGTTCTCTGTTCCCTAAGGCCCTGCAAGCTCTGTCCC	1561
Db	2187	TCATCTGCTGTGTGCTCTCTGTGGGTCTTCTTCTCCCAAGCCCTGCAGCGCCTGTCCC	2246
Qy	1562	GCAGCATTTCCGCTCACGGGCACATPAGACCGCAGTTGGCATTTTCCTGCTCTGCTTG	1621
Db	2247	GCAGTATCGTCCGCTCACGGGTGCACAGCAGCGCTGTTGGAGTCTTCTCGGTTCTGCTTG	2306
Qy	1622	TGTTTACTTCTGCCATTCGCACATGTCACCTGTTCACCTGTAAACCACACCCCATACGGAGCTGTG	1681
Db	2307	TGTTTACTTCTGCCATTTGCCACATGTTCCACCTGTTCACCTGTAAACCACACCCCATACGGAGCTGTG	2366
Qy	1682	CAGCCCGGATGCTGAATTTAAACACCTGCTGACATCACCTGCCCTGCCACCTGCAGCAGCTCA	1741
Db	2367	CGGCCGGATGCTGAATTTAAACACCTGCGATGTCACCGCTGCACCGCTGCACCTACGACAGCTCA	2426
Qy	1742	ATTACTCTCTGGGCCCTGGAATGCTCCCTGCTGTGAGGGGACCATGCCACCTGCAGCTTTC	1801
Db	2427	ATTACTCTCTGGGACTGGAAGCTCCCTCTGTGTGAGGGGACCGCAGCTTTC	2486
Qy	1802	CTGAGGTGTT	1811
Db	2487	CTGAGTACTT	2496
RESULT 7			
US-09-473-716-1			
; Sequence 1, Application US/09473716			
; Patent No. 6436672			
; GENERAL INFORMATION:			
; APPLICANT: Tomlinson, James			
; APPLICANT: Cor Therapeutics, Inc.			
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL			
; TITLE OF INVENTION: CYCLASE			
; FILE REFERENCE: 44481-5027-01-US			
; CURRENT APPLICATION NUMBER: US/09/473,716			
; CURRENT FILING DATE: 1999-12-29			
; PRIORITY APPLICATION NUMBER: PCT/US98/13540			
; PRIOR FILING DATE: 1998-07-01			
; PRIOR APPLICATION NUMBER: 60/070,901			
; PRIOR FILING DATE: 1997-07-01			
; PRIOR APPLICATION NUMBER: 08/886,362			
; PRIOR FILING DATE: 1997-07-01			
; NUMBER OF SEQ ID NOS: 2			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 1			
; LENGTH: 4523			
; TYPE: DNA			
; ORGANISM: human type V adenylyl cyclase			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (139)..(3921)			
US-09-473-716-1			

Query: Match 49.48: Score 895: DB 4: Length 4523:

Best Local Similarity 69.8%; Pred. No. 2.4e-229;
Matches 1277; Conservative 0; Mismatches 525; Indels 27; Gaps 4;

QY	5	ACGTGCTGCTGGGCATCTTGGCGGCAGTGCAGTCTGGGGCGCTTTTCGCACGACAGACCCGC	64
Db	1046	ATCGCTCATCGCCGTGGTGTCTGGCCGTGCACAGTGGTGGGCTGCTGCTGCGCCGACGAC	1105
QY	65	GCAGCCCTTCGCGGCGCTCTGGTCCCTGTGTCTTTGTATACATCGCATACACGCTCC	124
Db	1106	GCAGCCCTCTGAGGCGATCTGGTGGACGGTGTCTTCATCTACACATCTACACGCTGC	1165
QY	125	TCCCCATCCGCATGGCGGCTGCCCTCTCAGCGGCTTGGGCTCTCCACCTTGCATTTGA	184
Db	1166	TGCGCGTGGCATGGGCGCCAGTGCACGGGGTGTCTCTGTCGGCTCCACCTGC	1225
QY	185	TCTTGGCTTGGCAACTTAACCGTGTGATGCTTCTCTGGAAGCAGCTCGTGGCCAAATG	244
Db	1226	CCATCCCTTGGGCACCAACGCCACACAGTTCCTGCTGAAGCAGCTGTCTCTCAATG	1285
QY	245	TGCTGCTGTCTCTGACCAACGTCATTAGCATCTGCACACATATCCACGACGAGGTGT	304
Db	1286	TTCTCATTTTCTCTGACCAACATCTGGTGGTGTCTGCACCCATATCTCCGGCTGAGGTCT	1345
QY	305	CTCAGCGCCAGCCCTTTCAGGAGACCCGAGTTACATCCAGGCCGGCTCCACCTGCAGC	364
Db	1346	CCAGAGACAGGCTTTCAGGAGACCCGAGATGCATCCAGCGCGCTCCACTCCGAGC	1405
QY	365	ATGAGAACTCGGACGAGAGCGGCTGTCTGTCTGGTATATGCCCCAGCAGCTTGGCCATGG	424
Db	1406	GGGAGAACAGCAGCAGGAACGGCTTCTGCTGTCTCTTCCCGCTCATGTTCGCAATGG	1465
QY	425	AGATGAACAGACATCAACACAAAAAAGAGA- --CATGTTCCACAAGATCTACATAC	481
Db	1466	AGATGAACAGACATCAACGCCACGAGGAGATATGATGTTCCATAAAGATTACATCC	1525
QY	482	AGAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTTAGGGGCTTCACGAGCCTGGCAT	541
Db	1526	AGAAATCACAACGTGAGCATCCTGTTTGTGTGATCGAGGGCTTCACGAGCCTGCGT	1585
QY	542	CCCAGTGCACCTCGGACGAGCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACA	601
Db	1586	CCGAGTGCATGCACAGAACTGGTCATGAGCCCTCAAGAGCTCTTCGCCGCTTTGACA	1645
QY	602	AGTGTGCTCGGAGAACTCACTGCCTGAGGATCAAGATCTTGGGGACTGTTACTACTGTG	661
Db	1646	AGCTGCCCGCAGAACTCACTGTTTACGTATTAGATCCTTGGGGATGTTATTACTGCG	1705
QY	662	TGTCAGGCTCGCGAGGCGCGGCCGACCATGCCACTGCTGTGTGGAGATGGGGTAG	721
Db	1706	TCTCGGGCTGCTGAAGCAAGGGCTGACCACGCCCACTGCTGTGTGGAGATGGGCATGG	1765
QY	722	ACATGATTAGGCCATCTCGTGGTACGTGAGGTGCAGAGTGTGAATGTGNACTGGCG	781
Db	1766	ACATGATCAGGCCATCTGTTGGTCCGGGAGGTGCAGGGGTGAACGTGAACATCGCTG	1825
QY	782	TGGGCATCCACAGCGGCGCTGCACTCGCGGCTCTTGGCTTCGGAAATGGCAGTTCG	841
Db	1826	TGGGAATTCACAGCGGCGAGTACACTCGGCTGCTTGTCTCAGGAAGTGGCAGTTCG	1885
QY	842	ATGTGTGTCCAATGATGTACCCCTGGCCCAACCATGGAAGCAGGAAGCGGCGCTGGCC	901
Db	1886	ACGTCTGTCTTAACGATGTACGCTAGCCAACACATGAGGCTGGCGCAAGCAGGAC	1945
QY	902	GCATCCACATCACTCGGCGAACACTTGCAGTACCTTGAACGGGGACTACGAAGTGGAGCCAG	961
Db	1946	GCATCCACATCAACAGGCTACACTCAACTACCTGAATGGGGACTACGAGTGGAGCCAG	2005
QY	962	GCGTGTGTGGCAGCGCAACGGTACCTCAAGGAGCAGCAATTTGAGACTTTCTCATCC	1021
Db	2006	GCTGTGGGGCGAGCGCAACGCTTACCTCAGAGGACACAGTATCGAGACCTTTCTCATCC	2065
QY	1022	TGGCGCCCAAGCAACCGAAAGGAGAAAGGCACTGCTGGCCAAAGCTGACGCGGACTC	1081

Db	2066	TGCGCTGCA	CCCAAGACGGAAAGAGAGAGAGAGCCCATGATCGCCAAGATGAACCCGCCAGA	2126
Qy	1082	GGCCCAACTCCAT	TGGAAGGGCTGATGCCCGGATGGGTTCCCTGATCGTGCCTTTCTCC----	1137
Db	2126	GAACCAACTCCA	TCGCGCACCAACCCACACACTCGGGGGCTGAGCGCCCTTCTTACAACC	2185
Qy	1138	-----CGGACC	AAGGACTCCAAGGCCTTCGCGCCAGATGGGCATTTGATGATTTCCAGCA	1189
Db	2186	ACCTGGGTGCA	CAACCAAGTGTCTCAAGGAGATGAACGGATGGGCTTTTGAAGACCCCA----	2242
Qy	1190	AAGACAACCGG	GGCACCAAGATGCCCTGAACCCCTGAGGATGAGTGGATGGATGCTCTGA	1249
Db	2243	---AGACA	AAGACGCCACAGAGATGGCAACCTTGAGGATGAAGTGGATGAGTTCTCG	2299
Qy	1250	GCGTGCCATCG	ATGCCCGACGATTTGATCAGCTGCGGAAGGACCATGTGCGCGCGTTTT	1309
Db	2300	GCCGTGCCAT	TGAGCCACGAGCATTTAGSCTTTCGGTCTGAGCAGTCCGCAAGTTCC	2359
Qy	1310	TGCTCACCCTC	CAGAGAGAGATTTTGAGAGAAGTACTCCCGAAGGTGGATCCCCGCT	1369
Db	2360	TCCTGACCTT	CAGGAGCCTGACTTAGAGAAGATACTCCAAGCAGGTAGACGACCGAT	2419
Qy	1370	TCGGAGCCTAG	GTGCTGCCCCCTGGTCTCTGCTTCATCTGCTTCATCCAGCTTC	1429
Db	2420	TTGGTGCTAT	GTGGGGTGTGCTCGCTGCTCTTCCCTCTTCATCTGCTTTGTCAGATCA	2479
Qy	1430	TAATTTTCCCA	CACTCCACCCCTGATGCTTGGGATTTATGCCAGGATCTTCCTGCTGCTGC	1489
Db	2480	CCATGTCGCC	CACTCCATATTCATGTCACGCTTCTACCTGACCTGTTCCCTGCTGCTGA	2539
Qy	1490	TAATCACCGT	GCTGATCTGCTGTGTACTCTGTGTGTTCTGTGTTCCCTAAGGCCCTGC	1549
Db	2540	CCTTGGTGTG	TTGTGTCTGTGATCTACTCTGCGTAAAGCTCTTCCCTCCCACTGC	2599
Qy	1550	AACGCTGTCC	CGACATTTGCCGTACGGGCACATAGCACCGCAGTTTGGCATCTTTT	1609
Db	2600	AGACCCCTC	CCAGAGATCGTGGGTCCAAGATCAACAGACCCCTGGTGGGGTGTCA	2659
Qy	1610	CCGTCTGCTG	TGTTTACTTCTGCCATTTGCCAATGTTTCACTGTAAACACACCCCA	1669
Db	2660	CCATCACCC	TGTTTCTCTGGGGGTTTTTGTCAACATGTTACGTTGCAACTCCAGGAC	2719
Qy	1670	TACGAGCCTG	TGCAGCCCGGATGCTCAATTTAACACCTGCTGCATCATCTGCCTGCCACC	1729
Db	2720	TGCTGGCTG	CTTTGGCACAGGACACATCAGCGCAGCCAGGTCAACCGTGTCAAG	2779
Qy	1730	TGCACGAG	-----CTCAATTACTCTGTGGGCTTGGATGCTCCCTGTGTGAGGGCACCA	1783
Db	2780	TGGCGAGT	CGGCCGTCAACTACAGCCTGGCGGATGACGAGGGCTTCTGTGGCAGCCCT	2839
Qy	1784	TGCCCACTG	CAGCTTTCTCTGAGGTTC	1812
Db	2840	GGCCCAACTG	CAACTTCCCGAGTACTC	2868

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RESULT 8
US-08-726-214-9
; Sequence 9, Application US/08726214
; Patent No. 6107076
; GENERAL INFORMATION:
; APPLICANT: Tang, Wei-Jen
; APPLICANT: Gilman, Alfred G.
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3924 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-726-214-9

Query Match 47.4%; Score 858.2; DB 3; Length 3924;
Best Local Similarity 68.6%; Pred. No. 1.5e-219;
Matches 1254; Conservative 0; Mismatches 548; Indels 27; Gaps 4;
QY 5 ACCTGGTCTGGGCATCTCTGGGGAGTGGAGTGGGGGGCGCTTTTCGAGCAGACCCGC 64
DB 421 ATCGCGTCATTGACGTGGTCTGGCGGTCCAGGTAGTGGCGCTTGTGCTGCCACAGCCAC 480
QY 65 GCAGCCCTCTGGGGCCCTCTGGTGGCCCTGTGTTCTGTATACATCGCATACACCTCC 124
DB 481 CGAGCCCTCCGAGGGCATCTGTGTGACCGTGTCTCTATACATCTACACCTGC 540
QY 125 TCCCATCCGCGATCGCGGTGCGCTCTCAGCGCCCTGGGCCCTCTCCACCTTGCATTTGA 184
DB 541 TGCGCTGCGCATGAGGGTGGGTGCTCAGGGGGTGTCTGTGCGGCTCTCCACTTGG 600
QY 185 TCTTGGCCTGGCACTTACCGTGGTGTGATGCCCTTCTCTGGAAGAGCTGGTGGCCATG 244
DB 601 CCATCTCTCTGCACACCAACGCCAGGACAGTTTCTGTGTAACACAGCTTGTCTCCAAG 660
QY 245 TGCTGCTGTCTCTGCACCACTCATTAGCATCTGCACACATATCCAGCAGAGGTGT 304
DB 661 TCTCATCTCTCTTGCACCAACATCGTGGGTGTGCTACTACTACCCAGCGAGGTCT 720
QY 305 CTCAGCCGAGCGCTTTCAGGAGACCCGAGTTACATCCAGGCGCGGCTCCACCTGCAGC 364
DB 721 CCCAGACAAAGCTTCCAGGAGACCCGGAGTGCATCCAAAGCTCGGCTCCACTCACAGC 780
QY 365 ATGAGAAATCGGAGCAGGAGCGGCTGCTGCTGCTGATTTGCCAGCAGGTGGCCATGG 424
DB 781 GGGAGAACGACGACACAGAGCGCTCTCTGCTGCTCTCTCTCCCGCTCATGTTGCCATG 840
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QY 542 CCCAGTGCATGGCAGGAGCTGGTGCATGACCCCTGAATGAGCTCTTGGCCGGTGTGACA 601
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DB 1021 AGTTGGCTGGGAGATCACTGCTTACGATTAAGATCTCCGGGGATTTGTTACTACTGTG 1080

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QY 722 ACATGATTTAGGCCATCTCGCTGGTGTAGGTGACAGGTGTAATGTGAACATCGCGG 781
DB 1141 ACATGATCGAGGCCATCTCGTGGTCCGGAGGTGACAGGTTGAACATCGGTG 1200
QY 782 TGGGCATCCACAGCGGCGGTGCTGCTGCGGCGTCTTGGCTTGGCGAAATGCACTTCG 841
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QY 1138 -----CGGACCAAGGACTTCCAAAGGCTTCCGCGAGATGGGCAATGATGATTCACGCA 1189
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QY 1190 AAGACAACCGGGGCAACCAAGATGCCCCCTGAACCCCTGAGGATGAGGTGGATTTCTCTGA 1249
DB 1618 ---AGGACAAGAATGCCAGGAAAGTGCACAACTCCAGGATGAAGTGGAGAGTCTCTG 1674
QY 1250 GCGGTGCCATCGATGCCCGCAGCATTTGATCAGCTGCGGGAAGGACCATGTCGCGCGGTTT 1309
DB 1675 GTCGAGCCATCGATGCCAGGATTTGACAGACTCGGATCCGAAACAGCTCCGAAAGTTCC 1734
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DB 2095 TGGTGGTTCGCTGGCAGGAGGACACAAATCACGCTGAACCGGTAACGCGATGTCATG 2154

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1330 TTTCAGATATTTGGCGCTTACCAGCTGTCCCTGCTGAGTGGCCAGGAGCTCGTG 1389
568 ATGACCTGAATGAGCTTTGGCCGCTTGCACAGCTGGCTGGGAGATCACTGCTG 627
1390 AAGCTACTCAAGAGCTTTGGCCGCTTTGCACAGCTGGCGGCAATACCACAGCTG 1449
628 AGGATCAAGATCTTTGGGGAGCTGTACTACTGTGTGACAGGCTGGCGAGGCCGGGCC 687
1450 AGGATCAAGATCTTAGCGGAGCTGTACTACTGTGATCTGCGGCGCTGCTGACTACCGGAG 1509
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1570 CGGAGAAGACCAAGACCGGAGTGGACATCGTGTGGGGTGGACACAGGACATGTGTA 1629
808 TGCGGCTCTGCTTGGCTTGGGAATGGAGTTCATGTGTGCTGCTCAATGATGTGACCGCTG 867
1630 GGTGGCTCTGCGGCGGAGAGCGCTGGCAGTATGATGTGCTACCGATGTGCTGCTG 1689
868 GCCAACACATGGAAGCAGGAGCGGCGCTGGCGCATCCACATCACTTCGGGCAACACTG 927
1690 GCAACAGATGGAGGTGGCGGCTCCAGGGCGGCTGGACATTTCCAGAGGACCATG 1749
928 CAGTACCTGAACGGGAGTACGAAGTGGAGCGGCGCTGGTGGCAAGCGCAAGCGCTAC 987
1750 GACTGCTGAAGGGAGTTCGATGTGGAACCTGGTGTGATGCTGCTGCGTGGACTAC 1809
988 CTCAGGAGCAGCAGATGTAGACTTTCTCATCTGCGGCGGCGGCGGCAAGGAAGAG 1047
1810 CTAGATGAGAAGGCGATCGAAGCTACCTCATCTATCTGCTCCAGAGCGGAGGTGAAGAAG 1869

RESULT 12

US-08-726-214-15
Sequence 15, Application US/08726214
Patent No. 610706
GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:450

TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 4601 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-726-214-15
Query Match 17.7%; Score 320.6; DB 3; Length 4601;
Best Local Similarity 59.5%; Pred. No. 7.8e-76;
Matches 567; Conservative 0; Mismatches 374; Indels 12; Gaps 1;
QY 79 GGCTCTCTGGTCCCTCTGTTCTTTGTATATACATCGATACACGCTCTCCCTCCCATCGGATG 138
DB 1575 GGCATAGGCTACGTGCTTTTACACTCTTCGCCACCTACAGCATGCTTCCGTTGCCCTCTC 1634
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DB 1635 ACCTGGGCCATCTTGGCGGCTGGGCATCTTGTGTGAAGTCACACTTCAAGTGTCTC 1694
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QY 379 CAGGAGCGGTGTGCTGTCTGCTGATTTGCCAGCAGCTTTCGCTGAGAGTGAAGAAAGAC 438
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QY 439 ATCAACACAAAAAAGAG-----ACATGTTCCACAGATCTACATACAGAG 486
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QY 487 CATGACAAATGTGAGCATCTCTGTTGCAGACATTTGAGGCTTCCAGCAGCTGGCATCCAG 546
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DB 2115 GCCATGAGCATCTGCTTTTCGATTTAAATTCCTGGGGAGCTGCTACTACTGTGTCTCA 2174
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Db	1510	CAGATGTGACGATCTTGATGACAGACATCGTGGGCTTCACAGAGCTGCCACGCACTGC	1569
Qy	550	ACTGCGAGGAGCTGCTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCT	609
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Qy	850	TCCAATGATGTGACCTCGGCCAACACATGGAAGCAGGAAGCGGCTGGCCGATCCAC	909
Db	1870	TCCCATGATGTGCTCGCCACACAGGATGGAGGACAGCTGGAGTCCCTGGCCGGGTGCAC	1929
Qy	910	ATCACTCGGGCAACACTGCACTACCTGAAACGGGGACTACGAAGTGGAGCCAGGCGCTGGT	969
Db	1930	ATCACAGAGCAACATTGAATCACCTGGACAGGCATACGAGGTGGAGATGGCATGGG	1989
Qy	970	GCGAAGCGCAACGCGTACCTCAAGGAGCAGCACAATTGACACTTTCCTCATCTCGGGCGCC	1029
Db	1990	GAGCAGCGAGACCCCTATCTGAAAGAGATGAACATCCGAACCTACCTGGTATCGATCCC	2049
Qy	1030	AG 1031	
Db	2050	CG 2051	
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; Sequence 5, Application US/08307896C			
; Patent No. 6034071			
; GENERAL INFORMATION:			
; APPLICANT: Iyengar, Srinivas Ravi			
; TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND ADENLYL			
; TITLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS			
; FILE REFERENCE: 29770			
; CURRENT APPLICATION NUMBER: US/08/307,896C			
; CURRENT FILING DATE: 1994-09-16			
; NUMBER OF SEQ ID NOS: 9			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 5			
; LENGTH: 4008			
; TYPE: DNA			
; ORGANISM: Rattus norvegicus			
US-08-307-896-5			
Query Match 15.8%; Score 286; DB 3; Length 4008;			
Best Local Similarity 60.7%; Pred. No. 1.3e-66;			
Matches 503; Conservative 0; Mismatches 295; Indels 30; Gaps			
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Qy	279	CTGCACACACATATCCAGCAGAGGTGCTCAGCGCCGCGGCTTTTCAGGAGAGACCCGAGTTA	338
Db	684	CTACCACAGCACCTCATGGAGCTTGCCTTTGAGCAAAACCTATCGGACACGTTGTAATTG	743

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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Title: US-09-750-240-3

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 442118 seqs, 280819700 residues

Total number of hits satisfying chosen parameters: 884236

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	1808.4	99.8	3549	10	US-09-750-240-5
3	1763.4	97.3	3552	10	US-09-750-240-10
4	1763	97.3	4942	9	US-10-201-000-1
5	1657.8	91.5	3582	10	US-09-750-240-12
6	895	49.4	4523	9	US-10-175-158-1
7	319.4	17.6	2601	10	US-09-925-297-352
8	284	15.7	3518	9	US-10-121-911-2
9	216.8	12.0	4473	10	US-09-751-1008-1
10	209.4	11.6	4985	12	US-10-071-223-1
11	207.8	11.5	5515	10	US-09-751-1008-98
12	124.4	6.9	330	9	US-09-764-868-182
13	124.4	6.9	330	9	US-09-989-442-71
14	124.4	6.9	330	10	US-09-764-869-445
15	79.2	4.4	11881	9	US-09-764-868-1351
16	79.2	4.4	11881	9	US-09-764-868-1353
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20	64.4	3.6	2013	9	US-10-051-643-176	Sequence 176, App
21	64.4	3.6	2013	9	US-09-880-505-176	Sequence 176, App
22	64.4	3.6	2172	9	US-10-051-643-173	Sequence 173, App
23	64.4	3.6	2172	9	US-09-880-505-173	Sequence 173, App
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25	46.6	2.6	915	9	US-09-764-868-181	Sequence 181, App
26	46.6	2.6	915	9	US-09-989-442-20	Sequence 69, Appl
27	42.2	2.3	923	9	US-09-989-442-20	Sequence 20, Appl
28	42.2	2.3	1180	10	US-09-915-582-11	Sequence 11, Appl
29	39.4	2.2	2602	10	US-09-866-582-19	Sequence 19, Appl
30	39.2	2.2	2028	10	US-09-840-125-1	Sequence 1, Appl
31	39.2	2.2	2821	10	US-09-880-107-3358	Sequence 3358, Ap
32	38.6	2.1	434	10	US-09-960-352-2292	Sequence 2292, Ap
33	38.4	2.1	455	9	US-09-954-531-848	Sequence 848, App
34	38	2.1	3121	9	US-10-033-245-6	Sequence 6, Appli
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38	38	2.1	3121	9	US-10-033-435-6	Sequence 6, Appli
39	38	2.1	3121	9	US-10-032-990-6	Sequence 6, Appli
40	38	2.1	3121	12	US-10-033-246-6	Sequence 6, Appli
41	38	2.1	3121	12	US-10-033-301-6	Sequence 6, Appli
42	38	2.1	3121	12	US-10-033-326-6	Sequence 6, Appli
43	37.6	2.1	397	10	US-09-960-352-14458	Sequence 14458, A
44	37.6	2.1	1041	9	US-09-738-626-349	Sequence 349, App
45	37.4	2.1	1759	9	US-10-227-884-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-750-240-3
; Sequence 3, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750.240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-240-3

Query Match	100.0%;	Score 1812;	DB 10;	Length 1812;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1812;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
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Db	1	GTTAACGTTGGTCTGGGATCTCTGGCGAGTGCAGGTCGGGGCGCTTTTCGACGAC	60	
Oy	61	CCGCGACGCCCTCTCTGGCGGCTCTGGTGCCTGTGTCTTTGTATACATCGCATACG	120	

QY	3	TAACGTGGTCTGGCGCATCCTCGCGGCAGTGCAGTCTGGGGCGCTTTCGACGACAGCCC	62
Db	636	TAACGTGGTCTGGCGCATCCTCGCGGCAGTGCAGTCTGGGGCGCTTTCGACGACAGCCC	695
QY	63	GCSCAGCCCTCTGGGGGCTCTGCTGGCCCTGTGTTCTTTGTATACATCGCATACAGCCT	122
Db	696	GCSCAGCCCTCTGGGGGCTCTGCTGGCCCTGTGTTCTTTGTATACATCGCATACAGCCT	755
QY	123	CTTCCCATCCGATGCGGGCTGCGGTCTCTCAGCGGCTGGGCTCTCCACTTGCATTTT	182
Db	756	CTTCCCATCCGATGCGGGCTGCGGTCTCTCAGCGGCTGGGCTCTCCACTTGCATTTT	815
QY	183	GATCTTTGGCTGSCAACTTAAACCGTGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCCAA	242
Db	816	GATCTTTGGCTGSCAACTTAAACCGTGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCCAA	875
QY	243	TGTGCTGCTTTCCCTCTGCACCAAGCTCATTAGCATCTGCACACACTATCCACGAGAGT	302
Db	876	TGTGCTGCTTTCCCTCTGCACCAAGCTCATTAGCATCTGCACACACTATCCACGAGAGT	935
QY	303	GTCTCAGCGCCAGGCTTTTCAGAGACCCGAGTTACATTCAGGCCCGGCTCCACCTGCA	362
Db	936	GTCTCAGCGCCAGGCTTTTCAGAGACCCGAGTTACATTCAGGCCCGGCTCCACCTGCA	995
QY	363	GCATGAGAATCGSCAGCAGGCGGTGCTGCTGCTGGTATTGCCCCAGCAGTTGGCAT	422
Db	996	GCATGAGAATCGSCAGCAGGCGGTGCTGCTGCTGGTATTGCCCCAGCAGTTGGCAT	1055
QY	423	GGAGATGAAGAAGACATCAACACAAAAAAGACAGATGTTCCACAGAGTCTACATACA	482
Db	1056	GGAGATGAAGAAGACATCAACACAAAAAAGACAGATGTTCCACAGAGTCTACATACA	1115
QY	483	GAAGCATGAATGTGAGCATCTGCTTTGCACACATTCAGGGCTTCACAGCCTGGCATC	542
Db	1116	GAAGCATGAATGTGAGCATCTGCTTTGCACACATTCAGGGCTTCACAGCCTGGCATC	1175
QY	543	CCAGTGCATCGCGCAGGAGCTGGTCATGACCTGAATGAGCTCTTGGCCGGTTTGACAA	602
Db	1176	CCAGTGCATCGCGCAGGAGCTGGTCATGACCTGAATGAGCTCTTGGCCGGTTTGACAA	1235
QY	603	GCTGGCTCGGAGAACTACTGCTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGT	662
Db	1236	GCTGGCTCGGAGAACTACTGCTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGT	1295
QY	663	GTGAGGGCTGCCGGAGCCCGGCGACCATGCCACTGCTGCTGTGAGATGGGGGTAGA	722
Db	1296	GTGAGGGCTGCCGGAGCCCGGCGACCATGCCACTGCTGCTGTGAGATGGGGGTAGA	1355
QY	723	CATGATTGAGGCATCTCGCTGGTACGTGAGGTGACAGTGTGAATGTGAACATGCGCGT	782
Db	1356	CATGATTGAGGCATCTCGCTGGTACGTGAGGTGACAGTGTGAATGTGAACATGCGCGT	1415
QY	783	GGSCATCCACAGGCGCGTGCATGCGGCGTCTTGGCTTGCAGAAATGGCAGTTGCA	842
Db	1416	GGSCATCCACAGGCGCGTGCATGCGGCGTCTTGGCTTGCAGAAATGGCAGTTGCA	1475
QY	843	TGTGTGTCTCAATGATGTGACCTGGCCAAACACATGGAAGCAGGAAGCCGGCTGGCG	902
Db	1476	TGTGTGTCTCAATGATGTGACCTGGCCAAACACATGGAAGCAGGAAGCCGGCTGGCG	1535
QY	903	CATCCACATCCTCGGCGCAACATGCGAGTACCTGAACGGGGACTACGAAGTGGAGCCAG	962

; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE OF INVENTION: FAILURE
; FILE REFERENCE: 22002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 3552
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-750-240-10

Query Match 97.3%; Score 1763.4; DB 10; Length 3552;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 21; Indels 3; Gaps 1:

QY	3	TACGTGGTGGTGGGCATCTGTGGCGCAGTGCAGGTGCGGGGGCGCTTTCGACGACACCC	62
DB	636	TTACGTGGTGGTGGGCATCTGTGGCGCAGTGCAGGTGCGGGGGCGCTTCGACGACACCC	595
QY	63	GGCAGCCCTCTGCGGGCTCTGTGGCCCTGTGTTCTTTGTATACATCGCATACACGCT	122
DB	696	GGCAGCCCTCTGCGGGCTCTGTGGCCCTGTGTTCTTTGTCTACATCGCTTACAGCT	755
QY	123	CCTCCCATCCGATCGGGCTGCGCTCTCAGCGCCCTGGGCTCTCACCTTGCAATT	182
DB	756	CCTCCCATCCGATCGGGCTGCGCTCTCAGCGCCCTGGGCTCTCACCTTGCAATT	815
QY	183	GATCTTGGCTGGCACTTAACCGTGGTGTGATGCTTCTCTGGAAGCAGCTGGTGCCAA	242
DB	816	GATCTTGGCTGGCACTTAACCGTGGTGTGATGCTTCTCTGGAAGCAGCTGGTGCCAA	875
QY	243	TGTGCTGTGTTCTCTGCACCAACGTCATTAGCATCTGCACACATATCCAGCAGGT	302
DB	876	TGTGCTGTGTTCTCTGCACCAACGTCATTAGCATCTGCACACATATCCAGCAGGT	935
QY	303	GTCTCAGCGCCAGGCTTTCAGAGACCCGCGATTACATCCAGGCCGCTCCACCTGCA	362
DB	936	GTCTCAGCGCCAGGCTTTCAGAGACCCGCGATTACATCCAGGCCGCTCCACCTGCA	995
QY	363	GCATGAGATCGGCAGCAGGCGGTGCTGTGTCGGTATTGCCCCAGCAGCTTGCCAT	422
DB	996	GCATGAGATCGGCAGCAGGCGGTGCTGTGTCGGTATTGCCCCAGCAGCTTGCCAT	1055
QY	423	GGAGATGAAGAGAGATCAACACAAAAAAGAGAC---ATGTTCCACAAGATCTACAT	479
DB	1056	GGAGATGAAGAGAGATCAACACAAAAAAGAGACATGATTTCCACAAGATCTACAT	1115
QY	480	ACAGAAGCATGACAATGTTCAGATCTCTGTTGCAGACATTGAGGCTTCACGAGCTGGC	539
DB	1116	ACAGAAGCATGACAATGTTCAGATCTCTGTTGCAGACATTGAGGCTTCACGAGCTGGC	1175
QY	540	ATCCCATGCTACCTGCGCAGGAGCTGTCATGACCTCGAATGAGCTCTTTGCCCGGTTTGA	599
DB	1176	ATCCCATGCTACCTGCGCAGGAGCTGTCATGACCTCGAATGAGCTCTTTGCCCGGTTTGA	1235
QY	600	CAAGCTGGCTGGGGAATCACTGCTGAGGATCAAGATCTTGGGGGATGTTTACTACTG	659
DB	1236	CAAGCTGGCTGGGGAATCACTGCTGAGGATCAAGATCTTGGGGGATGTTTACTACTG	1295
QY	660	TGTGTGAGGCTGCGGAGGCGCGGCCAGCATGCCACTGCTGTGTGAGATGGGGT	719

DB 1296 TGTGTCAGGCTGCCGAGGCGCGGCCGACCATGCCACTGCTGTGTGAGATGGGGT 1355
QY 720 AGACATGATTGAGGCCATCTCGCTGTAGTGTGAGGTGACAGGTGTAATGTGAACATCG 779
DB 1356 AGACATGATTGAGGCCATCTCGCTGTAGTGTGAGGTGACAGGTGTAATGTGAACATCG 1415
QY 780 CGTGGCATCCACAGCGCGCTGCACCTGCGGCTCTTGGCTTGGGAAATGGCAGTT 839
DB 1416 CGTGGCATCCACAGCGCGCTGCACCTGCGGCTCTTGGCTTGGGAAATGGCAGTT 1475
QY 840 CGATGTGTGTCATGATGTGACCTGCGCAACACATGGAAGCAGGAGCGGCTGG 899
DB 1476 CGATGTGTGTCATGATGTGACCTGCGCAACACATGGAAGCAGGAGCGGCTGG 1535
QY 900 CCGCATCCACATCACTCGGCAACACTGCAGTACCTGAAGGGGACTACGAGGTGAGCC 959
DB 1536 CCGCATCCACATCACTCGGCAACACTGCAGTACCTGAAGGGGACTACGAGGTGAGCC 1595
QY 960 AGCCCTGTGTGCAAGCGCAACGCTACCTCAAGGAGCAGCACATTTGAGACTTTCTCAT 1019
DB 1596 AGCCCTGTGTGCAAGCGCAACGCTACCTCAAGGAGCAGCACATTTGAGACTTTCTCAT 1655
QY 1020 CCTGGCGCCAGCAGAAAG 1079
DB 1656 CCTGGCGCCAGCAGAAAG 1715
QY 1080 TCGGGCAACTCCATGGAAGGCTGATCGCGGATGGTTCCTGATCGTCCCTTCTCCCG 1139
DB 1716 TCGGGCAACTCCATGGAAGGCTGATCGCGGCTGATCGCGGCTGATCGTCCCTTCTCCCG 1775
QY 1140 GACCAAGGACTCCAGGCTTCGCGCAGATGGGCATTTGATGATTTCCAGCAAGACAAACG 1199
DB 1776 GACCAAGGACTCCAGGCTTCGCGCAGATGGGCATTTGATGATTTCCAGCAAGACAAACG 1835
QY 1200 GGGCAGCCAGATGACCTGAACCTGAGGATGAGGTGGATGAGTTCTGAGCGCTGCCAT 1259
DB 1836 GGGCAGCCAGATGACCTGAACCTGAGGATGAGGTGGATGAGTTCTGAGCGCTGCCAT 1895
QY 1260 CGATGCGCCAGCATTTGATGATGCGGAGAGACCATGTCGCGCGGTTTTTGTCTACCTT 1319
DB 1896 CGATGCGCCAGCATTTGATGATGCGGAGAGACCATGTCGCGCGGTTTTTGTCTACCTT 1955
QY 1320 CCAGAGAGAGATTTTGAAGAAGTACTCCCGGAAGGTGGATCCCGGCTTCGGAGCCTA 1379
DB 1956 CCAGAGAGAGATTTTGAAGAAGTACTCCCGGAAGGTGGATCCCGGCTTCGGAGCCTA 2015
QY 1380 CGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1439
DB 2016 CGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2075
QY 1440 ACACCTCACCCCTGATGCTTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCT 1499
DB 2076 ACACCTCACCCCTGATGCTTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCT 2135
QY 1500 GCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1559
DB 2136 GCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2195
QY 1560 CCGCAGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1619
DB 2196 CCGCAGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2255
QY 1620 TGTGTTTACTTCTGCAATTTGCCAACATGTTACCTGTAACCAACACACCCCATACGAGCTG 1679
DB 2256 TGTGTTTACTTCTGCAATTTGCCAACATGTTACCTGTAACCAACACACCCCATACGAGCTG 2315
QY 1680 TCGAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCTGCTGCTGCTGCTGCTGCT 1739
DB 2316 TCGAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCTGCTGCTGCTGCTGCTGCT 2375
QY 1740 CAATTACTCTGCGGCTGATGCTCCCTGCTGAGGAGCACCATGCCACCTGCACTGCACTG 1799
DB 2376 CAATTACTCTGCGGCTGATGCTCCCTGCTGAGGAGCACCATGCCACCTGCACTGCACTG 2435


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Db 2342 GCAGCATTTGCCGCTCACGGCACATAGCACCGAGTTGGCATCTTTTCCGTCCTGCTTG 2401
QY 1622 TGTFTTACTTCTGCCATTGGCCAAACATCTTCACTGTAAACACACCCCAACATACGAGCTGTG 1681
Db 2402 TGTFTTACTTCTGCCATTGGCAATGTTCACTGTAAACACACCCCAACATACGAGCTGTG 2461
QY 1682 CAGCCCGGATGCTGAAATTTAAACACCTTGCCTGACATCACTGCCTGCCACCTTGCAGCACTCA 1741
Db 2462 CAGCCCGGATGCTGAAATTTAAACACCTTGCCTGACATCACTGCCTGCCACCTTGCAGCACTCA 2521
QY 1742 ATTACTCTCTGGGCCCTGGAGTGTCTCCCTGTGTGAGGGCACCATTGCCACCTTGCAGCTTTC 1801
Db 2522 ATTACTCTCTGGGCCCTGGAGTGTCTCCCTGTGTGAGGGCACCATTGCCACCTTGCAGCTTTC 2581
QY 1802 CTGAGGTGTTTC 1812
Db 2582 CTGAGTACTTTC 2592

RESULT 5
US-09-750-240-12
; Sequence 12, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE REFERENCE: FAILURE
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 3582
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified AC-VI
US-09-750-240-12
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Query Match          91.5%; Score 1657.8; DB 10; Length 3582;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1730; Conservative 0; Mismatches 77; Indels 6; Gaps 2;

QY 3 TAACGTGGTGTGGGCATCTTGGCGGAGTGCAGGTTCGGGGGGCGCTTTCGACGACACCC 62
Db 657 TTACGTGGTGTGGGCATCTTGGCGGAGTGCAGGTTCGGGGGGCGCTTTCGACGACACCC 716
QY 63 GCGCAGCCCTCTGCGGGCTCTGGTGCCTGTGTTGTATACATCGCATACACGCT 122
Db 717 GCGCAGCCCTCTGCGGGCTCTGGTGCCTGTGTTGTATACATCGCATACACGCT 776
QY 123 CTCCCCATCCGATCGGGCTGCCCTCTCTCAGCGGCTTGGGCTCTCCACCTTGCATTT 182
Db 777 CTCCCCATCCGATCGGGCTGCCCTCTCTCAGCGGCTTGGGCTCTCCACCTTGCATTT 836
QY 183 GATCTTGGCTTGGCACTTTAACCGTGGTGTATGCTTCTTGAAGCAGCTCGGTGCCAA 242
Db |||||||
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Db 837 GATCTTGGCTTGGCAACTTTAAACGTTGGTGTATGCTTTCCTCTGGAAGCAGCTCGGTGCCAA 896
QY 243 TGTGCTGCTGTTCCTCTCTGCACCAACGTCATTAGCATCTGCACACACTATTCACACAGAGT 302
Db 897 TGTGCTGCTGTTCCTCTCTGCACCAACGTCATTGGCATCTGCACACACTATTCACACAGAGT 956
QY 303 GTCTCAGCCCGAGGCCCTTTTCAGGAGACCCGCGATTATCATCCAGGCCCGGTCCACCTGCA 362
Db 957 GTCTCAGCCCGAGGCCCTTTTCAGGAGACCCGCGGTTACATCCAGGCCCGGTCCACCTGCA 1016
QY 363 GNATGAGATCGGCACAGAGAGCGGCTGTGCTGTGCGGTATTCGCCACAGCAGCTTGGCAT 422
Db 1017 GCATGAGATCGGCACAGAGAGCGGCTGTGCTGTGCGGTATTCGCCACAGCAGCTTGGCAT 1076
QY 423 GGAGATGAAGAGAGACATCAACACAAAAAAGAGAC---ATGTTCCACAAGATCTACAT 479
Db 1077 GGAGATGAAGAGAGACATCAACACAAAAAAGAGACATGATGTTCCACAAGATCTACAT 1136
QY 480 ACAGAGCATGACATGCTCAGCATCTCTGTTTGACAGACATTTAGGGGCTTACCAGCCTGGC 539
Db 1137 ACAGAGCATGACATGCTCAGCATCTCTGTTTGACAGACATTTAGGGGCTTACCAGCCTGGC 1196
QY 540 ATCCAGTGCATGCGCAGAGAGCTGTGTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGA 599
Db 1197 ATCCAGTGCATGCGCAGAGAGCTGTGTCATGACCTTGAATGAGCTCTTTGCCCGGTTTGA 1256
QY 600 CAAGCTGGCTGCGGAGAATCACTGCTGAGGATCAAGATCTTGGGGGACTGTTTACTACTG 659
Db 1257 CAAGCTGGCTGCGGAGAATCACTGCTGAGGATCAAGATCTTAGGAGACTGTTTACTACTG 1316
QY 660 TGTGTCAGGGCTGCCGGAGGCCCGGCGACCATGCCACTGCTGTGTGAGAGATGGGGT 719
Db 1317 CGTGTCAAGGCTGCCCGAGGGCGGCGAGATCACGCCCACTGCTGTGTGAGATGGGGT 1376
QY 720 AGACATGATTGAGGCCATCTCGCTGTGTAGTGAGGTGACAGGTGTAATGTGAACATGG 779
Db 1377 AGACATGATTGAGGCCATCTCGCTGTGTAGTGAGGTGTAACAGGTGTAACATGG 1436
QY 780 CBTGGCATCCACAGCGGGCGCTGCACTCGGCGCTCTTGGCTTCGGAATGGCAGTT 839
Db 1437 TGTGGCATCCACAGCGGAGCTGTGCTATTGCGGCGCTTGGCCTACGGAATGGCAGTT 1496
QY 840 CGATGTGTGTCATGATGTGACCTTGGCCCAACACATGGAAGCAGGAAGCGGCGTGG 899
Db 1497 TGATGTCTGTCTAAACGATGTGACCTTGGCTAACCACATGAGGCGCGGGGC---GGCCG 1553
QY 900 CCGCATCCACATCACTCGGCAACACTGGCAGTACCTGGAAGGGGAGCTACCAAGTGAGGC 959
Db 1554 GCGCATCCACATCACTCGGGCTACCTGCGATGCTTGAACGGGGAGCTATGAGGTGGAGCC 1613
QY 960 AGGCCGTGTGGCAAGCGCAACCGTACCTCAAGAGCAGCAGCATTTGAGACTTTCTCTCAT 1019
Db 1614 AGGCCGTGTGTGAACGCAATGCGTACCTCAAGGAGCAGTGCATTTGAGACCTTCTCTCAT 1673
QY 1020 CBTGGCGCCAGCCAGAAACGGAAAGAGGAGAAAGCATGCTGGCCAAGCTGCAGCGGAC 1079
Db 1674 ACTTGGCGCCAGCCAAACGGAAAGAGGAGAAAGCATGCTGGCCAAGCTTTCAGCGGAC 1733
QY 1080 TCGGGCCCACTCCATGGAAGGGCTGATGCGCGCATGGGTTCCTGATGCTGCTTCTCCCG 1139
Db 1734 ACGGGCCCACTCCATGGAAGGGCTGATGCGCGCGCTGGGTTCCTGATGCTGCTTCTCCCG 1793
QY 1140 GACCAAGGACTCCCAAGGCCCTTCGCGCAGATGGCATTTGATGATTTCCAGCAAGACAACCG 1199
Db 1794 GACCAAGGACTCTAAGGCATTCGCCCAGATGGCATTTGATGATTTCTAGCAAGACAACCG 1853
QY 1200 GGGCACCCCAAGATGCCCTGAACCCCTCAGGATGAGGTGATGATGCTTCTGAGCCGTGCCAT 1259
Db 1854 GGGTGGCCCAAGATGCTCTGAACCCCTGAAGATGAGGTGATGATGCTTCTGAGCCGTGCCAT 1913
QY 1260 CGATGCGCCGAGCATTTGATCAGCTGCGGAAGGACCATGTCGCCCGGTTTGTGCTACCTT 1319
Db 1914 CGATGCGCCGAGCATTTGATCAGCTGCGGAAGGACCATGTCGCCCGGTTTGTGCTACCTT 1973
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Db 2126 GAACCAACTCCATCGGSCACAAACCCACACACTGGGGGGCTGAGCGCCCTTCTACAAAC 2185
QY 1138 -----CGACCAAGGACTTCAAGGCTTTCGCGCAGATGGGCAATGATGATTCCAGCA 1189
Db 2186 ACCTGGGTGCACACAGGTGTCGAAGAGATGAAGCGATGGGCTTTGAAGACCCCA--- 2242
QY 1190 AAGACAACCGGGGACCCCAAGATGCCCTGAACCTTGAGGATGAGGTGGATGATTCCTGA 1249
Db 2243 ---AGGACAAGAACGCCAGAGAGTGCGAACCTTGAGGATGAAGTGGATGAGTTCTGG 2299
QY 1250 GCGGTGCCATCGATGCCCGCAGCATGATCAGCTGCGGAAGGACCATGTCGCGCGGTTTT 1309
Db 2300 GCGGTGCCATGACGCCAGAGCATGATGATAGGCTTCGGTCTGAGCAGGTCCGCAAGTTC 2359
QY 1310 TGCTACCTTCCAGAGAGAGATTTTGAAGAAGTACTCCCGGAAGGTGGATCCCGGCT 1369
Db 2360 TCTGACCTTCAGGAGCCTGACTTAGAGAAGTACTCCAGCAGGTAGACGACCGAT 2419
QY 1370 TCGAGGCTACGTTGGCTGTGCCCTGTGTCTTCTGCTTTCATCTGCTTCATCCAGCTTC 1429
Db 2420 TTGGTGCTATGTGGCTGTGCCCTGCTGCTCTTCTTCTTCTCATCTGCTTGTCCAGATCA 2479
QY 1430 TAATTTTCCACACTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGC 1489
Db 2480 CCATGTCGCCCACTCCCATATTCATGCTCAGCTTCTACCTGACCTGTTCCTCTGCTGTA 2539
QY 1490 TAATACCGTGTGATGCTGTGTGTACTCTCTGTGTGTCTTCTTCTTCCCTTAAGGCCCTGC 1549
Db 2540 CTTTGGTGTGTTGTGTCTGTGATCTACTTCTGCTTCCGTAAGCTCTTCCCTCCCACTGC 2599
QY 1550 AAGCTGTCCCGCAGCATTTGCGCTCAGCGGCACATAGCAGCGCATGTTGGCATCTTTT 1609
Db 2600 AGACCTCTCCAGGAAGATGTCGGGTCCAAAGATGAACAGCACCCTGTTGGGTGTTC 2659
QY 1610 CCGTCTGCTGTGTACTTCTGCCATTCGCAACATGTTCACTGTGAACCAACCCCA 1669
Db 2660 CCATACCTTGTGTGTTTCTTCTGCGGCTTGTGTCAACATGTTCACTGTGAACCTCCAGGAC 2719
QY 1670 TAGGGACTGTGACCGCGGATGCTGAATTTAAACCTGCTGTGACATCACTGCCCTGCCACC 1729
Db 2720 TGCTGGCTCTTGGCACAGAGCACAACATCAGCGCGAGCCAGGTCAACGCGTGTACG 2779
QY 1730 TGACAGG-----CYCAATTACTCTGCGGCTGGATGCTCCCTGTGTGAGGGACCA 1783
Db 2780 TGGCGGATCGCGGCTCAACTACAGCCTGGCGATGAGCAGGGCTTCTGTGCGAGCCCT 2839
QY 1784 TGCCCACTGCGAGCTTTCCTGAGGTGTC 1812
Db 2840 GGCCCACTGCAACTTCCCGAGTACTTC 2868
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RESULT 7

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US-09-925-297-352
; Sequence 352, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 352
; LENGTH: 2601
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: misc feature
; LOCATION: (2520)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2572)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-352
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Query Match 17.6%; Score 319.4; DB 10; Length 2601;
Best Local Similarity 64.5%; Pred. No. 3.6e-76;
Matches 515; Conservative 0; Mismatches 271; Indels 13; Gaps 2;
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QY 294 AGCAGAGGTCTCTCAGCGCCAGGCGCTTTTCAGGAGACCCGAGTTACATCAAGGCCCGCT 353
Db 34 AACAGCCGCAAGCACCGCAAGGCTTCTCTGGAGGCGCCGAGTCGCTGGAGGTGAAGAT 93
QY 354 CCACCTGCACATCAGATCGGCAGCAGGAGCGGCTCTGCTGCTGCGTATTGCCCCAGCA 413
Db 94 GAACCTGGAAGAGCAGAGCCAGCAGCAGAGAACCTCATGCTTTTCCATCTGCCCCAAGCA 153
QY 414 CGTTGCCATGGAGATGAAGAAGACATCAACACA-----AAAAAAGAGACAT 461
Db 154 CGTGGCTGACGAGATGCTGAAGACATGAAGAAGACGAGAGCCAGAGCCAGCAGCA 213
QY 462 GTTCCACAAGATCTACATACAGAAGCATACAATGTGAGCATCTGTTTGCAGACATGTA 521
Db 214 GTTCAACACCATGTACATGTACCGTACAGAGACGTGAGCATCTCTTTGCCGACATCGT 273
QY 522 GGGCTTCCACAGCTGCGATCCCATCCAGTGCCTGCGCAGAGCTGTCATGACCTGAATGA 581
Db 274 GGGCTTTACCCAGCTGTCTTCTGCTCAGTGCCCGAGGAGCTGTGGAAGCTGTCTCAACGA 333
QY 582 GCTCTTTGCCCGGTTTGACAAGCTGGCTGGGAGAAATCACTGCTGAGGATCAAGATCTT 641
Db 334 GCTCTTTGCCCGCTTTGACAAGCTGGCAGCTAAATACCAACAGCTGCGATTAAAGATCT 393
QY 642 GGGGAGCTGTACTACTGTGTGTCAGGGCTGCGGAGGCGCGGCGCCAGCATGCCCACTG 701
Db 394 GGGCGAGTGTACTACTGTGCTGCGGCTTGGCGGCTTACCGGAGGACACCGCGCTCG 453
QY 702 CTGTGTGAGATGGGGTAGACATGATTGAGGCCATCTCGCTGCTGCTGAGGTGACAGG 761
Db 454 CTCCATCTCATGGGCTGGCCATGTTGAGAGCCATCTCGTATGTGCGGAGAGACCAA 513
QY 762 TGTGAATGTGAACATGCGCTGGGSCATCCACAGCGGCGCGTGCACCTGCGGCTCTTGG 821
Db 514 GACTGGGTGGACATGCTGTGGGGGTGCACACGCGGACCGTGTGTTGGGGCGCTCTGGG 573
QY 822 CTTGCGGAATGGCAGTTCCATGTGTGTCATGATGTGACCTGCGCCACCATGGA 881
Db 574 CCAGAAGCGTGGCAGTACGACGTGTGCTGACTGTGCTACTGTAGCCCAACAGATGGA 633
QY 882 AGCAGGAAGCGGCTGGCGGCATCCACATCACTCGGCGAACACTGCAGTACCTGAACGG 941
Db 634 GGGCGGGGATCTCCTGGGCGCTGACATCTCCAGCAGCACCATGAGCTGCTGTAAGG 693
QY 942 GGACTACGAAGTGGAGCGCGCTGTGTGGCAAGCGGCTGCTGCTTACCTCAAGGAGCAGCA 1001
Db 694 GGAGTTTGATGTGGAGCGAGCGATGGGCGAGCGCTGTGATTACCTAGAGAAGAGGG 753
QY 1002 CATTGAGACTTTCTCTATCTCTGGGCGCC-AGCCAGAAACGGAAGAGAGGAGGATGC 1060
Db 754 TATTGAAACCTTACCTCATCTATCTTCCCTCCAAAGCCAGAGGTGAAGAAAAACAGCCCAAGAA 813
QY 1061 TGGCCRAGCTGACGCGAC 1079
Db 814 TGGCTCAATGGCTCGGCC 832
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RESULT 8

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US-10-121-911-2
; Sequence 2, Application US/10121911
; Patent No. US20020164632A1
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; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE
; FILE REFERENCE: 5800-47
; CURRENT APPLICATION NUMBER: US/10/121.911
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US/09/412,210
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3518
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 21529 adenylate cyclase
; NAME/KEY: CDS
; LOCATION: (247)...(3480)
US-10-121-911-2

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Query Match	15.7%	Score 284;	DB 9;	Length 3518;
Best Local Similarity	56.4%;	Pred. No. 1.5e-66;		
Matches 617;	Conservative	0;	Mismatches 435;	Indels 42;
Gaps				

Qy	6	CGTGTGCTGGGCATCCTGGCGCAGTGCAGTGTGGGGCGCTTTTCGACGACAGACCGCG	65
Db	528	CTTTGGTATGGGTGCGGCTCTASCCTTAGCCACAGCCCTTCTGTTCACCGGGGCGTGGT	587
Qy	66	CAGCCCTCTGGGGCCTCTGTGTGCCCTGTGTCTTTCTATACATGCATACAGGCTCCT	125
Db	588	GAGCGCTGGGACCAAGTGTCTATTTCCTTCGTCACTTCAGGGGTATGCCATGCT	647
Qy	126	CCCCATCCGATGCGGGCTGCGGTCCTCAGGGGCTGGGCTCTCCACCTTTCATTTGAT	185
Db	648	GCCTTTGGGCATGCGGGACGCGCGTGTGGGGCTCGCTCTCTCACTTCGCATCTGCT	707
Qy	186	CTTTGGCTCGCAACTT-----AACCTGTGTGATGCTTCTCTCTG--GAAGACGT	233
Db	708	GGTCTCGGGCTGTATCTTTGGGCCACAGCGGACTCAGGGCTGCATGCTGCGCGAGTT	767
Qy	234	CGGTGCCAATGTGCTGCTTCTTCCTTCGACCAACGTCATTAGCATCTGCACACATATCC	293
Db	768	GGCAGCAAAACGCGAGTGTCTTCTGTGCGGAACGTGGCAGGAGTACCAACAAGGCGCT	827
Qy	294	AGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAGACCCGCGAGTTTACATCCAGGCCGCT	353
Db	828	GATGGAGCGGCGCTTCGCGGGCACGTTCCGGGAGCACTCAGCTCCCTGCATCAGCGCG	887
Qy	354	CCACCTGCAGCATGGAATTCGCGACGAGGCGGTGCTGTCTGGTATTGCCCCAGCA	413
Db	888	CGGCTGGACCGGAGAAGAACCAAGACACCTTCTTGTTCATCTCTCTGCGCTA	947
Qy	414	CGTTGCCATGGAGATGAAGAGACATCAACACAAAAAAG-----	457
Db	948	CCTGGGCGGAGATGAAGGAGAGATCATGGACGGTGCAGGACGACAGGGGTCAAG	1007
Qy	458	-----ACATGTTCCACAAGATCTACATACAGAAGCATGACAAATGTCAGCAT	503
Db	1008	GCCAGAGAGCATTAACAATTTCCACAGCTCTATGTCAAGAGGCCAGGGAGTTCAGCGT	1067
Qy	504	CCTGTTTTCAGACATTTAGGGCTTCACAGCTTGGCATCCAGTGCATCGGCGAGGAGCT	563
Db	1068	GCTGTATGCTGACATCGTGGGCTTCACGCGGTGCGCCAGCGAGTGTCCCGCTAAGGAGCT	1127
Qy	564	GGTCATGACCTGAATGAGCTCTTTGCCCGTTTCACAAGCTGCTGCGGAGATCACTG	623
Db	1128	GGTGCTCATGCTCAATGAGCTCTTTGGCAAGTTGCACCAAGTTCGCAAGGAGCATGATG	1187
Qy	624	CCTGAGATCAAGATCTTGGGAGCTGTTTACTGTGTCTAGGGGCTGCGGAGGCGCG	683
Db	1188	CATCGGATCAAGATCCTGGGAGCTGTTACTACTGTCTCTGGGTCGCACTCTCACT	1247

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RESULT 9
US-09-751-100B-1
; Sequence 1, Application US/09751100B
; Patent No. US2002014236A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Human Adenylylate Cyclase and Use Therefor
; FILE REFERENCE: P27948A
; CURRENT APPLICATION NUMBER: US/09/751,100B
; CURRENT FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (43)..(4101)
; OTHER INFORMATION: Adenylylate cyclase coding region
US-09-751-100B-1

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Query Match	12.0%;	Score 216.8;	DB 10;	Length 4473;
Best Local Similarity	63.8%;	Pred. No. 2.2e-48;		
Matches 329;	Conservative 0;	Mismatches 187;	Indels 0;	Gaps 0;
Qy	463	TTCCACAAGACTCTACATACAGAAGCATGACAAATGTGACATCCTCTTTTGCAGACATTGAG	522	
Db	1186	TTCCGCCCTTTAAGATGTCAGACATTCGAAGAAGTCAGTATTTTATTTTGCAGACATTGTG	1245	
Qy	523	GGCTTTCACCGCTGGGCATCCAGTGCACCTGCGGAGGAGCTGGTCATGACCCGTGAATGAG	582	
Db	1246	GGTTTCACCAAGATGAGCGCCAACAAATCTCGCGCATGCTTTGGTAGGGCTACTCAATGAC	1305	
Qy	583	CTCTTTGCGCCGGTTTGACAAGCTGGCTCGGAGGAATCACTGCTCAGGATCAAGATCTTTG	642	
Db	1306	CTGTTTCGGTCGCTTTGACCGCCTGTGTGAGCAGACCAAGTGTGAGAAATCAGCACTCTG	1365	
Qy	643	GGGACTGTTTACTACTGTGTGTGAGGGCTGCGGAGGCCCGCGCGGACCATGCCCCACTGC	702	
Db	1366	GGGACTGTTTATTACTGTGTGGCAGGGTGTCCGAGGCCCGCGGACAGCAATGCGCTACTGC	1425	
Qy	703	TGTGTGGAGATGGGGGTAGACATGATTGAGCGCCATCTCGCTGGTACGTGAGGTGACAGGT	762	

Db 1426 TGCATTGAATGGCTTAGGCATGATAAAGCCATCAGAGAGTCTGCCAGGAGAGAAA 1485
QY 763 GTGAATCTGAACATGCGCTGGGATCCACAGCGGGCGGTGCACCTGCGCGCTTGGC 822
Db 1486 GAGATGGTGAACATGCGCTGGGTTTCAACAGGGGACTCTCTGTGTGCGCATCTGGC 1545
QY 823 TTGCGGAAATGGCAGTTTCATGTGTGTCCTCAATGATGTGACCTGGCCCAACACATGAA 882
Db 1546 ATGAGGAGGTTTAAATTTGATGTGTGTCCTCAACGATGTGAATCTCATCGAG 1605
QY 883 GCAGGAGCGGCTGGCCGATCCACATCCTGCGGCAACATGCTACCTGAGTGAAGGG 942
Db 1606 CAGCTGGGAGTGGCTGGCAAGTTTACATATCTGAGGCCACTGCMAAATACTTAGACG 1665
QY 943 GACTTACCAAGTGGAGCCAGCGCTGTGTGGCAAGCG 978
Db 1666 AGGTATGAATGAAGATGGAGAGTTATTGAGCGC 1701

RESULT 10

US-10-071-223-1
; Sequence 1, Application US/10071223
; Patent No. US20020137174A1
; GENERAL INFORMATION:
; APPLICANT: Storm, Daniel R.
; APPLICANT: Hacker, Beth
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
; APPLICANT: University of Washington
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLIVL
; FILE REFERENCE: 44481-5029-02-US
; CURRENT APPLICATION NUMBER: US/10/071,223
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 09/473,717
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: PCT/US98/13541
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/098,559
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,440
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: human type IX adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (17)..(3898)
US-10-071-223-1

Query Match 11.6%; Score 209.4; DB 12; Length 4985;
Best Local Similarity 62.1%; Pred. No. 2.3e-46;
Matches 330; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

QY 426 GATGAAGAAGACATCAACACAAAAAAGAGACATCTTCCACAAGATCTACATACAGAA 485
Db 1123 GAAGAAAAAGCTTCCATCCAAAAAGCTCTATAGCCCTCCGCCCTTTTAAAGATGCAGCA 1182
QY 486 GCATGACAATGTCAGCATCTCTTTGTCAGACATTTGAGGGCTTCCACAGCCTGGCATCCCA 545
Db 1183 GATCGAAGAAGTCAGTATTTTATTTCAGATATCGTGGGCTTCCACCAAGATGAGTCCAA 1242
QY 546 GTCACCTGCCAGAGCTGCTCATGACCTGTAATGAGCTCTTTGCCCGGTTTGACAAAGCT 605
Db 1243 CAAGTCTGCCACGCCCTTGGTGGGTCTCTCTGAACGATCTTTCGGTGGCTTCGACCGCCT 1302
QY 606 GCGTCGGGAGAATCACTGCCTCAGGATCAAGATCTTGGGGGACTGTTTACTACTGTGTGTC 665
Db 1303 GTGTGAGGAGCAACAGTGTGAGAAAAATCAGCACCCCTGGGAGACTGTTTACTTACTTGC 1362

QY 666 AGGCTGCCGAGGCGCGGCCGACCATGCCACTGCTGTGTGAGATGGGGGTAGACAT 725
Db 1363 GGGCTGTCCGAGCGCGGCCGACCATGCTACTGCTGCATCAGATGGCCCTGGGCAT 1422
QY 726 GATTGAGGCATCTCGCTGTGTAGTGTGAGTGTGAGTGTGAAATGTGAACATGCGCGTGGG 785
Db 1423 GATCAAGGCCATCGAGCAGTTCTGCCAGAGAGAAGAGATGGTGAACATGAGATCGG 1482
QY 786 CATCCACAGCGGCGGCTGCACCTGCGGCGTCTTGGCTTCCGGAATGGCAGTTCGATGT 845
Db 1483 GGTGCACACAGGCGACCGTCTTTGCGGCATCTCGGCATCAGGAGGTTTAAATTTGACGT 1542
QY 846 GTGGTCCAATGATGTGACCTTGGCCCAACACATCGGAAGCAGGAGCGGCTGGCCGCAT 905
Db 1543 GTGGTCCAACGATGTGAACCTGGCCCAATCTCATGGAGCAGCTGGGAGTGGCCGCAAGT 1602
QY 906 CCACATCACTCGGGCAACACTGCAGTACCTGACGGGGGACTACGAAGTGA 956
Db 1603 TCACATTTCTGAGGCCACCGCAAAATACTTAGATGACCCGTACGAAATGGA 1653

RESULT 11

US-09-751-100B-98
; Sequence 98, Application US/09751100B
; Patent No. US20020142436A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Human Adenylylate Cyclase and Use Therefor
; FILE REFERENCE: P27948A
; CURRENT APPLICATION NUMBER: US/09/751,100B
; CURRENT FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 98
; LENGTH: 5515
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (539)..(4600)
; OTHER INFORMATION:
US-09-751-100B-98

Query Match 11.5%; Score 207.8; DB 10; Length 5515;
Best Local Similarity 62.0%; Pred. No. 6.6e-46;
Matches 329; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

QY 426 GATGAAGAAGACATCAACACAAAAAAGAGACATGTTCCACAAGATCTACATACAGAA 485
Db 1645 GAAGAAAAAGCTTCCATCCAAAAAGCTCTATAGCCCTCCGCCCTTTTAAAGATGCAGCA 1704
QY 486 GCATGACAATGTCAGCATCTCTTTGTCAGACATTTGAGGGCTTCCACAGCCTGGCATCCCA 545
Db 1705 GATCGAAGAAGTCAGTATTTTATTTCAGATATCGTGGGCTTCCACCAAGATGAGTGCCT 1764
QY 546 GTCACCTGCCAGAGCTGCTCATGACCTGTAATGAGCTCTTTGCCCGGTTTGACAAAGCT 605
Db 1765 CAAGTCTGCCACGCCCTTGGTGGGTCTCTCTGAACGATCTGTCGGTGGCTTCGACCCGCT 1824
QY 606 GCGTCGGGAGAATCACTGCTGAGGATCAAGATCTTTGGGGACTGTTTACTACTGTGTGTC 665
Db 1825 GTGTGAGGAGACCAAGTGTGAGAAAAATCAGCACCCCTGGGAGACTGTTTACTACTGCGTGGC 1884
QY 666 AGGCTGCCGAGGCGCGGCCGACCATGCCACTGCTGTGTGAGATGGGGGTAGACAT 725
Db 1885 GGGCTGTCCGAGCGCGGCCGACCATGCTACTGCTGCATCAGATGGCCCTGGGCAT 1944
QY 726 GATTGAGGCATCTCGCTGCTGAGTGTGAGTGTGACAGTGTGAATGTGAACATGCGCGTGGG 785
Db 1945 GATCAAGGCCATCGAGCAGTTCTGCCAGGAGAGAAGAGATGTTGAAACATGAGAGTTCGG 2004
QY 786 CATCCACAGCGGCGGCTGCACCTGCGGCGTCTTGGCTTCCGGAATGGCAGTTCGATGT 845

>	PRIOR FILING DATE:	2000-11-17	
>	PRIOR APPLICATION NUMBER:	60/249,217	
>	PRIOR FILING DATE:	2000-11-17	
>	PRIOR APPLICATION NUMBER:	60/249,211	
>	PRIOR FILING DATE:	2000-11-17	
>	PRIOR APPLICATION NUMBER:	60/249,215	
>	PRIOR FILING DATE:	2000-11-17	
>	PRIOR APPLICATION NUMBER:	60/249,264	
>	PRIOR FILING DATE:	2000-11-17	
>	PRIOR APPLICATION NUMBER:	60/249,214	
>	PRIOR FILING DATE:	2000-11-17	
>	PRIOR APPLICATION NUMBER:	60/249,297	
>	PRIOR FILING DATE:	2000-11-17	
>	PRIOR APPLICATION NUMBER:	60/232,400	
>	PRIOR FILING DATE:	2000-09-14	
>	PRIOR APPLICATION NUMBER:	60/231,242	
>	PRIOR FILING DATE:	2000-09-08	
>	PRIOR APPLICATION NUMBER:	60/232,081	
>	PRIOR FILING DATE:	2000-09-08	
>	PRIOR APPLICATION NUMBER:	60/232,080	
>	PRIOR FILING DATE:	2000-09-08	
>	PRIOR APPLICATION NUMBER:	60/231,414	
>	PRIOR FILING DATE:	2000-09-08	
>	PRIOR APPLICATION NUMBER:	60/231,244	
>	PRIOR FILING DATE:	2000-09-08	
>	PRIOR APPLICATION NUMBER:	60/233,054	
>	PRIOR FILING DATE:	2000-09-14	
>	PRIOR APPLICATION NUMBER:	60/233,063	
>	PRIOR FILING DATE:	2000-09-14	
>	PRIOR APPLICATION NUMBER:	60/232,397	
>	PRIOR FILING DATE:	2000-09-14	
>	PRIOR APPLICATION NUMBER:	60/232,399	
>	PRIOR FILING DATE:	2000-09-14	
>	PRIOR APPLICATION NUMBER:	60/232,401	
>	PRIOR FILING DATE:	2000-09-14	
>	PRIOR APPLICATION NUMBER:	60/241,808	
>	PRIOR FILING DATE:	2000-10-20	
>	PRIOR APPLICATION NUMBER:	60/241,826	
>	PRIOR FILING DATE:	2000-10-20	
>	PRIOR APPLICATION NUMBER:	60/246,475	
>	PRIOR FILING DATE:	2000-11-08	
>	PRIOR APPLICATION NUMBER:	60/231,243	
>	PRIOR FILING DATE:	2000-09-08	
>	PRIOR APPLICATION NUMBER:	60/233,065	
>	PRIOR FILING DATE:	2000-09-14	

Query Match	Score 124.4;	DB 9;	Length 330;
6.98;			

Best Local Similarity 64.2%; Pred. No. 5.2e-24;

Matches 185; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 669 GCTGCCGGAGGCCCGGGCCGACCATGCCCTGTGTGGAGATGGGGGTAGACATGAT 728

Db 1 GCTGCCACTCTCACTGCCAGACCATGCCATCAACTGGCTGGCGATGGGGCCGTGGACATGTG 60

QY 729 TGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTAATGTGAACATGCGCGTGGCAT 788

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DD 61 CCRGGCCATCAGGAAAC TGCGGCAGCCACTGGCGTGGACATCAACATGCGTGTGGCGGT 120

789 CCACAGCGGGCGGTGCACCTGCGGGCTTGGCTTGGCAATGGCAGTTCGATGTGTG 848

100

Db 121 GCACTCAGGCAGCGTACTGTGTGGAGTCATCGGGCTGCAGAAGTGGCAGTACGACGTTTG 180

Qy 849 GTCCAATGATGTGACCTGGCCAACCAACATGGAAGCAGGAGCCGGCTGGCCGATCCA 908

[illegible]

DB 181 GTCACATGATGTCACACATGGCTAACCACATGGAGGCAGGCGGTGTACAGGGCGAGTGCA 240

ov 909 CATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGG 956

Db 241 CATCACAGGGCTACCCCTGGCCCTGCTGGCANGGGCTTATGCTGNGGA 288


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RESULT 14
US-09-764-869-445
; Sequence 445, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 445
; LENGTH: 330
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (272)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (285)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (289)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-869-445

Query Match          6.9%; Score 124.4; DB 10; Length 330;
Best Local Similarity 64.2%; Pred. No. 5.2e-24;
Matches 185; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 669 GCTGCCGGAGGCGCGGCGGACCATGCGCCACTGCTGTGTGGAGATGGGGGTAGACATGAT 728
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DB 1 GCTGCCACTCTCACTGCCAGACCATGCCATCAACTGCTGCGTCATGGCGCTGGACATGTG 60

QY 729 TGAGCCCATCTCGCTGTGTACGTGTGACAGGTGTGAATGTGAATGAAATGCGCGTGGCAT 788
      |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 61 CCKGCCATCAGGAACACTGCGGGGAGCCACTGGCGTGGACATCAACATGCGGTGGCGGT 120

QY 789 CCACAGCGGGCGCGTGCACTGCGGCGTCTTGGCTTGGCGAAATGGCAGTTGCGATGTGTG 848
      |||  ||  |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 121 GCACTCAGGCAGCGTACTGTGTGGAGTCACTCGGCGCTGCAGAAAGTGGCAGTACGACGTTTG 180

QY 849 GTCCAAATGATGTGACCTTGGCCCAACCATGGAAGCAGGAGCCGGGTGGCCGCATCCA 908
      |||  |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 181 CTCACATGATGTACACTGGCTAACCACATGGAGGAGCGGCGGTGTACCAGGCGAGTGCA 240

QY 909 CATCACTCGGGCAACACTGCACTGAAACGGGCACTACGAAGTGA 956
      |||||  |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 241 CATCACAGGGGCTACCCCTGGCCCTGCTGGCANGGGCTTATGCTGNNGA 288

RESULT 15
US-09-764-868-1351
; Sequence 1351, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1351
; LENGTH: 11881
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-764-868-1351

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Query Match          4.4%; Score 79.2; DB 9; Length 11881;
Best Local Similarity 63.4%; Pred. No. 4.8e-11;
Matches 137; Conservative 0; Mismatches 78; Indels 1; Gaps 1;

QY 746 TACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGCGGTGC 805
      |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 227 TCGCGGCAGCCCACTGCGCGTGGACATCAACATGCGTGTGGCGTGCACCTCAGGCAGCGTAC 286

QY 806 ACTGCGGCGTCTTGGCTTGGCGAAATGCCAGTTTCGATGTGTGGTCCCAATGATGTGACCC 865
      ||  ||  ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 287 TGTGTGGAGTCACTCGGGCTGCAGAAAGTGGCAGTACGACGTTTGGTCACATGATGTACAC 346

QY 866 TGGCCCAACCATGGAAGCAGGAGCCGGGCTGGCGC-CATCCACATCACTCGGGCAACA 924
      |||||  |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 347 TGGCTAACCATGAGGAGCGCGGTGTACCAAGGCTGAGACCTAGGGCCCTAGGCAGCTA 406

QY 925 CTGCACTACCTGAACGGGACTACGAAGTGGAGCCA 960
      |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 407 CAGCAGAAAGGCCAACCCAGGCCTFACCACAGGCTGCCA 442
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Job time : 127.15 secs

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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 22:19:04 ; Search time 3575.79 Seconds
(without alignments)
12740.746 Million cell updates/sec

Title: US-09-750-240-3
Perfect score: 1812
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 43: /cgn2_6/ptodata/1/pna/US102B_COMB.seq:*

- 44: /cgn2_6/ptodata/1/pna/US6000_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1812	100.0	1812	29	US-09-750-240-3	Sequence 3, Appli
3	1808.4	99.8	3549	18	US-09-472-667-5	Sequence 5, Appli
4	1808.4	99.8	3549	29	US-09-750-240-5	Sequence 5, Appli
5	1763.4	97.3	3552	18	US-09-472-667-10	Sequence 10, Appli
6	1763.4	97.3	3552	29	US-09-750-240-10	Sequence 10, Appli
7	1763	97.3	3356	68	US-60-245-228-549	Sequence 549, App
8	1763	97.3	3706	68	US-60-248-592-183	Sequence 183, App
9	1763	97.3	4942	42	US-10-201-000-1	Sequence 1, Appli
10	1657.8	91.5	3582	29	US-09-750-240-12	Sequence 12, Appli
11	1599.6	87.7	5353	18	US-09-491-404-837	Sequence 837, App
12	1599.6	87.7	5353	34	US-09-922-279-837	Sequence 837, App
13	1599.6	87.7	5353	34	US-09-922-279A-837	Sequence 837, App
14	1454.2	80.3	5826	80	US-60-360-207-5921	Sequence 5921, Ap
15	1437.2	79.3	4131	9	US-08-538-815-11	Sequence 11, Appli
16	895	49.4	4523	41	US-10-175-158-1	Sequence 1, Appli
17	886.6	48.9	3969	3	US-07-751-460-1	Sequence 1, Appli
18	886.6	48.9	4356	3	US-07-899-058-1	Sequence 1, Appli
19	886.2	47.4	3924	9	US-08-538-815-9	Sequence 9, Appli
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ALIGNMENTS

RESULT 1
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; Sequence 3, Application US/09472667
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. Kirk
; APPLICANT: Insel, Paul A.
; APPLICANT: Ping, Peipei
; APPLICANT: Post, Steven R.
; APPLICANT: Gao, Melhua
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056722
; CURRENT APPLICATION NUMBER: US/09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: PCT/US99/02702
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 09/021,773
; PRIOR FILING DATE: 1998-02-11
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: PCT/US97/15610
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/058,209
; PRIOR FILING DATE: 1996-09-05
; PRIOR APPLICATION NUMBER: PCT/US96/02631
; PRIOR FILING DATE: 1996-02-27
; PRIOR APPLICATION NUMBER: US 08/396,207
; PRIOR FILING DATE: 1995-02-28
; PRIOR APPLICATION NUMBER: US 08/485,472
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-472-667-3

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Best Local Similarity 100.0%; Pred. No. 0;
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; Sequence 5, Application US/09750240
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750.240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-240-5

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Db 756 CCTCCCCATCCGATGCGGGCTGCGCTCTCAGCGCCCTGCGCCCTTCCACCTTGCATTT 815

QY 183 GATCTTGGCGCTGCAACTTAACCGTGGTGATGCTTCCCTCGAAGCAGCTCGTGCCAA 242
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DB 1236 GCTGGCTGCGGAGAACTACCTGCTGAGGATCAAGATCTTGGGGACTGTTACTACTGTG 1295
QY 663 GTCAGGGCTGCCGAGGCGCGCGCCAGCACATGCCCCACTGCTGTGTGAGATGGGGTAGA 722
DB 1296 GTCAGGGCTGCCGAGGCGCGCGCCAGCACATGCCCCACTGCTGTGTGAGATGGGGTAGA 1355
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QY 1203 CACCCAGATGCCCTGAACCCCTGAGGATGAGTGTGATGCTTCCAGCGCTGCCATCGA 1262
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RESULT 5

US-09-472-667-10

; Sequence 10, Application US/09472667

; GENERAL INFORMATION:

; APPLICANT: Hammond, H. Kirk

; APPLICANT: Insel, Paul A.

; APPLICANT: Ping, Peipei

; APPLICANT: Post, Steven R.

; APPLICANT: Gao, Melhua

; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART

; FILE REFERENCE: 22002056722

; CURRENT APPLICATION NUMBER: US/09/472, 667

; PRIOR FILING DATE: 1999-12-27

; PRIOR APPLICATION NUMBER: PCT/US99/02702

; PRIOR FILING DATE: 1999-02-09

; PRIOR APPLICATION NUMBER: US 09/008,097

; PRIOR FILING DATE: 1998-01-16

; PRIOR APPLICATION NUMBER: US 09/021,773

; PRIOR FILING DATE: 1998-02-11

; PRIOR APPLICATION NUMBER: US 08/924,757

; PRIOR FILING DATE: 1997-09-05

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; PRIOR FILING DATE: 1997-09-05

; PRIOR APPLICATION NUMBER: US 08/708,661

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; PRIOR APPLICATION NUMBER: US 60/048,933

; PRIOR FILING DATE: 1997-06-16

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; PRIOR FILING DATE: 1996-02-27

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; PRIOR APPLICATION NUMBER: US 08/485,472
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 11
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; ORGANISM: Homo sapiens
US-09-472-667-10

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Query Match 97.3%; Score 1763.4; DB 18; Length 3552;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 21; Indels 3; Gaps 1;

Qy	3	TACGCTGTGCTGGGCATCCTGGCGCAGTGCAGTCCGGGGCGCTTTGCGAGCAGACCC	62
Db	636	TTACGTGTGCTGGGCATCCTGGCGCAGTGCAGTCCGGGGCGCTCTGCGACGACACCC	695
Qy	63	GCSCAGCCCTCTGGGGCTCTGCTGGCCCTGTGTCTTTGTATACATCGCATACACGCT	122
Db	696	GCACAGCCCTCTGGGGCTCTGCTGGCCCTGTGTCTTTGTATACATCGCTACACGCT	755
Qy	123	CCTCCCATCCGATCGGGCTGCGGCTCCTCAGCGGCTGGGCTCTCCACCTTGCATTT	182
Db	756	CCTCCCATCCGATCGGGCTGCGGCTCCTCAGCGGCTGGGCTCTCCACCTTGCATTT	815
Qy	183	GATCTTGGCTGGCAACTTAAACGCTGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCCAA	242
Db	816	GATCTTGGCTGGCAACTTAAACGCTGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCCAA	875
Qy	243	TGTGCTGCTGTCTCTGCAACAGCTCATTAGCATCTGCACACACTATCCAGCAGAGGT	302
Db	876	TGTGCTGCTGTCTCTGCAACAGCTCATTAGCATCTGCACACACTATCCAGCAGAGGT	935
Qy	303	GTCTCAGCCGAGGCTTTTCAGGAGACCCGCAAGTTACATCCAGGCCCGGCTCCACCTGCA	362
Db	936	GTCTCAGCCGAGGCTTTTCAGGAGACCCGCGGTTACATCCAGGCCCGGCTCCACCTGCA	995
Qy	363	GCATGAAATCGCAGCAGAGCGGCTGCTGCTGCGTATTGCCCAGCAGCTTGGCAT	422
Db	996	GCATGAAATCGCAGCAGAGCGGCTGCTGCTGCGTATTGCCCAGCAGCTTGGCAT	1055
Qy	423	GGAGTGAAGAGACATCAACACAAAAAGAAC --- ATGTTCCACAGATCTACAT	479
Db	1056	GGAGTGAAGAGACATCAACACAAAAAGAACATGTTCCACAGATCTACAT	1115
Qy	480	ACAGAGCATGACAATGTCAAGATCTGTTTTCAGACATTTAGGGCTTCCACAGCCTGGC	539
Db	1116	ACAGAGCATGACAATGTCAAGATCTGTTTTCAGACATTTAGGGCTTCCACAGCCTGGC	1175
Qy	540	ATCCAGTGCATCGCAGAGCTGTCTATGACCTGAATGAGCTTTTGGCCGGTTTGA	599
Db	1176	ATCCAGTGCATCGCAGAGCTGTCTATGACCTGAATGAGCTTTTGGCCGGTTTGA	1235
Qy	600	CAAGCTGGCTCGGAGAATCACTGCTGAGGATCAAGATCTTGGGGACTCTTACTACTG	659
Db	1236	CAAGCTGGCTCGGAGAATCACTGCTGAGGATCAAGATCTTGGGGACTCTTACTACTG	1295
Qy	660	TGTGTAGGGCTCGCGAGGCCGGCCGACCATGCCACTGCTGTGTGGAGATGGGGT	719
Db	1296	TGTGTAGGGCTCGCGAGGCCGGCCGACCATGCCACTGCTGTGTGGAGATGGGGT	1355
Qy	720	AGACATGATTGAGCCATCTCGCTGTGTGCTGAGTGACAGTGTGAATGTGAACATCG	779
Db	1356	AGACATGATTGAGCCATCTCGCTGTGTGCTGAGTGACAGTGTGAATGTGAACATCG	1415
Qy	780	CGTGGGCATCCACAGGGGCGGTGCATCTGCGGCGCTCTTGGCTTGCAGAAATGGCAGTT	839
Db	1416	CGTGGGCATCCACAGGGGCGGTGCATCTGCGGCGCTCTTGGCTTGCAGAAATGGCAGTT	1475
Qy	840	CGATGTGTGTCAAATGATGTACCTTGACCTTGCCCAACCAATGTGAAGCAGGAACCGGCTGG	899

RESULT 6
US-09-750-240-10
; Sequence 10, Application US/09750240
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.

```
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 3552
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-750-240-10

Query Match      97.3%; Score 1763.4; DB 29; Length 3552;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 21; Indels 3; Gaps 1;

QY   3  TACGTGGTCTGGGCATCTCGGGAGTGCAGGTGCGGGGGCGCTTCCAGCAGACCC 62
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
636  TTACGTGGTCTGGGCATCTCGGGAGTGCAGGTGCGGGGGCGCTTCCAGCAGACCC 695
QY   63  GCCAGCCCTCTGCGGGCTCTGGTCCCTGTGCTTGTATACATCGCATACAGCT 122
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
696  GCCAGCCCTCTGCGGGCTCTGGTCCCTGTGCTTGTATACATCGCATACAGCT 755
QY   123  CTTCCCATCCGATCGGGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 182
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
756  CTTCCCATCCGATCGGGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 815
QY   183  GATCTTGGCTGCACTTAACCGTGGTATGCTTCTGCTGCTGCTGCTGCTGCTGCTG 242
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
816  GATCTTGGCTGCACTTAACCGTGGTATGCTTCTGCTGCTGCTGCTGCTGCTGCTG 875
QY   243  TGTGCTGCTTCTCTGCAACCAAGTCAATTAGCATCTGCACACATATCCAGCAGAGT 302
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
876  TGTGCTGCTTCTCTGCAACCAAGTCAATTAGCATCTGCACACATATCCAGCAGAGT 935
QY   303  GTCTCAGCGCCAGGCTTTTCAGGAGACCGCAGTTACATCCAGGCCGGCTCCACCTGCA 362
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
936  GTCTCAGCGCCAGGCTTTTCAGGAGACCGCAGTTACATCCAGGCCGGCTCCACCTGCA 995
QY   363  GCATGAGATCGCAGCAGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 422
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
996  GCATGAGATCGCAGCAGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1055
QY   423  GGAGATGAAGAAGACATCAACCAAAAAAAGAGAC - - - ATGTTCCACAAGATCTACAT 479
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1056  GGAGATGAAGAAGACATCAACCAAAAAAAGAGACATGATCTCCACAAGATCTACAT 1115
QY   480  ACAGAGATGACAATGTACAGATCTCTGTTGTTGAGACATTTGAGGGCTTACCAGCCTGGC 539
Db-  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1116  ACAGAGATGACAATGTACAGATCTCTGTTTGCAGACATTTGAGGGCTTACCAGCCTGGC 1175
QY   540  ATCCAGTGCACGTCGAGAGCTGCTGATGACCTGAAAGCTTCTTCCCGGCTTGA 599
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1176  ATCCAGTGCACGTCGAGAGCTGCTGATGACCTGAAAGCTTCTTCCCGGCTTGA 1235
QY   600  CAAGCTGGCTGCGGAGAATCACTGCTGAGGATCAAGATCTTGGGGGACTGTTTACTACTG 659
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1236  CAAGCTGGCTGCGGAGAATCACTGCTGAGGATCAAGATCTTGGGGGACTGTTTACTACTG 1295
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QY   660  TGTGTTCAGGCTGCGGAGGCCCGGCGGACCATGCCCATCTGCTGTGTGGAGATGGGGT 719
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1296  TGTGTTCAGGCTGCGGAGGCCCGGCGGACCATGCCCATCTGCTGTGTGGAGATGGGGT 1355
QY   720  AGACATGATTGAGGCCATCTCGTGTGTACGTGAGGTGACAGGTGTGAATGTGAACATGCG 779
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1356  AGACATGATTGAGGCCATCTCGTGTGTACGTGAGGTGACAGGTGTGAATGTGAACATGCG 1415
QY   780  CGTGGGCATCCAGAGCGGGCGGTGACCTGCGGGGCTCTTGGCTTGGGAAATGGCAGTT 839
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1416  CGTGGGCATCCAGAGCGGGCGGTGACCTGCGGGCTCTTGGCTTGGGAAATGGCAGTT 1475
QY   840  CGATGTGTGTCCTCAATGATGTGACCTTGGCAACACCATGGAAGCAGAGAGCCGGGCTGG 899
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1476  CGATGTGTGTCCTCAATGATGTGACCTTGGCAACACCATGGAAGCAGAGAGCCGGGCTGG 1535
QY   900  CCGCATCCACATCACTCGGGCAACACTGCACTACCTGAAGCGGAGCTACGAAGTGGAGCC 959
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1536  CCGCATCCACATCACTCGGGCAACACTGCACTACCTGAAGCGGAGCTACGAAGTGGAGCC 1595
QY   960  AGCCCGTGTGGCAAGCGCAACCGTACCTCAAGGAGCAGACATTCAGACTTTCCTCAT 1019
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1596  AGCCCGTGTGGCGGCGCGGTGACCTCAAGGAGCAGACATTCAGACTTTCCTCAT 1655
QY   1020  CTTGGGCGCGCAGCCAGAAACGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1079
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1656  CTTGGGCGCGCAGCCAGAAACGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1715
QY   1080  TCGGGCCAACTCCTCGAAGGGCTGATGCGCGCATGGTTCCTGATGCTGCTGCTGCTGCT 1139
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1716  TCGGGCCAACTCCTCGAAGGGCTGATGCGCGCATGGTTCCTGATGCTGCTGCTGCTGCT 1775
QY   1140  GACCAAGGAGCTCAAGGCCCTTCGCCAGATGGGCACTTATGATTCAGCAGCAACACACCG 1199
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1776  GACCAAGGAGCTCAAGGCCCTTCGCCAGATGGGCACTTATGATTCAGCAGCAACACACCG 1835
QY   1200  GGGCACCCAAAGATGCCCTGAAACCTGAGGATGAGGTGGATGAGTTCTGAGCCGTGCCAT 1259
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1836  GGGCACCCAAAGATGCCCTGAAACCTGAGGATGAGGTGGATGAGTTCTGAGCCGTGCCAT 1895
QY   1260  CGATGCCCGCAGCATTTGATCAGCTGCGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1319
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1896  CGATGCCCGCAGCATTTGATCAGCTGCGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1955
QY   1320  CCAGAGAGGAGGATTTTGAAGAAGTACTCCCGAAGGTGGATCCCGCTTCGGAGGCTA 1379
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1956  CCAGAGAGGAGGATTTGAGAGAAGTACTCCCGAAGGTGGATCCCGCTTCGGAGGCTA 2015
QY   1380  CGTTGGCTGTGCGCTGTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 1439
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2016  CGTTGGCTGTGCGCTGTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 2075
QY   1440  ACATCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCT 1499
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2076  ACATCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCT 2135
QY   1500  GCTGATCTGCTGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 1559
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2136  GCTGATCTGCTGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 2195
QY   1560  CCGCAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1619
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2196  CCGCAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2255
QY   1620  TGTGTTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1679
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2256  TGTGTTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2315
QY   1680  TGCAGCCCGGATGCTGAAATTAACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1739
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2316  TGCAGCCCGGATGCTGAAATTAACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2375
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QY 1740 CAATTACTCTGGGCTGGATGCTCCCTGTGTGGGCGACCATGCCACCTGCAGCTT 1799
Db 2376 CAATTACTCTGGGCTGGATGCTCCCTGTGTGGGCGACCATGCCACCTGCAGCTT 2435
QY 1800 TCCTGAGTGTC 1812
Db 2436 TCCTGAGTACTTC 2448
RESULT 7
US-60-245-228-549
; Sequence 549, Application US/60245228
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000878
; CURRENT APPLICATION NUMBER: US/60/245,228
; CURRENT FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 630
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 549
; LENGTH: 3356
; TYPE: DNA
; ORGANISM: HUMAN
US-60-245-228-549
Query Match 97.3%; Score 1763; DB 68; Length 3356;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 20; Indels 3; Gaps 1;
QY 5 AGCTGGTGTCTGGGCTCTCTGGGCGAGTGCAGGTGGGGGCGCTTTTCGAGCAGACCCGC 64
Db 421 AGCTGGTGTGGGCTCTCTGGGCGAGTGCAGGTGGGGGCGCTCTCGCAGCAGACCCGC 480
QY 65 GCAGCCCTCTGGGCGCTCTGGTGCCTGTCTTTGTATATACATACAGCTGCC 124
Db 481 GCAGCCCTCTGGGCGCTCTGGTGCCTGTCTTTGTATACATCGCTACAGCTCC 540
QY 125 TCCCATCCGATCGGCGTCCGCTCAGCGGCTGGGCTCTCCACCTTGCATTGA 184
Db 541 TCCCATCCGATCGGCGTCCGCTCAGCGGCTGGGCTCTCCACCTTGCATTGA 600
QY 185 TCTTGGCTTGGCACTTAACCGTGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATG 244
Db 601 TCTTGGCTTGGCACTTAACCGTGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATG 660
QY 245 TGCTGCTGTCTGACCAACGCTATTAGCATCTGCACACATATCCAGCAGAGGTGT 304
Db 661 TGCTGCTGTCTGACCAACGCTATTGGCATCTGCACACATATCCAGCAGAGGTGT 720
QY 305 CTCAGCGCAGGCTTTCAGGAGACCCGAGTTACATCCAGCCCGGCTCCACCTGCAGC 364
Db 721 CTCAGCGCAGGCTTTCAGGAGACCCGAGTTACATCCAGCCCGGCTCCACCTGCAGC 780
QY 365 ATGAGAATCGGAGCAGGCGGCTGCTGCTCGGTATTGCCCGCAGACGTTGGCATGG 424
Db 781 ATGAGAATCGGAGCAGGCGGCTGCTGCTCGGTATTGCCCGCAGACGTTGGCATGG 840
QY 425 AGATGAAAGAAGACATCAACAAAAAAGAGAC- - - ATGTTCCAAAGATCTACATAC 481
Db 841 AGATGAAAGAAGACATCAACAAAAAAGAGACATGATGTTCCACAAAGATCTACATAC 900
QY 482 AGAAGCATGACAATGTCAGCATCTCTGTTGACAGATTGAGGGCTTCCAGCCCTGGCAT 541
Db 901 AGAAGCATGACAATGTCAGCATCTCTGTTGACAGATTGAGGGCTTCCAGCCCTGGCAT 960
QY 542 CCCAGTGCACTCGCAGGAGCTGGTCATGCCCTCAATCAGCTCTTTCGCCGTTTGACA 601
Db 961 CCCAGTGCACTCGCAGGAGCTGGTCATGCCCTCAATCAGCTCTTTCGCCGTTTGACA 1020
QY 602 AGCTGGCTCGGAGAATCACTGCCTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTG 661

Db 1021 AGCTGGCTCGGAGAATCACTGCCTGAGGATCAAGATCTTGGGACATGTTACTACTGTG 1080
QY 662 TGTACAGGCTGCCGAGGCGCGGCGGACCATGCCACCTGCTGTGTGAGATGGGGTAG 721
Db 1081 TGTACAGGCTGCCGAGGCGCGGCGGACCATGCCACCTGCTGTGTGAGATGGGGTAG 1140
QY 722 ACATGATTGAGGCCATCTCGTGTGTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCG 781
Db 1141 ACATGATTGAGGCCATCTCGTGTGTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCG 1200
QY 782 TGGGCATCCACAGCGGCGCGTGCACCTGCGGCGTCTTGGTTCGGGAAATGGCAGTTCG 841
Db 1201 TGGGCATCCACAGCGGCGCGTGCACCTGCGGCGTCTTGGTTCGGGAAATGGCAGTTCG 1260
QY 842 ATGTGTGTCCAATGATGACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 901
Db 1261 ATGTGTGTCCAATGATGACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1320
QY 902 GCATCCACATCACTCGGCGCACACTGCAGTACCTGAACGGGCGGCGGCGGCGGCGGCGGCGG 961
Db 1321 GCATCCACATCACTCGGCGCACACTGCAGTACCTGAACGGGCGGCGGCGGCGGCGGCGGCGG 1380
QY 962 GCCGTGTGGCAAGCGCAACCGGTACCTCAAGGAGCAGACATTCAGACTTTCTCTCATCC 1021
Db 1381 GCCGTGTGGCAAGCGCAACCGGTACCTCAAGGAGCAGACATTCAGACTTTCTCTCATCC 1440
QY 1022 TGGGCGCGCAGCAGAAAGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1081
Db 1441 TGGGCGCGCAGCAGAAAGGAGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1500
QY 1082 GGGCAACTCCATGGAAGGCGTGTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1141
Db 1501 GGGCAACTCCATGGAAGGCGTGTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1560
QY 1142 CCAAGGACTCCAAGGCGTTCGCCAGATGGGCGATTTGATGATTTCCAGCAAGAACACCGGG 1201
Db 1561 CCAAGGACTCCAAGGCGTTCGCCAGATGGGCGATTTGATGATTTCCAGCAAGAACACCGGG 1620
QY 1202 GCACCAAGATGCCCTGAACCGTGAAGGATGAGGTGAGTTCCTGAGCCGTGCCATCG 1261
Db 1621 GCACCAAGATGCCCTGAACCGTGAAGGATGAGGTGAGTTCCTGAGCCGTGCCATCG 1680
QY 1262 ATGCCCGCAGCATTTGATCAGCTGCGGAAGGACCATGTGCGCGGCGGCGGCGGCGGCGGCGGCGG 1321
Db 1681 ATGCCCGCAGCATTTGATCAGCTGCGGAAGGACCATGTGCGCGGCGGCGGCGGCGGCGGCGGCGG 1740
QY 1322 AGAGAGAGATTTTGAAGAAGTACTCCCGGAAGGTGATCCCGCTTCGGAGCGCTAGG 1381
Db 1741 AGAGAGAGATTTTGAAGAAGTACTCCCGGAAGGTGATCCCGCTTCGGAGCGCTAGG 1800
QY 1382 TTGCGCTGTGCCCTGTGGTCTTCTGCTCATCTGCTTCCAGCTTCTAATTTTCCAC 1441
Db 1801 TTGCGCTGTGCCCTGTGGTCTTCTGCTCATCTGCTTCCAGCTTCTAATTTTCCAC 1860
QY 1442 ACTCCACCTGTGCTTGGGATTTATGCCAGCATCTTCTGCTGTGCTGCTAATCACCGTGC 1501
Db 1861 ACTCCACCTGTGCTTGGGATTTATGCCAGCATCTTCTGCTGTGCTGCTAATCACCGTGC 1920
QY 1502 TGATCTGTGCTGTACTCTCTGTGTCTTCCCTAAGGCCCTGCAACGCTGTCTGCC 1561
Db 1921 TGATCTGTGCTGTACTCTCTGTGTCTTCCCTAAGGCCCTGCAACGCTGTCTGCC 1980
QY 1562 GCAGCATTTGCCCTCACGGGCACATAGCACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1621
Db 1981 GCAGCATTTGCCCTCACGGGCACATAGCACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2040
QY 1622 TGTACTTCTGCCATTTGCCAATGTTTCACTGTAACCCACACACACACACACACACACACACACAC 1681
Db 2041 TGTACTTCTGCCATTTGCCAATGTTTCACTGTAACCCACACACACACACACACACACACACAC 2100
QY 1682 CAGCCCGGATGCTGAATTTAACAACCTGTGATCACTGCTGCCCTGCCACCTGCGAGCAGCTCA 1741

Db	2101	CAGCCCGAGTCGTAATTAACACCTGTCGACATCACTGCGCTGCCACCTGCAGCAGCTCA	2160
Qy	1742	ATTACTCTCTGGCGCTGGATGCTCCCTCTGTGTGAGGGACACATGCGCCACCTGCAGCTTTC	1801
Db	2161	ATTACTCTCTGGCGCTGGATGCTCCCTCTGTGTGAGGGACCATGCGCCACCTGCAGCTTTC	2220
Qy	1802	CTGAGGTGTTC	1812
Db	2221	CTGAGTACTTC	2231

```

RESULT 8
US-60-248-592-183
; Sequence 183, Application US/60248592
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000961
; CURRENT APPLICATION NUMBER: US/60/248,592
; CURRENT FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 3706
; TYPE: DNA
; ORGANISM: HUMAN
US-60-248-592-183

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Query Match	97.3%	Score 1763;	DB 68;	Length 3706;
Best Local Similarity	98.7%;	Pred. No. 0;		
Matches 1788;	Conservative 0;	Mismatches 20;	Indels 3;	Gaps 1;
Qy	5	ACGTGGTCTCGGCATCTCGCGGCAGTGCAGTCTGGGGCGCTTTCCACGACGACCCGC	64	
Db	771	ACGTGGTCTCGGCATCTCGCGGCAGTGCAGTCTGGGGCGCTCTCCACGACGACCCGC	830	
Qy	65	GCAGCCCTCTGCGGGCTCTGGTGCCTGTGTTCTTTGTATACATCGCATACAGCTCC	124	
Db	831	GCAGCCCTCTGCGGGCTCTGGTGCCTGTGTTCTTTGTCTACATCCCTACAGCTCC	890	
Qy	125	TCCCATCCGATCGGGCTCGGTCCTCAGCGGCTGGGCTCTCCACCTTGCAATTGA	184	
Db	891	TCCCATCCGATCGGGCTCGGTCCTCAGCGGCTGGGCTCTCCACCTTGCAATTGA	950	
Qy	185	TC TTGGCTGGCAACTTAACCGTGGTATGCTTCCTCTGGAAGCAGCTCGTGCCAAATG	244	
Db	951	TC TTGGCTGGCAACTTAACCGTGGTATGCTTCCTCTGGAAGCAGCTCGTGCCAAATG	1010	
Qy	245	TGCTGCTGTTCTCTGCAACCAAGTCATTAGCATCTGCACACATATCCACGACAGGTTG	304	
Db	1011	TGCTGCTGTTCTCTGCAACCAAGTCATTTGGCATCTGCACACATATCCACGACAGGTTG	1070	
Qy	305	CTCAGCGCAGCGCTTTACAGGAGACCCGCACTACATCAGCGCGGCTCCACCTGACAGC	364	
Db	1071	CTCAGCGCAGCGCTTTACAGGAGACCCGCGTTACATCAGCGCGGCTCCACCTGACAGC	1130	
Qy	365	ATGAAATCGCAGCAGGAGCGGTGCTGCTCGGTTATGCCCGACAGCTTGCCATGG	424	
Db	1131	ATGAAATCGCAGCAGGAGCGGTGCTGCTCGGTTATGCCCGACAGCTTGCCATGG	1190	
Qy	425	AGATGAAGAAGACATCAACAAAAAAGAGAC ---ATGTTCCCAAGATCTACATAC	481	
Db	1191	AGATGAAGAAGACATCAACAAAAAAGAGACATGATGTTCCCAAGATCTACATAC	1250	
Qy	482	AGAAGCATGACAATGTCAGCATCTGTTTTCAGACATTTAGGGGCTTACCAGCGCTGGCAT	541	
Db	1251	AGAAGCATGACAATGTCAGCATCTGTTTTCAGACATTTAGGGGCTTACCAGCGCTGGCAT	1310	
Qy	542	CCCAGTGCATTCGCGAGGAGCTGGTCAATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACA	601	
Db	1311	CCCAGTGCATTCGCGAGGAGCTGGTCAATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACA	1370	

Qy	602	AGCTGGCTGGGGAAATCACTGCTCAGGATCAAGATCTTGGGGACTGTTACTACTGTG	661
Db	1371	AGCTGGCTGGGGAAATCACTGCTCAGGATCAAGATCTTGGGGACTGTTACTACTGTG	1430
Qy	662	TGTCAGGGCTGCCGGAGGCCCGCCGACACATCCGCCACTGCTGTGGAGATGGGGGTAG	721
Db	1431	TGTCAGGGCTGCCGGAGGCCCGCCGACACATCCGCCACTGCTGTGGAGATGGGGGTAG	1490
Qy	722	ACATGATTGAGGCCATCTCGCTGGTACGTGAGTGACAGGTGTAATGTGAACATGCGCG	781
Db	1491	ACATGATTGAGGCCATCTCGCTGGTACGTGAGTGACAGGTGTAATGTGAACATGCGCG	1550
Qy	782	TGGGCATCCACAGGGGCGGTGCACCTGGGGCGTCTTGGCTTGGCGAAATGGCAGTTCC	841
Db	1551	TGGGCATCCACAGGGGCGGTGCACCTGGGGCGTCTTGGCTTGGCGAAATGGCAGTTCC	1610
Qy	842	ATGTGTGGTCCATGATGTGACCTTGGCCAAACACATGGAAGCAGGAAGCCGGGCTGCC	901
Db	1611	ATGTGTGGTCCATGATGTGACCTTGGCCAAACACATGGAAGCAGGAAGCCGGGCTGCC	1670
Qy	902	GCATCCACATCACTCGGGCAACACTGCAGTACTGTGAACGGGACTACGAAGTGGAGCCAG	961
Db	1671	GCATCCACATCACTCGGGCAACACTGCAGTACTGTGAACGGGACTACGAAGTGGAGCCAG	1730
Qy	962	GCCGTGTTGCAAGCGCAACGCGTACTCAAGGAGCAGCACATTCAGACTTTTCCTCATCC	1021
Db	1731	GCCGTGTTGCGGAGCGCAACGCGTACTCAAGGAGCAGCACATTCAGACTTTTCCTCATCC	1790
Qy	1022	TGGCGCCAGCCAGAAACGAGAGAGGAAAGGCAATGCTGGCCAAGCTGCAGCGGACTC	1081
Db	1791	TGGCGCCAGCCAGAAACGAGAGAGGAAAGGCAATGCTGGCCAAGCTGCAGCGGACTC	1850
Qy	1082	GGGCCAACTCCATGGAGGGCTGATCGCGGATGGGTCTCTGATCGCTCTTCCCGGA	1141
Db	1851	GGGCCAACTCCATGGAGGGCTGATCGCGGATGGGTCTCTGATCGCTCTTCCCGGA	1910
Qy	1142	CCAAGGACTCCAAGGCTTCCGCCAGATGGGCATTGATGATTTCCAGCAAGACAAACCGG	1201
Db	1911	CCAAGGACTCCAAGGCTTCCGCCAGATGGGCATTGATGATTTCCAGCAAGACAAACCGG	1970
Qy	1202	GCACCAAGATGCCCTGAACCCCTGAGGATGAGTGGATGATCTCTGAGCGGTGCCATCG	1261
Db	1971	GCACCAAGATGCCCTGAACCCCTGAGGATGAGTGGATGATCTCTGAGCGGTGCCATCG	2030
Qy	1262	ATGCCCGCAGCATTGATCAGCTCGGAAGAGACATGTGCGCGGTTTTTGTCTCACCCTCC	1321
Db	2031	ATGCCCGCAGCATTGATCAGCTCGGAAGAGACATGTGCGCGGTTTTTGTCTCACCCTCC	2090
Qy	1322	AGACAGAGGATTTTGAGAGAAGTACTCCGGAAGGTGGATCCCGCTTCGGAGGCTTACG	1381
Db	2091	AGACAGAGGATTTTGAGAGAAGTACTCCGGAAGGTGGATCCCGCTTCGGAGGCTTACG	2150
Qy	1382	TTGCTGTGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTTAATTTTCCAC	1441
Db	2151	TTGCTGTGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTTCATCTTCCAC	2210
Qy	1442	ACTCCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTTAATCAACCGTGC	1501
Db	2211	ACTCCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTTAATCAACCGTGC	2270
Qy	1502	TGATCTGTGCTGTACTCTCTGTGGTCTCTGTTCCCTAAGGCCCTGCAAGCTCTGTCCC	1561
Db	2271	TGATCTGTGCTGTACTCTCTGTGGTCTCTGTTCCCTAAGGCCCTGCAAGCTCTGTCCC	2330
Qy	1562	GCACGATTTGCCGTCAACGGGACATAGCAGCGAGTTGGCATCTTTTCCGTCTGCTTGC	1621
Db	2331	GCACGATTTGCCGTCAACGGGACATAGCAGCGAGTTGGCATCTTTTCCGTCTGCTTGC	2390
Qy	1622	TGTTTACTTCTGCGATTTGCCAATGTTTCACTGTAAACACACCCCATACGGAGCTGTG	1681
Db	2391	TGTTTACTTCTGCGATTTGCCAATGTTTCACTGTAAACACACCCCATACGGAGCTGTG	2450

Qy 1682 CAGCCCGGATGCTGAATTAACACCTGCTGACATCACTGCTGCCACCTGCGACGAGCTCA 1741
Db 2451 CAGCCCGGATGCTGAATTAACACCTGCTGACATCACTGCTGCCACCTGCGACGAGCTCA 2510
Qy 1742 ATTACTCTCTGGGCTGGATGCTCCCTGCTGTGTGAGGCGCACCATGCCACCTGCGAGCTTTC 1801
Db 2511 ATTACTCTCTGGGCTGGATGCTCCCTGCTGTGTGAGGCGCACCATGCCACCTGCGAGCTTTC 2570
Qy 1802 CTGAGGCTGTTT 1812
Db 2571 CTGAGTACTTC 2581

RESULT 9
US-10-201-000-1
; Sequence 1, Application US/10201000
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/10/201,000
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US/09/474,076
; PRIOR FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-10-201-000-1

Query Match 97.3%; Score 1763; DB 42; Length 4942;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 20; Indels 3; Gaps 1;
Qy 5 ACGTGGTCTGGGATCTCTGGGCGAGTGCAGGTGCGGGGGCGCTTCGCAGCAGACCGCG 64
Db 782 ACGTGGTCTGGGATCTCTGGGCGAGTGCAGGTGCGGGGGCGCTTCGCAGCAGACCGCG 841
Qy 65 GCAGCCCTCTGCGGGCTCTGGTGCCTGTGTTTGTATACATCGCATACAGCTCC 124
Db 842 GCAGCCCTCTGCGGGCTCTGGTGCCTGTGTTTGTATACATCGCATACAGCTCC 901
Qy 125 TCCCATCCGATCGGGCTCCGCTGCTCAGCGGCTGGGCTCTCCACCTTGCAATTGA 184
Db 902 TCCCATCCGATCGGGCTCCGCTGCTCAGCGGCTGGGCTCTCCACCTTGCAATTGA 961
Qy 185 TCTTGGCTCGCACTTAACCGTGGTGTGCTTCTCTGGAAGCAGCTCGGTGCCAATG 244
Db 962 TCTTGGCTCGCACTTAACCGTGGTGTGCTTCTCTGGAAGCAGCTCGGTGCCAATG 1021
Qy 245 TGCTGCTCTCTGTCACCAACGTCATTAGCATCTGCACACATATCCAGCAGAGTGT 304
Db 1022 TGCTGCTCTCTGTCACCAACGTCATTAGCATCTGCACACATATCCAGCAGAGTGT 1081
Qy 305 CTCAGCGCAGGCTTTTCAGGAGACCCGCGAGTTACATCCAGCGCGGCTCCACCTGCGAGC 364
Db 1082 CTCAGCGCAGGCTTTTCAGGAGACCCGCGAGTTACATCCAGCGCGGCTCCACCTGCGAGC 1141
Qy 365 ATGAGAAATCGGACGAGGCGGTGCTGCTGCGGTATGCCCCAGCAGCTTGCCATGG 424

Db 1142 ATGAGAATCGCAGCAGGAGCGGCTGCTGCTGCTATTTCCCGCAGCACGTTGCCATGG 1201
Qy 425 AGATGAAGAAGACATCAACACAAAAAAGAGAC-- --ATGTTCCACAAAGATCTACATAC 481
Db 1202 AGATGAAGAAGACATCAACACAAAAAAGAGACATGTTTCCACAAAGATCTACATAC 1261
Qy 482 AGAAGCATGACAATGTGAGCATCTCTGTTTGCAGACATTTGAGGGCTTCCACCGCTGGCAT 541
Db 1262 AGAAGCATGACAATGTGAGCATCTCTGTTTGCAGACATTTGAGGGCTTCCACCGCTGGCAT 1321
Qy 542 CCCAGTGCAGTGCAGGAGCTGCTGATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACA 601
Db 1322 CCCAGTGCAGTGCAGGAGCTGCTGATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACA 1381
Qy 602 AGCTGGCTGCGGAGAACTCAAGATCGAGGATCAAGATCTTGGGGACTGTTTACTACTGTG 661
Db 1382 AGCTGGCTGCGGAGAACTCAAGATCGAGGATCAAGATCTTGGGGACTGTTTACTACTGTG 1441
Qy 662 TGTGAGGCTGCCGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 721
Db 1442 TGTGAGGCTGCCGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1501
Qy 722 ACATGATTTGAGGCGCATCTCGCTGCTGAGGTGACAGGTGATGATGTGAACATGCGCG 781
Db 1502 ACATGATTTGAGGCGCATCTCGCTGCTGAGGTGACAGGTGATGATGTGAACATGCGCG 1561
Qy 782 TGGCATCCACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 841
Db 1562 TGGCATCCACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1621
Qy 842 ATGTGTGCTCAATGATGTGACCCCTGGCCAAACCATGGAAGCAGGAGCGGCGGCGGCGGCG 901
Db 1622 ATGTGTGCTCAATGATGTGACCCCTGGCCAAACCATGGAAGCAGGAGCGGCGGCGGCGG 1681
Qy 902 GCATCCACATCACTCGGCGCAACACTGCACTGAGGTGACAGGTGATGATGTGAACATGCGCG 961
Db 1682 GCATCCACATCACTCGGCGCAACACTGCACTGAGGTGACAGGTGATGATGTGAACATGCGCG 1741
Qy 962 GCGGTGCTGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1021
Db 1742 GCGGTGCTGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1801
Qy 1022 TGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1081
Db 1802 TGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1861
Qy 1082 GGGCCAACTCCATGGAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1141
Db 1862 GGGCCAACTCCATGGAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1921
Qy 1142 CCAAGGACTCCAAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1201
Db 1922 CCAAGGACTCCAAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1981
Qy 1202 GCACCCAAAGTGCCTGAAACCTGAGGATGAGGTGAGTTCCTGAGCGCGTGCATCG 1261
Db 1982 GCACCCAAAGTGCCTGAAACCTGAGGATGAGGTGAGTTCCTGAGCGCGTGCATCG 2041
Qy 1262 ATGCCCGCAGCATTTGATCAGCTGCGGAGGACCATGTCGCGCGGTTTGTGCTCACTTCC 1321
Db 2042 ATGCCCGCAGCATTTGATCAGCTGCGGAGGACCATGTCGCGCGGTTTGTGCTCACTTCC 2101
Qy 1322 AGAGAGAGATTTTTCAGAAAGAACTACTCCCGAAGGTGGATCCCGGCTTCGGAGCTACG 1381
Db 2102 AGAGAGAGATTTTTCAGAAAGAACTACTCCCGAAGGTGGATCCCGGCTTCGGAGCTACG 2161
Qy 1382 TTGCCCTGCGGCTGTTGCTTCTGCTTCATCTGCTTCATCCAGCTTCTTAATTTCCAC 1441
Db 2162 TTGCCCTGCGGCTGTTGCTTCTGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCAC 2221
Qy 1442 ACTCCACCTGATGCTGGGATTTATGCCAGCATCTTCCGTGCTGCTAATACCGCTGC 1501
Db 2222 ACTCCACCTGATGCTGGGATTTATGCCAGCATCTTCCGTGCTGCTAATACCGCTGC 2281

Db 1854 GGGTCCCAAGATGCTCTGAACCTGAAGATGAGTGGATGAGTCTCTGGGCGAGGCAT 1913
Qy 1260 CGATGCCCGCAGCATGATCAGCTGCGGAGGACCATGTCGCGCGGTTTTCGCTCACTT 1319
Db 1914 CGATGCCCGCAGCATGATCAGCTGCGGAGGACCATGTCGCGCGGTTTTCGCTCACTT 1973
Qy 1320 CCAGAGAGAGATTTTGGAGAGAGTACTCCCGGAAGGTGGATCCCGCTTCGGAGGCTA 1379
Db 1974 CCAGAGAGAGATCTTGAGAGAGAGTACTCCCGGAAGGTGGATCCCGCTTCGGAGGCTA 2033
Qy 1380 GGTGGCTGTGCCCTGTTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAAATTTTCCC 1439
Db 2034 GGTGGCTGTGCCCTGTTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTCACTTTCCC 2093
Qy 1440 ACATCCACCTGATGCTTGGGATTTATGCGCAGCATCTTCCCTGCTGCTGCTTAATCACCGT 1499
Db 2094 ACATCCACCTGATGCTTGGGATCTATGCGCAGCATCTTCCCTGCTGCTGCTTAATCACCGT 2153
Qy 1500 GCTGATCTGTGCTGTGACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1559
Db 2154 GCTGATCTGTGCTGTGACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2213
Qy 1560 CCGCAGCATGCTCGCTCACGGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCT 1619
Db 2214 CCGCAGCATGCTCGCTCACGGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCT 2273
Qy 1620 TGTGTTACTTCTGCCATTGCAACATGTTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1679
Db 2274 TGTGTTACTTCTGCCATTGCAACATGTTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2333
Qy 1680 TGCAGCCCGGATGCTGAATTTAACACCTGCTGACATCATCTGCTGCTGCTGCTGCTGCTGCT 1739
Db 2334 TGCAGCCCGGATGCTGAATTTAACACCTGCTGACATCATCTGCTGCTGCTGCTGCTGCTGCT 2393
Qy 1740 CAATTAATCTCTGGGCTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1799
Db 2394 CAATTAATCTCTGGGCTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2453
Qy 1800 TCCTGAGGTGTC 1812
Db 2454 TCCTGAGTACTTC 2466

RESULT 11
US-09-491-404-837
; Sequence 837, Application US/09491404
; GENERAL INFORMATION:
; APPLICANT: Tang, Yuanhua T.
; APPLICANT: Tillinghast, John
; APPLICANT: Sinku, Ankura
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 785
; CURRENT APPLICATION NUMBER: US/09/491.404
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 3796
; SOFTWARE: PL_SP_genes Version 1.0
; SEQ ID NO 837
; LENGTH: 5353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1669)...(1804)
; OTHER INFORMATION: this location contains the signal peptide sequence,
; OTHER INFORMATION: MLGIVASIFLLILLITVLICAVYSGSLPALKQLRSIVRSRAH, Run with SignalP
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)...(2946)
; OTHER INFORMATION: similar to g12887419 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters

US-09-491-404-837
Query Match 87.7%; Score 1589.6; DB 18; Length 5353;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1625; Conservative 1; Mismatches 20; Indels 4; Gaps 2;
Qy 5 ACGTGGTCTCGGCGATCTCGCGCAGTGCAGGTGCGGGGCGCTTTCGACAGACAGCCGC 64
Db 217 ACGTGGTCTCGGCGATCTCGCGCAGTGCAGGTGCGGGGCGCTTTCGACAGACAGCCGC 276
Qy 65 GCAGCCCTCTCGCGGCTCTGGTGCCCTGTTGTTGTTATATACATCCATACAGGCTCC 124
Db 277 GCAGCCCTCTCGCGGCTCTGGTGCCCTGTTGTTGTTATATACATCCATACAGGCTCC 336
Qy 125 TCCCATCCGATCGCGGCTCGCGTCCGTCAGCGGCTCGCGCTCTCCACCTTGCATTTGA 184
Db 337 TCCCATCCGATCGCGGCTCGCGTCCGTCAGCGGCTCGCGCTCTCCACCTTGCATTTGA 396
Qy 185 TCTTGGCTTGCAACTTAACCGTGGTGATGCTTCTC - TGAAGCAGCTCGGTGCCAAT 243
Db 397 TCTTGGCTTGCAACTTAACCGTGGTGATGCTTCTC - TGAAGCAGCTCGGTGCCAAT 456
Qy 244 GTGCTGCTGTTCTCTGCACCAACGTCATAGCATCTGCACACATATCCAGCAGAGTG 303
Db 457 GTGCTGCTGTTCTCTGCACCAACGTCATAGCATCTGCACACATATCCAGCAGAGTG 516
Qy 304 TCTCAGCCCGAGGCTTTTACAGAGACCGCAGTTACATCCAGGCGCGCTCCACCTGCAG 363
Db 517 TCTCAGCCCGAGGCTTTTACAGAGACCGCAGTTACATCCAGGCGCGCTCCACCTGCAG 576
Qy 364 CATGAGAAATCGCAGCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423
Db 577 CATGAGAAATCGCAGCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 636
Qy 424 GAGTGAAGAAGACATCAACAAAAAAGAGAC - - - ATGTTCCAAAGATCTACATA 480
Db 637 GAGTGAAGAAGACATCAACAAAAAAGAGACATGATGTTCCAAAGATCTACATA 696
Qy 481 CAGAAGCATGACATGTCAGCATCTGTTTGCAGACATGAGGGCTTCCACAGCTGSCA 540
Db 697 CAGAAGCATGACATGTCAGCATCTGTTTGCAGACATGAGGGCTTCCACAGCTGSCA 756
Qy 541 TCCAGTGCATGCGCAGGAGCTGGTCATGACCTGATGAGCTCTTTCGCCGGTTGAC 600
Db 757 TCCAGTGCATGCGCAGGAGCTGGTCATGACCTGATGAGCTCTTTCGCCGGTTGAC 816
Qy 601 AAGCTGGCTCGGAGATCACTGCTGAGGATCAAGATCTTGGGGAGCTGTTACTACTGT 660
Db 817 AAGCTGGCTCGGAGATCACTGCTGAGGATCAAGATCTTGGGGAGCTGTTACTACTGT 876
Qy 661 GTGTCAGGCTGCGGAGGCGCGGCGCAGCATGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 877 GTGTCAGGCTGCGGAGGCGCGGCGCAGCATGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 936
Qy 721 GACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTTGAATCTGAACATGGCG 780
Db 937 GACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTTGAATCTGAACATGGCG 996
Qy 781 GTGGCATCCACAGCGGCGGCTGACCTGCGGCTGCTTGGCTTCCGGAATGGCAGTTC 840
Db 997 GTGGCATCCACAGCGGCGGCTGACCTGCGGCTGCTTGGCTTCCGGAATGGCAGTTC 1056
Qy 841 GATGCTGCTCAATGATGTCACCTGGCCCAACCATGGAAGCAGGAGCGGGCTGCG 900
Db 1057 GATGCTGCTCAATGATGTCACCTGGCCCAACCATGGAAGCAGGAGCGGGCTGCG 1116
Qy 901 GCATCCACATCACTCGGCGCAACACTGACGTACCTGAACGGGAGCTAGCAAGTGAGGCA 960
Db 1117 GCATCCACATCACTCGGCGCAACACTGACGTACCTGAACGGGAGCTAGCAAGTGAGGCA 1176
Qy 961 GCGCGTGTGCGAGCGCAACCGCTACCTAAGGAGCAGCAGATGAGACTTTCCTCATC 1020
Db 1177 GCGCGTGTGCGAGCGCAACCGCTACCTAAGGAGCAGCAGATGAGACTTTCCTCATC 1236


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QY 1021 CTGGGCCAGCCAGAAACGAGAGGAGAAAGCATGCTGGCCAAAGCTGCAGCGGACT 1080
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Db 1237 CTGGGCCAGCCAGAAACGAGAGGAGAAAGCCATGCTGGCCAAAGCTGCAGCGGACT 1296
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QY 1081 CGGGCCAACTCCATGGAAGGCGCTGATGCCCGCATGGGTTCCCTGATGTGCTTCTCCCGG 1140
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Db 1357 ACCAAGGACTCCAAAGGCTTCCGCCAGATGGGATTCATATCCCAAGACACACCGG 1416
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Db 1417 GGCACCCAAAGATGCCCTGAACCTTGAGGATGAGTGATGCTTCCAGCCGCTGCCATC 1476
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QY 1321 CAGAGAGAGATTTGAGAAGAGTACTCCCGGAAGGTGGATCCCGCTTCGGAGCCTAC 1380
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Db 1537 CAGAGAGAGATTTGAGAAGAGTACTCCCGGAAGGTGGATCCCGCTTCGGAGCCTAC 1596
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QY 1381 GTTGCCCTGCGCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTCCCA 1440
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Db 1597 GTTGCCCTGCGCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTCCCA 1656
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Db 1657 CACTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTTAATCAGCGTG 1716
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Db 1717 CTGATCTGCTGTGACTCCTGTGGTCTCTGTTCCCTAAGGCCCTGCAACGCTGTGTC 1776
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QY 1561 CGCAGCATTTCCGCTCAGCGGCACATAGACCCGATTTGGCATCTTTCCGCTCCTGCTT 1620
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|
Db 1777 CGCAGCATTTCCGCTCAGCGGCACATAGACCCGATTTGGCATCTTTCCGCTCCTGCTT 1836
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|
QY 1621 GTCTTTACTTCTGCCATTTGCCAATGTTTC 1650
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Db 1837 GTGTTTACTTCTGCCATTTGCCAATGTTTC 1866
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RESULT 12
US-09-922-279-837
; Sequence 837, Application US/09922279
; GENERAL INFORMATION:
; APPLICANT: Tang, Yuanhua T.
; APPLICANT: Tillinghast, John
; APPLICANT: Sinku, Ankura
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 785
; CURRENT APPLICATION NUMBER: US/09/922, 279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 3796
; SOFTWARE: pt_sp_genes Version 1.0
; SEQ ID NO 837
; LENGTH: 5353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1669)...(1804)
; OTHER INFORMATION: this location contains the signal peptide sequence,
; OTHER INFORMATION: MLCIYASIFLLLTILICAVISGSLFPKALQRLSRIVRSRAH, Run with SignalP
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; NAME/KEY: misc_feature
; LOCATION: (3)...(2946)
; OTHER INFORMATION: similar to gi2887419 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-922-279-837
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Query Match 87.7%; Score 1589.6; DB 34; Length 5353;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1625; Conservative 1; Mismatches 20; Indels 4; Gaps 2;
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QY 5 ACGTGTGCTGGGCATCCTGGCGCAGTGCAGGTGGGGGCGCTTTCGACGACAGACCCGC 64
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|
Db 217 ACGTGTGCTGGGCATCCTGGCGCAGTGCAGGTGGGGGCGCTTTCGACGACAGACCCGC 276
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|
QY 65 GCAGCCCTCTCGGGGCTCTGTGTGCCCTGTCTTCTTGTATACATCGCATACACGTCC 124
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|
|
Db 277 GCAGCCCTCTCGGGGCTCTGTGTGCCCTGTCTTCTTGTCTACATCGCTACACGTCC 336
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|
|
QY 125 TCCCATTCGCATTCGGGGCTGCCCTCCTCAGCGGCTGGGCGCTTCCACCTTGCATTTGA 184
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|
|
Db 337 TCCCATTCGCATTCGGGGCTGCCCTCCTCAGCGGCTGGGCGCTTCCACCTTGCATTTGA 396
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|
|
QY 185 TCTTGGCTGGCAACTTAACCGTGGTGCATGCCCTCCCTC-TGGAGCAGCTCGGTGCCAAT 243
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|
|
Db 397 TCTTGGCTGGCAACTTAACCGTGGTGCATGCCCTCCCTTGGAGGCGAGCTCGGTSCCAAT 456
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|
QY 244 GTGCTGTCTTCTCTGCACCAACGTCATTTAGCATCTGCACACACTATCCAGCAGAGGTG 303
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|
|
Db 457 GTGCTGTCTTCTCTGCACCAACGTCATTTGGCATCTGCACACACTATCCAGCAGAGGTG 516
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|
QY 304 TCTCAGCGCCAGCGCTTTCAGGAGACCCGAGTTTACATCCAGGCGCGGCTTCCACCTGCAG 363
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|
|
Db 517 TCTCAGCGCCAGCGCTTTCAGGAGACCCGCGGTTACATCCAGGCGCGGCTTCCACCTGCAG 576
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|
QY 364 CATGAGAATCGGAGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 423
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Db 577 CATGAGAATCGGAGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 636
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|
QY 424 GAGATGAAAGAACATCAACACAAAAAAGAAAGAC---ATGTTCCAAAGATCTACATA 480
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|
Db 637 GAGATGAAAGAACATCAACACAAAAAAGAAAGATGATGTTCCACACAGATCTACATA 696
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|
QY 481 CAGAAGCATGACAATGTGACGATCTGTTTGGCAGACATTCAGGCGCTTCCACGCTGGCA 540
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|
Db 697 CAGAAGCATGACAATGTGACGATCTGTTTGGCAGACATTCAGGCGCTTCCACGCTGGCA 756
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|
|
QY 541 TCCCACTGCACTCGCAGGAGCTGGTCATGACCTGAAATCAGCTCTTTGCCCCGCTTTCAG 600
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|
|
Db 757 TCCCACTGCACTCGCAGGAGCTGGTCATGACCTGAAATGAGCTCTTTGCCCCGCTTTCAG 816
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|
QY 601 AAGCTGGCTCGGAGAAATCACTGCCTGAGGATCAAGATCTTTGGGGGACTGTTACTACTGT 660
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|
|
Db 817 AAGCTGGCTCGGAGAAATCACTGCCTGAGGATCAAGATCTTTGGGGGACTGTTACTACTGT 876
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|
QY 661 GTGTCAGGGCTCGCGGAGGCCCGCGGCGACCATGCCACATGCTGTGTGGAGATGGGGGTA 720
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Db 877 GTGTCAGGGCTCGCGGAGGCCCGCGGCGACCATGCCACATGCTGTGTGGAGATGGGGGTA 936
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QY 721 GACATGATTGAGGCCATCTCGCTGGTACGTGACGTGACAGGTGATGATGCAACATCGCG 780
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QY 781 GTGGGCATCCACAGCGGCGCTGCACTGCGGCGTCTCTGCTTGGGAAATGGCAGTTTC 840
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QY 841 GATGTGTGTGTCATGATGTGACCTTGGCCAAACCATGGAAGCAGGAAGCCCGGCTGGC 900
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QY 901 CGCATCCATCACTCGGCGCAACACTGACGTACCTGAAACGGGAGCTACGAGGTGGAGCCA 960
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Qy 1082 GGGCAACTCCATCGAAGGGCTGATGCCGATGGGTTCCGTGATCGTGCCTTCCCGGA 1141
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Qy 1142 CCAAGGACTCAAGGCTTCGGCCAGATGGCCATTGATTCAGCAAGAACACACCGGG 1201
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Qy 1202 GCACCAAGATGCCCTGAACCCCTGAGGATGAGTGGATGAGTTCCTGAGCCGTCGCAATCG 1261
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Qy 1442 ACTCCACCTGATGCTTTGGATTATGCCAGCATCTTCTGCTGCTGCTAATCAACCGTGC 1501
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Qy 1742 ATTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1801
Db 2467 ATTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2526
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RESULT 15

US-08-538-815-11
; Sequence 11, Application US/08538815

GENERAL INFORMATION:

APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL
CYCLASE AND USES THEREFOR
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/538.815
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:450
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: N/A
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4131 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-538-815-11

Query Match 79.3%; Score 1437.2; DB 9; Length 4131;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 1584; Conservative 0; Mismatches 223; Indels 3; Gaps 1;

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Qy 185 TCTTGGCTGCACTTAACCTGCTGATGCTCTCTCGAAGCAGCTCGGTGCAATG 244
Db 867 TTTGGCTGGCATCTCAACATGCTGACCCCTCTCTTTGGAAGCAGCTCGGTGTAAG 926
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Db 927 TGGTGTCTCTCTGCAACATGCCATCGGTGCTGCACGCACTACCCGCTGAAGTGT 986
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Qy 365 ATGAGATCGCAGCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 424
Db 1047 ATGAGATCGCAGCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1106
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Db 1107 AAATGAAGAAGATCAACACAAAAAAGAGAGATGTTCCACAAGATTTACATCC 1166
Qy 482 AGAGATGACAATGTCAGCATCTCTGTTTTCAGACATTTAGGGGCTTACCAGCCTGGCAT 541
Db 1167 AGAAGATGACAATGTCAGCATCTCTGTTTTCAGACATTTAGGGGCTTACCAGCCTGGCAT 1226
Qy 542 CCCAGTGCAGTGCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
Db 1227 CCCAGTGCAGTGCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1286
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Db 1287 AGCTGGTGCAGGAGATCACCTGCTGAGGATCAAGATCTTGGGGAGCTGTTACTACTGTG 1346
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Db 1346 TGTACGGCTGCCGAGGCGCGGACCATGCCCCATGCTGTGTGTGAGATGGGGTGTAG 721
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Qy	782	TGGGCATCCACAGCGGGCGGTGCACATGCGGGCTCCTTGGCTTCCGGAATGSCAGTTTCG	841
Db	1467	TGGGCATCCACAGCGGGCGGTGACATGCGGTGTCTTGGCTTCCGGAATGSCAGTTTG	1526
Qy	842	ATGTGTGCTCCAATGATGTGACCTTGCCCAACCACTGGAAGCAGGAAAGCCGGGCTGCC	901
Db	1527	ATGTGTGCTCCAACGATGTGACCTTGCCCAACCACTGGAAGCAGGAAAGCCGGGCTGCC	1586
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Db	1587	GCATCCACATCACTCGGGCCACACTGCAGTACCTGAACGGGGACTATGAGTGGAGCCAG	1646
Qy	962	GCGTGTGTGCAAGCGCAACCGTACCTCAAGGAGCAGCATTGAGACTTTCTCATCC	1021
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Qy	1022	TGGGGCCACGCAAGCAAGGAGGAGAAAGGCATGCTGGCCAAAGCTGCAGCGGACTC	1081
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Qy	1082	GGGCCAACTCCATGGAGGCTGATGCGCGATGGGTTCCTGATCGTGTGCTTCTCCGGA	1141
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Qy	1142	CAAGGACTCCAAAGGCTTCCGCGACATGGCATTTGATGATTCAGCAAGCAAGCCGG	1201
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Qy	1202	GCACCAAGATGCCGAACCTGAGGATGAGGTGATGATTCCTGAGCCGTGCCATCG	1261
Db	1887	GTGCCAAGATGCTGGAACCTGAGGATGAGGTGAGCAGATTCCTGGCCGAGCCATCG	1946
Qy	1262	ATGCCGCGACGATGATGAGCTGGGAAGCAACATGTGCCCGGTTTTGCTCACCTTC	1321
Db	1947	ATGCCGCGACGATGAGCCAGCTGCTGAAGCAACATGTGCCCGGTTTTGCTCACCTTC	2006
Qy	1322	AGAGAGGAGTTTGTAGAAGATGACTCCCGGAAGTGGATCCCGCTCGGAGCCCTACG	1381
Db	2007	AGAGGAGGATCTCGAGAAGAATATTACGGGAAGTAGACCTCGTTTCGGAGCCCTACG	2066
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Db	2127	ACTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTG	2186
Qy	1502	TGATCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG	1561
Db	2187	TCATCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG	2246
Qy	1562	GCAGCATGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG	1621
Db	2247	GCAGTATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG	2306
Qy	1622	TGTTTACTTCTGCCATGCTGCAACATGTTTACCTGTAAACACACCCCGATACGGAGCTGTG	1681
Db	2307	TGTTTACTTCTGCCATGCTGCAACATGTTTACCTGTAAACACACCCCGATACGGAGCTGTG	2366
Qy	1682	CAGCCGGATGCTGAATTTAAACACCTGCTGACATCACTGCTGCCACCTGCGACGCTCA	1741
Db	2367	CGCCCGGATGCTGAATTTAAACACCTGCTGACATCACTGCTGCCACCTGCGACGCTCA	2426
Qy	1742	ATTACTCTTGGGCTTGGATGCTCCCTGTGTGAGGGCACCATGCCCCACCTGCAGCTTTC	1801
Db	2427	ATTACTCTTGGGCTTGGATGCTCCCTGTGTGAGGGCACCATGCCCCACCTGCAGCTTTC	2486

Search completed: February 23, 2003, 07:31:52
Job time : 3608.79 secs

Qy 1802 CTGAGGTGTT 1811
Db 2487 CTGAGTACTT 2496

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 22:29:24 ; Search time 308.758 Seconds
(without alignments)
9128.329 Million cell updates/sec

Title: US-09-750-240-3
Perfect score: 1812
Sequence: 1 gtttaacgtggtctggtgcat.....gcagcttctcgtgaggtgttc 1812

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2850587 seqs, 777171511 residues
Total number of hits satisfying chosen parameters: 5701174

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1454.2	80.3	5826	6	US-10-144-771-5921
2	829.8	45.8	4349	6	US-10-144-771-19529
3	432.8	23.9	1386	1	PCT-US02-36759-83
4	346	19.1	2253	6	US-10-144-771-16113
5	339	18.7	2949	5	US-09-724-676-11593
6	339	18.7	2949	5	US-09-724-676-11593
7	339	18.7	3756	5	US-09-724-676-11592
8	339	18.7	3756	5	US-09-724-676-11592
9	338.2	18.7	4079	6	US-10-305-720-1412
10	338.2	18.7	5370	5	US-09-724-676-11576
11	338.2	18.7	5370	5	US-09-724-676-11576
12	338.2	18.7	5680	5	US-09-724-676-11577
13	338.2	18.7	5680	5	US-09-724-676-11577
14	332.6	18.4	4633	6	US-10-144-771-16338
15	320.6	17.7	3158	6	US-10-144-771-14946
16	316.6	17.5	6196	1	PCT-US02-34621-1
17	316.6	17.5	6196	6	US-10-282-942-1
18	314.4	17.4	5124	6	US-10-144-771-18424
19	311.4	17.2	2731	6	US-10-305-720-1344
20	286	15.8	4008	7	US-60-436-643-3039
21	284.8	15.7	3820	6	US-10-144-771-855
22	284	15.7	3518	6	US-10-121-911A-2
23	273.6	15.1	320	6	US-10-264-237-588
24	264.2	14.6	3458	6	US-10-144-771-3825
25	256.2	14.1	3357	6	US-10-338-044-2053
26	216.8	12.0	4457	6	US-10-144-771-18978

27	209.4	11.6	1767	5	US-09-724-676-11581	Sequence 11581, A
28	209.4	11.6	1767	5	US-09-724-676A-11581	Sequence 11581, A
29	93	5.1	2954	6	US-10-240-965-82	Sequence 82, Appl
30	92.2	5.1	993	6	US-10-144-771-4939	Sequence 4939, Ap
31	79.8	4.4	2430	6	US-10-144-771-12661	Sequence 12661, A
32	76.6	4.2	4775	6	US-10-152-319A-1657	Sequence 1657, Ap
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35	73.2	4.0	805	6	US-10-144-771-10979	Sequence 10979, A
36	64.4	3.6	1259	5	US-09-880-505A-123	Sequence 123, App
37	64.4	3.6	2013	5	US-09-880-505A-176	Sequence 176, App
38	64.4	3.6	2172	5	US-09-880-505A-173	Sequence 173, App
39	64	3.5	3047	6	US-10-305-720-1465	Sequence 1465, Ap
40	52.8	2.9	3845	6	US-10-144-771-10682	Sequence 10682, A
41	52.2	2.9	695	6	US-10-218-140-3629	Sequence 3629, Ap
42	50.4	2.8	4064	5	US-09-724-676-24466	Sequence 24466, A
43	50.4	2.8	4064	5	US-09-724-676A-24466	Sequence 24466, A
44	50.4	2.8	4135	5	US-09-724-676-24474	Sequence 24474, A
45	50.4	2.8	4135	5	US-09-724-676A-24474	Sequence 24474, A

ALIGNMENTS

RESULT 1
US-10-144-771-5921
; Sequence 5921, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CLO01321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 5921
; LENGTH: 5826
; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-5921

Query Match	80.3%	Score 1454.2;	DB 6;	Length 5826;
Best Local Similarity	88.1%	Pred. No. 0;		
Matches 1595;	Conservative 0;	Mismatches 213;	Indels 3;	Gaps 1;
Qy	5	ACGTGGTCTGGGCATCTTGGCGCAGTGCAGTGGCGGCGCTTTCGACGAGACCCGC	64	
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Qy	65	GCAGCCCTCTGCGGGCCTCTGGTCCCTGTGTTCTTTGTATACATCATACAGCTCC	124	
Db	787	ACAGCCCTCTGCGGGCCTTGGTCCCTGTGTTCTTTGTATACATCATACAGCTCC	846	
Qy	125	TCCCATCCGATCGGGCTGCCCTCTCAGCGGCTGGGCTCTCCACCTTGCATTGA	184	
Db	847	TTCCCATTCGATCGAGCGCGCTACTCAGCGGCTGGGCTCTCTACTCTGCAATTGA	906	
Qy	185	TCTTGGCTGGCAACTTAACCGTGGTGGTCTCTCTGGAAGCAGCTCGGTGCAATG	244	
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Qy	245	TGCTGCTGTCTCTGCACCAACGTCATTAGCATCTGCACACATATCCAGCAGAGGTG	304	
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Qy	305	CTCAGCGCGAGCCCTTTCAGGAGAGCCCGAGTTACATCAGCGCGGCTCCACCTGCAGC	364	
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QY 602 AGCTGGCTGGGAGAACTACCTGCTGAGGATCAAGATCTTTGGGGGACTGTTACTACTGTG 661
Db 1327 AGCTGGCTGGGAGAACTACCTGCTGAGGATCAAGATCTTTAGGAGACTGTTACTACTGCG 1386
QY 662 TGTGAGGGCTGCGGAGGCGCGGCCACCATGCCACTGCTGTGTGGAGATGGGGTAG 721
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QY 722 ACATGATTGAGGCCATCTCGCTGCTGCTGAGGTGACAGGTGTAATGTGAACATGCGCG 781
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QY 1142 CCAAGGACTCAAGGCGCTTCCGCGAGATGGGCATTTGATGATTTCCAGCAAGAACCGGG 1201
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QY 1202 GCACCAAGATGCCCTGAACCCCTGAGGATGAGGTGATGATTTCTTGAGCCGTGCCATCG 1261
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QY 1262 ATGCCCGCAGCATGTGATGCTGCGGAAGACCATGTGCGCGGTTTGTGCTCACCTTCC 1321
Db 1987 ATGCCCGCAGCATGACCAACTGCGTAAGACCATGTGCGCGGTTTCTGCTCACCTTCC 2046
QY 1322 AGAGAGAGGATTTGAGAGAACTACTCCCGGAAGTGGATCCCGCTTCGGAGCCTACG 1381
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QY 1622 TGTTTACTTCTGCAATTTGCCAACATGTTACCTGTAAACCACACCCCCCATACGGAGCTGTG 1681
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QY 1682 CAGCCCGGATGCTGAATTTAAACACCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCA 1741
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QY 1742 ATTACTCTCGGCTGCGATGCTCCCTGTGTGAGGSCACCATGCCACCTGCAGCTTTC 1801
Db 2467 ATTACTCTCGGACGTGATGCTCCCTGTGTGAGGSCACCGCACCTGCGACTTCC 2526
QY 1802 CTGAGTGTTC 1812
Db 2527 CTGAGTACTTC 2537

RESULT 2
US-10-144-771-19529
; Sequence 19529, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 19529
; LENGTH: 4349
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(4349)
; OTHER INFORMATION: n = A,T,C or G
US-10-144-771-19529

Query Match 45.8%; Score 829.8; DB 6; Length 4349;
Best Local Similarity 67.8%; Pred. No. 1.1e-198;
Matches 1240; Conservative 0; Mismatches 547; Indels; 42; Gaps 4;

QY 5 ACGTGTGTGTCGTCATCTCGCGCAGTCGAGGTGCGGGGCGCTTTCGACGACAGCCCGC 64
Db 416 ATCGCTCATTTGAGTGGTGTGCTGGCGCTCCAGGTAGTGGGCGCTTGTGCTGCCACAGCCAC 475
QY 65 GCAGCCCTCTGCGGGCTCTGCTGCGCTGTGTTTGTATACATCGCATACACAGCTCC 124
Db 476 GCAGCGCTCCGAGGGCATCTGTGGNCCGTGTTCATCTATACCATCTACACCTGCG 535
QY 125 TCCCATTCGCGCATCGGGCTGCGCTCTCCTCAGCGGCTTGGGCGCTTCCACCTTGCAATTGA 184
Db 536 TGCCTGTGCGCATGAGGGCTGCGGTGCTCAGCGGGGTGCTTCTGTCGGCTCTCCACTTGG 595
QY 185 TCTTGGCTGGGAACCTTAACCGTGGTGTATGCCCTTCTCTGTGGAAGCAGCTCGGTGCCAATG 244
Db 596 CCATCTCTCTGCACACCAACTCCACGAGACAGTTCCTGCTGAACACAGTGTGTCTCCAATG 655
QY 245 TGTGCTGTTCCTCTGCACCAAGTCAATTAGCATCTGCACACACTATCCACGACAGAGTGT 304
Db 656 TCTCATCTCTCTGCACCAACATTTGGGTGTGTGCACTCACTACCCAGCTGAGGTCT 715
QY 305 CTCAGCGCCAGGCTTTTCAGGAGACCCGCGAGTTTACATCCAGGCCGCGCTCCACTGCGAGC 364
Db 716 CCCAGACAGAGGCTTCCAGGAGACCCGGGAGTGTATCCAGGCTCGGCTCCATTTCCAGC 775
QY 365 ATGAGAAATCGGACAGGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 424
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Db 776 GGGAAACCAAGCAAGAGAGGCTCTCTGCTGTCTCTCTTCCCGTCATGTTGCCATGG 835
Qy 425 AGATGAAAGAACATCAACACAAAAGAGAG- -CATGTTCCACAGATCTACATAC 481
Db 836 AGATGAAAGACAGATCAACCCCAAGCAGGAGATATGATGTTCCACAGATCTACATCC 895
Qy 482 AGAAGCATGACAATGTCAGCATCTCTGTTTGGAGACATTTAGGGCTTCCACAGCCTGGCAT 541
Db 896 AGAAGCATGACAATGTCAGCATCTCTGTTTGGAGACATTTAGGGCTTCCACAGCCTGGCTT 955
Qy 542 CCCAGTGCATGCGGAGAGAGTGGTATGATGACCTGAAATGAGCTCTTTCCCGGTTTGACA 601
Db 956 CCCAGTGTACTGCCCCAAGAACTGTGATGACCTCAATGAGCTCTTCCCGGCTTTTGACA 1015
Qy 602 AGCTGGCTGCGGAGAACTCACTGCTGAGGATCAAGATCTTGGGGACTGTTACTACTGTG 661
Db 1016 AGTTGGCTGCGGAGAACTCACTGTTTACGGATTAAAGATCCTCGGGATTGTTACTACTCG 1075
Qy 662 GTTCAGGCTGCCGAGGCGCGGCGGACCATGCCCCACTGCTGTGTGGAGATGGGGTAG 721
Db 1076 TCTCGGGCTGCCCTCAAGCCAGAGCCGACCATGCCACTGCTGCTGGAGATGGGAATGG 1135
Qy 722 ACATGATTTAGGCCATCTCGCTGGTGTACGTGAGGTGACAGGTGTAATGTGAACATGCCCG 781
Db 1136 ACATGATCGAGGCCATCTCGTTGGTCCGGGAGGTGACAGGGGTGAACGTGAACATGCCCG 1195
Qy 782 TGGGCATCCAGCGGGCGCTGCACCTCGCGCTCTTGGCTTGGGAAATGGCAGTTTCG 841
Db 1196 TGGGAATTCACAGCGGGAGAGTACACTGCGGTGCTCTGCTCAGAAAGTGGCAATTCG 1255
Qy 842 ATGTGTGTCCAATGATGTACCTTGCCCAACCATGGAAGCAGGAAGCGGGCTGGCC 901
Db 1256 ACGTGTGTCTAAGCATGTCACTCTGCGCAACCATGGAAGCTGGTGGCAAGCGGGCC 1315
Qy 902 GCATCCACATCACTCGGCGACATGCTAGTACCTGAACGGGACTACGAAGTGGAGCCAG 961
Db 1316 GCATCCACATCACCAGAGCCACATCAACTACCTGAATGGGACTATGAGTGGAAACAG 1375
Qy 962 GCGTGTGTGGCAAGCGCAACGCTACCTCAAGGAGCAGCATTTGAGACTTTCCCTCATCC 1021
Db 1376 GCTGTGTGGCATGCGCAATGCCATACCTCAAGGAGCAGCATTTGAGACCTTCTCATCC 1435
Qy 1022 TGGGCGCAGCAGAAACGGAAGAGAGAAAGGATGCTGCCAAGCTGCAGCGGAGTC 1081
Db 1436 TGAGCTGTACCCAGAAGCGGAAGAGAGAGAGGCGCATGATGCCAAGATGAACGCCAGA 1495
Qy 1082 GGGCAACTCCATGGAAGGGCTGTGCGCGATGGTTCCTGTGATCGTCCCTTCT- - - - - 1135
Db 1496 GAACCAACTCCATCGGACACAATCCGCTCACTGGGGAGCGGAGCGCCCTTCTACAACC 1555
Qy 1136 - - - - -CCCGACCAAGGACTCCAAGGGCTTCCGCGCATGGGCATTTGATGATTCAGCA 1189
Db 1556 ACTTGGGCGGCAACGAGTGTCAAGAGAGATGAAGAGATGCTTCCCTATCTCTGCCCTG 1615
Qy 1190 AAGCAACCGGGGCAACCCAGATGCCCTGAAACCCGTGAGGATGAGTGTGATGATTCCTGA 1249
Db 1616 GTTTTTCAGGAATGCCCAGGAAAGTGCAGACCCAGAGAGTGAAGTGCAGAGTTTCTGG 1675
Qy 1250 GCGTGGCATGATGCTCCGCGAGCATTTGATCAGCTGCGGAAGGACCATGTGGCCCGTTT 1309
Db 1676 GTCGGGCGCATGATGCCAGGAGATFCGACAGACTGCGATCTGAACACGTCGCGCAAGTTCC 1735
Qy 1310 TGCTCACCTCCAGAGAGGATTTTGAGAGAAAGTACTCCCGGAAGGTGGATCCCGCT 1369
Db 1736 TCCTGACCTTCAGGAGCGCCACTTAGAGAGAAAGTACTCCAAGCAGGTGATGACCAT 1795
Qy 1370 TCGGAGCCTACGTGCTGTCGCCCTGTTGGTCTTCTGCTCATCTGCTTCACTCCAGCTTC 1429
Db 1796 TTGTGCTCATGTGCGCTGCGCTGCTGTTTCTCTCTCATCTGCTTTGTGCCAGATCA 1855
Qy 1430 TAAATTTTCCACACTCCACCCTGATGCTGGATTTATGCCAGCATCTTCTGCTGCTGC 1489
Db 1856 CAAATTTGCCCCACTCCCTGTTTCATGCTGAGTTTCTACCTGTGCTGTTTCTGCTGCTGG 1915

Qy 1490 TAATCACCGTGTGATCTGTGCTGTACTCTCTGTGGTTCTCTGTTCCTTAAGGCCCTGC 1549
Db 1916 CTTGGTGGTGTGTGTCTGTGATCTATGCTGTG- - - - -TGA 1954
Qy 1550 AACGTCTGTCCGAGCATTTGTCGCTCACGGGCACATAGCACCCGAGTTGGCATCTTTT 1609
Db 1955 AGACACTCTCCAGGAAGATAGTGGATCCAAGAAGAACAGCACCTGCTCGGGGTATTCA 2014
Qy 1610 CCGTCTCTGTGTGTTTACTTCTGCCATTGCCAATGTTCACTGTAAACACACCCCA 1669
Db 2015 CCATCACCTGTGTCTCTCGGCTTTTGTCAAGATGTTGTAAGTCTTAAGAACC 2074
Qy 1670 TACGAGCTGTGCAGCCGCGATGCTGAATTTAAACACCTGCTGCATCACTGTGCTGCCACC 1729
Db 2075 TGGTGGGTGCTGCGCAGAGGAGCACACATCACGGTGAACAGGTCAACGATGTCATG 2134
Qy 1730 TGCAGCAG- - - - -CTCAATTACTCTCTGGGCTGGATGCTCCCTGTGTGAGGACCA 1783
Db 2135 TGATGGAGTCGCGCTTCAACTACAGCTTGGGCGAGCAGCAGGGCTTCTGTGCGACGCC 2194
Qy 1784 TGCCCACTGCGAGCTTTCTCTGAGGTGTTTC 1812
Db 2195 AGCCCACTGCAACTTCCAGAGTACTTC 2223

RESULT 3
PCT-US02-36759-83
; Sequence 83, Application PC/TUS0236759
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DUGGAN, Brendan M.
; APPLICANT: YANG, Junming
; APPLICANT: GIETZEN, Kimberly J.
; APPLICANT: LEE, Soo Yeun
; APPLICANT: TANG, Y. Tom
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: WALIA, Narinder K.
; APPLICANT: WARREN, Bridget A.
; APPLICANT: BARROSO, Ines
; APPLICANT: BECHA, Shanya D.
; APPLICANT: YUE, Henry
; APPLICANT: LEHR-MASON, Patricia M.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: LEE, Sally
; APPLICANT: EMERLING, Brooke M.
; APPLICANT: KABLE, Amy E.
; APPLICANT: KHARE, Reena
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: GANDHI, Aneena R.
; APPLICANT: TRAN, Uyen K.
; APPLICANT: RICHARDSON, Thomas W.
; APPLICANT: MARQUIS, Joseph P.
; APPLICANT: LAL, Preeti G.
; APPLICANT: FORSYTHE, Ian J.
; APPLICANT: LEE, Ernestine A.
; APPLICANT: SWARNAKAR, Anita.
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: GORVAD, Ann E.
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: ISON, Craig H.
; APPLICANT: JIN, Pei
; APPLICANT: JIANG, Xin
; APPLICANT: JACKSON, Alan
; APPLICANT: BHATIA, Umesh
; APPLICANT: BURRILL, John D.
; APPLICANT: BLAKE, Julie J.
; APPLICANT: HO, Ann
; APPLICANT: ZHENG, Wenjin
; APPLICANT: GAO, Jing
; TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS

Best Local Similarity 63.8%; Pred. No. 3.5e-75;
Matches 552; Conservative 0; Mismatches 300; Indels 13; Gaps 2;

Qy 228 GCAGCTCGTCCCAATGTGCTGCTTCTCTGCACCAACGCTCATAGCATCTGCACACA 287
Db 819 GGAGATCCTGGCCAACTGCTTCTCTCTCTGCGCCATCGCTGTGGCGCATCATGTCTCTA 878

Qy 288 CTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTCCAGAGACCCGCACTTACATCCAGGC 347
Db 879 CTACATGCTGACCGCAAGCAGCGCTTCTCTGAGGCGCCGCACTGCTGGAGGT 938

Qy 348 CCGGCTCCACCTGCAGCATGAGATCGGCAGCAGAGCGGCTGCTGTGCTGGTATTGCC 407
Db 939 GAAGATGAACCTGGAAGAGCAGCCAGCAGGAAACCTCATGCTTTCCATCCTGCC 998

Qy 408 CCAGCAGTTGCCATGGAGATGAAGAGACATCAACACA-----AAAAAGA 455
Db 999 CAAGCAGCTGGCTGACGAGATGCTGAAGACATGAAGAAAGACGAGAGCCAGAGACCA 1058

Qy 456 AGACATGTTCCACAAGATCTACATACAGAAGCATGACAAATGTCAGCATCTCTTTGCAGA 515
Db 1059 GCAGCAGTTCAACACCATGTACATGTAACGTCACGAGAAGCTCAGCATCTCTTTGCCGA 1118

Qy 516 CATTGAGGCTTACAGCCTGGCATCCCATGTCAGCTGCGCAGGAGCTGTGTCAGCCCT 575
Db 1119 CATGCTGGCTTTACCCAGCTGTCTTCTGCTGCGAGTGCCAGGAGCTTGTGAAGCTGT 1178

Qy 576 GAATGAGCTTTGCCGTTTGACAAGCTGGCTGCGGAGATCACTCCCTGAGGATCAA 635
Db 1179 CAACGAGCTTTGCCGCTTTTGACAAGCTGCGAGCTAAATACCAACAGCTGCGGATTA 1238

Qy 636 GATCTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCGGAGGCGCGTGCACTCGGGGT 815
Db 1359 GACCAAGACTGGGTGGATCGCTGTGGGGTGCACACGCGGCGGTGCACTGGGGGCGT 1418

Qy 816 CTTGGCTTGGGAAATGGCAGTTGATGTGTGGTCCCAATGATGTACCTGCGCCACCA 875
Db 1539 GAAAGGGAGTTGATGTGGAGCAGCGATGGGGGAGCGCTGTGATTAACCTAGAAGA 1598

Qy 996 GCAGCATTGAGACTTTCTCATCTCTGGGCGCC-AGCCAGAAAGGAGAGGAGAAAG 1054
Db 1599 GAAGGGTATTGAACCTACCTCATCATTTGCTCCAAAGCCAGAGGTGAAGAAACAGCCAC 1658

Qy 1055 GCATGCTGGCAAGCTGCAGCGGAC 1079
Db 1659 CCAGATGGCCTCAATGGCTCGGCC 1683

RESULT 6
US-09-724-676A-11593
; Sequence 11593, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09724.676A
; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222
; SEQ ID NO 11593
; LENGTH: 2949
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-11593

Query Match 18.7%; Score 339; DB 5; Length 2949;
Best Local Similarity 63.8%; Pred. No. 3.5e-75;
Matches 552; Conservative 0; Mismatches 300; Indels 13; Gaps 2;

Qy 228 GCAGCTCGTCCCAATGTGCTGCTTCTCTGCACCAACGCTCATAGCATCTGCACACA 287
Db 819 GGAGATCCTGGCCAACTGCTTCTCTCTCTGCGCCATCGCTGTGGCGCATCATGTCTCTA 878

Qy 288 CTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTCCAGAGACCCGCACTTACATCCAGGC 347
Db 879 CTACATGCTGACCGCAAGCAGCGCTTCTCTGAGGCGCCGCACTGCTGGAGGT 938

Qy 348 CCGGCTCCACCTGCAGCATGAGATCGGCAGCAGAGCGGCTGCTGTGCTGGTATTGCC 407
Db 939 GAAGATGAACCTGGAAGAGCAGCCAGCAGGAAACCTCATGCTTTCCATCCTGCC 998

Qy 408 CCAGCAGCTTTGCCATGGAGATGAAGAGACATCAACACA-----AAAAAGA 455
Db 999 CAAGCAGCTGGCTGACGAGATGCTGAAGACATGAAGAAAGACGAGAGCCAGAGACCA 1058

Qy 456 AGACATGTTCCACAAGATCTACATACAGAAGCATGACAAATGTCAGCATCTCTTTGCAGA 515
Db 1059 GCAGCAGTTCAACACCATGTACATGTAACGTCACGAGAAGCTCAGCATCTCTTTGCCGA 1118

Qy 516 CATTGAGGCTTACAGCCTGGCATCCCATGTCAGCTGCGCAGGAGCTGTGTCAGCCCT 575
Db 1119 CATGCTGGCTTTACCCAGCTGTCTTCTGCTGCGAGTGCCAGGAGCTTGTGAAGCTGT 1178

Qy 576 GAATGAGCTTTGCCGTTTGACAAGCTGGCTGCGGAGATCACTGCTGAGGATCAA 635
Db 1179 CAACGAGCTTTGCCGCTTTTGACAAGCTGCGAGCTAAATACCAACAGCTGCGGATTA 1238

Qy 636 GATCTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCGGAGGCGCGTGCACTCGGGGT 815
Db 1239 GATCCTGGGCGACTGCTACTACTGTGATCTGCGGCTTGGCYGACTACCCGGAGGACCA 1298

Qy 696 CCATGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTGGTACGTGAGGT 755
Db 1299 CGTCTGCTCCATCCTCATGGGCTGGCCATGCTGGAGGCCATCTCGTATGTGCGGGAGA 1358

Qy 756 GACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGCGCTGCACTGCGGGGT 815
Db 1359 GACCAAGACTGGGTGGATCGCTGTGGGGTGCACACGCGGCGCTGCTGGGGGCGT 1418

Qy 816 CTTGGCTTGGGAAATGGCAGTTGATGTGTGGTCCCAATGATGTACCTGCGCCACCA 875
Db 1419 CTTGGCGCAGAAAGCGCTGGCAGTACGAGCTGTGTGCTGATGTATGATGATGATGAT 1478

Qy 876 CATGAAGCAGGAAGCCGCGCTGGCGCATCCACATCACTCGGGCAACACTGCACTGACCT 935
Db 1479 GATGAGCGCGCGCATCCCTGGGCGCTGCACATCTCCCAGAGCACCATGGAGTGCCT 1538

Qy 936 GAAAGGGAGTTGATGTGGAGCAGCGATGGGGGAGCGCTGTGATTAACCTAGAAGA 1598
Db 1599 GAAGGGTATTGAACCTACCTCATCATTTGCTCCAAAGCCAGAGGTGAAGAAACAGCCAC 1658

Qy 1055 GCATGCTGGCAAGCTGCAGCGGAC 1079
Db 1659 CCAGATGGCCTCAATGGCTCGGCC 1683

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RESULT 7
US-09-724-676-11592
; Sequence 11592, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; NUMBER OF SEQ ID NOS: 2000-11-28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11592
; LENGTH: 3756
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-11592

Query Match      18.7%; Score 339; DB 5; Length 3756;
Best Local Similarity 63.8%; Pred. No. 3.9e-75;
Matches 552; Conservative 0; Mismatches 300; Indels 13; Gaps 2;

QY 228 GCAGCTCGGTGCCAATGTGCTGCTTCCTGCACCAAGCTCATTAGCATCTGCACACA 287
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 819 GGAGATCTCGCCCAACGCTTCTCTACCTGTGCGCATCGCTGGGCGATCATGTCCCTA 878

QY 288 CTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAGACCCGCGAGTTACATCCAGGC 347
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 879 CTACATGGCTGACCGCAAGCACCGCAAGGCTTCTTGGAGGCCCGCCAGTCGCTGGAGGT 938

QY 348 CCGGCTCCACCTGCAGCATGAGATGCGGACGAGCGGCTGCTGCTGCGGTATTGCC 407
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 939 GAAGATGAACCTCGAAGCAGAGCCAGCAGCAGGAGAACCTCATGCTTTCCATCCTGCC 998

QY 408 CCAGCAGCTTTGCCAAGATCTACATACAGAAAGACATCAACACA-----AAAAAGA 455
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 999 CAAGCAGCTTTGCCAAGATCTACATACAGAAAGACATCAAGAAAGAGAGAGAGACCA 1058

QY 456 AGACATGTTCCACAAGATCTACATACAGAGATGACAATGTGAGCATCTGTTGCAGA 515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1059 GCAGCATCTTCAACACCATGTATCATGTACCCTCAGGAGAACCTCATGCTTTGCCGA 1118

QY 516 CATTGAGGGCTTACCAGCTGCGATCCAGTCCAGTCCAGGAGCTGTCATGACCT 575
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1119 CATCTGGGGCTTTACCCAGCTGCTTCTGCTGCAGTGCCCGAGGAGCTTGTGAAGTGT 1178

QY 576 GAATGAGCTTTTGCCTGTTGACAAGCTGGCTGGGAGAAATCAGTCGCTGAGGATCAA 635
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1239 GATCTGGGGGACTGTACTACTGTGTGTCAGGGCTGCCGAGGCGCGGCCACCATGC 1298

QY 636 CACTGCTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTGTAGCTGAGGT 755
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1299 CGTCTGCTCCATCTCATGGGGCTGGCCATGCTGGAGGCCATCTCTGTATGTGCGGAGAA 1358

QY 696 CAATGAGCTTTTGCCTGTTGACAAGCTGGCAGCTGCAATACCAACAGCTGGGATTA 1418
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1359 GACCAAGCTGGGGTGGACATGCTGTGGGGTGCACACGGGACCGTGTGTTGGGGGCGT 1478

QY 816 CATTGGCTTTCGGAATGCGAGTTGATGTGGTCCCATGATGTGACCCCTGCCCAACCA 875
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1419 CTTGGGCCAAGACCGCTGGCAGTACGAGTGTGGTGCAGTGTCTACGTAGCAACAA 1478

QY 876 CATGGAAGCAGGAAGCCGGCTGGCGCATCCACATCACTCGGCGCAACACTGACGTACCT 935
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1479 GATGGAGGCGGGGCGGATCCCTGGGCGCGTGCACATCTCCAGAGACCACTGACGTGCCT 1538

QY 936 GAACGGGGACTACGAATGTGAGCGAGCGGCTGTGTGGCAAGCGCAACCGCTACCTCAAGGA 995
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1539 GAAAGGGAGTTTGTATGTGAGGCCAGGCGATGGGGCGAGCCGCTGTGATTACCTAGAGA 1598
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QY 996 GCAGCACATTTGAGACTTTCTCTCATCTCTGGCGCC-AGCCAGAAACGGAAGAGAGAAG 1054
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1599 GAAGGGTATTGAAACCTTACCTCATCTGCTCCAAAGCCAGAGGTGAAGAAACAGCCAC 1658

QY 1055 GAATGCTGGCCAAAGCTGCAGCGGAC 1079
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1659 CCAGAAATGGCCTCAATGGCTCGGCC 1683

RESULT 8
US-09-724-676A-11592
; Sequence 11592, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11592
; LENGTH: 3756
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-11592

Query Match      18.7%; Score 339; DB 5; Length 3756;
Best Local Similarity 63.8%; Pred. No. 3.9e-75;
Matches 552; Conservative 0; Mismatches 300; Indels 13; Gaps 2;

QY 228 GCAGCTCGGTGCCAATGTGCTGCTTCCTTCCTGCACCAAGCTCATTAGCATCTGCACACA 287
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 819 GGAGATCTCGCCCAACGCTTCTCTACCTGTGCGCATCGCTGGGCGATCATGTCCCTA 878

QY 288 CTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAGACCCGCGAGTTACATCCAGGC 347
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 879 CTACATGGCTGACCGCAAGCACCGCAAGGCTTCTTGGAGGCCCGCCAGTCGCTGGAGGT 938

QY 348 CCGGCTCCACCTGCAGCATGAGATGCGGACGAGCGGCTGCTGCTGCGGTATTGCC 407
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 939 GAAGATGAACCTCGAAGCAGAGCCAGCAGCAGGAGAACCTCATGCTTTCCATCCTGCC 998

QY 408 CCAGCAGCTTTGCCAAGATGAGATGAAAGAACATCAACACA-----AAAAAGA 455
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 999 CAAGCAGCTGGCTGACGAGATGCTGAAAGACATCAAGAAAGAGAGAGAGAGACCA 1058

QY 456 AGACATGTTCCACAAGATCTACATACAGAGATGACAATGTGAGCATCTGTTGCAGA 515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1059 GCAGCATCTTCAACACCATGTATCATGTACCCTCAGGAGAACCTCATGCTTTGCCGA 1118

QY 516 CATTGAGGGCTTACCAGCTGCGATCCAGTCCAGTCCAGGAGCTGTCATGACCT 575
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1119 CATCTGGGGCTTTACCCAGCTGCTTCTGCTGCAGTGCCCGAGGAGCTTGTGAAGTGT 1178

QY 576 GAATGAGCTTTTGCCTGTTGACAAGCTGGCTGGGAGAAATCAGTCGCTGAGGATCAA 635
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1179 CAACAGAGCTTTTGCCTGTTGACAAGCTGGCAGCTGCAATACCAACAGCTGGGATTA 1238

QY 636 GATCTTTGGGGACTGTACTACTGTGTGTCAGGGCTGCCGAGGCGCGGCCACCATGC 695
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1239 GATCTGGGGGACTGTACTACTGTGTGTCAGGGCTGCCGAGGCGCGGCCACCATGC 1298

QY 696 CACTGCTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTGTAGCTGAGGT 755
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1299 CGTCTGCTCCATCTCATGGGGCTGGCCATGCTGGGAGGCCATCTCTGTATGTGCGGAGAA 1358

QY 756 GACAGGTGTGAATGTGAACATGCGGCTGGGCATCCACAGCGGGCGGTGCACTGCGGCGT 815
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1359 GACCAAGCTGGGGTGGACATGCTGTGGGGTGCACACGGGACCGTGTGTTGGGGGCGT 1418

QY 816 CATTGGCTTTCGGAATGCGAGTTGATGTGGTCCCATGATGTGACCCCTGCCCAACCA 875
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1419 CTTGGGCCAAGACCGCTGGCAGTACGAGTGTGGTGCAGTGTCTACGTAGCAACAA 1478

QY 876 CATGGAAGCAGGAAGCCGGCTGGCGCATCCACATCACTCGGCGCAACACTGACGTACCT 935
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1479 GATGGAGGCGGGGCGGATCCCTGGGCGCGTGCACATCTCCAGAGACCACTGACGTGCCT 1538

QY 936 GAACGGGGACTACGAATGTGAGCGAGCGGCTGTGTGGCAAGCGCAACCGCTACCTCAAGGA 995
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1539 GAAAGGGAGTTTGTATGTGAGGCCAGGCGATGGGGCGAGCCGCTGTGATTACCTAGAGA 1598
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Db 3622 ATCCACTCCGGCTCGGTGCTGTCGGGTGTTTTGGGACTACGGGAAGTGGCAGTTTGATGTC 3681
QY 847 TGTGTCACATGATGTGACCCCTGGCCACACCATGGAAGAGCGGGCTGGCCGCATC 906
Db 3682 TGTGCTTGGGATGTGATATTGCAACAACTCGAATCTGGAGGAATCCCGGAGGATT 3741
QY 907 CACATCACTGGGCACACATGCAAGTACCTGAACCGGGGACTACGAAGTGGAGCCGCT 966
Db 3742 CACATTTCCAAACCCAGCGTGGACTGTCTCAACGGTGACTATACGTTGGAAGAGGCCAT 3801
QY 967 GTTGGGAAGCGCAACCGGTACCTCAAGGACGACACATGAGACTTTCCTCAT 1019
Db 3802 GGTAAAGAGGGAATGAATTCCTGAGGAAGCAATAATCGAACTTACTTAAT 3854

RESULT 14
US-10-144-771-16338
; Sequence 16338, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 16338
; LENGTH: 4633
; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-16338

Query Match 18.4%; Score 333.2; DB 6; Length 4633;
Best Local Similarity 63.5%; Pred. No. 1.2e-73;
Matches 531; Conservative 0; Mismatches 293; Indels 12; Gaps 1;

QY 220 CTCTGGAAGCAGCTCGGTGCGCAATGCTGCTCTCTGCAACCAAGCTCATTAGCATC 279
Db 664 CTGCTGAGGAGATCTGGCAACAGCTTCTCTACTCTGTGCTATCATCTGTTGGGCATC 723
QY 280 TGCACACATATCCAGCAGAGTGTCTAGCGGCCAGGCCCTTTCAGGAGACCCGACGTAC 339
Db 724 ATGCTCTACTACATGCGCAGACCGCAAGCACCGCAAGGCCCTTCTGAGGCCGCCAGTCA 783
QY 340 ATCCAGGCCCGCTCACCTGCAAGATGAGATCGCGCAGCAGGAGCGGTGCTGTGTCG 399
Db 784 CTGGAGGTGAAGATGAATCTGGAGAGCAGACCGACGAGGAAACCTTATGCTTTCC 843
QY 400 GTATTGCCCGCAGCACGTTGC-----CATGGAGATGAAGAAGACATCAACACA 447
Db 844 ATCCTGCCAAGCACCTGGCTGACGAGATGCTGAAGGACATGAAGAGGACGAGACCCAG 903
QY 448 AAAAAAGACATGTTCCACAAGATCTACATACAGAAGCATGACAAATGTACGATCCCTG 507
Db 904 AAGGACGACGACGATTCATACCATGTACATGTACCGGCACGAGAAATGTACGATCCCTG 963
QY 508 TTTGACAGATGAGGGCTTCAACAGCGTGGCATCCAGTCCAGTGGCAGTGGCAGGAGCTGTC 567
Db 964 TTTGACAGATTTGTTGGCTTTACCCAGCTGCTCTGCTTGGAGTCCCGAGGAGTCGTG 1023
QY 568 ATGACCTCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGGGAGATCACTGCCTG 627
Db 1024 AAGTTACTCAACAGCTCTTCGCCCGCTTTGACAAGCTGGCAGCCAAATACCACAGCTG 1083
QY 628 AGGATCAAGATTTGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGAGGCCCGCGGCC 687
Db 1084 AGGATCAAGATCTTAGCGACTGTTACTACTGATCTGCGGCTTGCCTGACTACCGGGAG 1143
QY 688 GACCATGCCCATGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTGTTA 747
Db 1144 GACCATGCCGTGTGCTCCATCTTATGGGGCTTGCCATGGTAGAGCCCATCTCGTACGTTG 1203
QY 748 CGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGCCGCTGCAC 807

Db 1204 CGGGAGAAGACCAGACTTGGAGTGGACATGCGGTGGGAGTGCACACAGGCATGTGCTTA 1263
QY 808 TCGCGGCTCTTTCGCTTGGGAAATGGCAGTTCCGATGTGTGGTCCAATGATGTACCCCTG 867
Db 1264 GCGGCTGCTCTGGCCAGAGCCCTGCGAGTATGATGATGTTACTACTGATGTACCGGTG 1323
QY 868 GCCAACACATGGAAGCAGGAAGCCGGGTGGCCGATCCACATCATCTCGGGCAACACTG 927
Db 1324 GCAACAAGATGAGGCTGGTGGCATCCAGGGCGGTGCACATTTCCAGAGACCATG 1383
QY 928 CAGTACTCTGAACGGGACTACGAAGTGGAGCCAGGCGGTGGTGGCAAGCCGACGCGTAC 987
Db 1384 GACTGCTGAAGGGGAGTTTGATGTGGACCTGGTGTATGGGGGCGTCCCTCGGACTAC 1443
QY 988 CTCAGGAGCAGCACATTTGAGACTTTCTCATCTCTGGGCCAGCCAGCAAGAACGAA 1043
Db 1444 CTAGATGAGAAGGGCATCGAAACCTACCTCATCATTTGCCTCCAAGCCAGAGGTGAA 1499

RESULT 15
US-10-144-771-14946
; Sequence 14946, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 14946
; LENGTH: 3158
; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-14946

Query Match 17.7%; Score 320.6; DB 6; Length 3158;
Best Local Similarity 59.5%; Pred. No. 1.5e-70;
Matches 567; Conservative 0; Mismatches 374; Indels 12; Gaps 1;

QY 79 GGCCTCTGGTGGCCCTGTGTTCTTTGTATACATGCAACACAGCTCTCTCCCCATCCGATG 138
Db 1857 GGCATAGGTACGTGCTTTTACACTCTTCGCCACCTACAGCATGCTTCCCTGCCTCTC 1916
QY 139 CGGGCTGCGCTCCTCAGCGGCTGGCCCTCTCCACCTTCGATTTGATCTGGCCTGGCAA 198
Db 1917 AACTGGGCCATCTTGGCGGCTGGGCACATCTTCTGCAAGTCCACCTTCAAGTACTC 1976
QY 199 CTTAACCGTGGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTGTTCTCT 258
Db 1977 ATACCCAGGCTAGCGGTCTTTTCCATCAACCAGGTCTTGGCCAGGTGGTGTATTATG 2036
QY 259 TGCACCAACGTCAATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCC 318
Db 2037 TGTATCAATACAGCAAGAACTTTCATCAGTTACCTTTCAGACCGTGCAGCGCCAGGCC 2096
QY 319 TTTTCAGAGACCCGAGTTACATCCAGGCCGCTCCACCTGCAGCATGAGATCGGCAG 378
Db 2097 TTCTCGAGACCCGGAGGTGTGTTGGAGCCAGGCTCCGCTTGGAGACAGAACCAAGA 2156
QY 379 CAGGAGCGGTGCTGCTGTCGGTATTGGCCCGCAGCAGTGGCCATGGAGATGAAGAAGAC 438
Db 2157 CAGGAGCGGTGCTGCTGCTGCTGCTCCCGAGGTTTGTGCTCTGGAATGATCAAGAC 2216
QY 439 ATCAACAAAAAAGAG-----ACATGTTCCACAAGATCTACATACAGAG 486
Db 2217 ATGACCAATGTGSAGGATGAGCACCTGCAGCATCAGTTCACCGCATCTACATCCATCG 2276
QY 487 CATGACAATGTACGATCCTGTTTGACAGACATTTGAGGGCTTCACAGCCTGGCATCCCG 546
Db 2277 TATGAGAAGCTCAGTATCTTTTGGCAGATGTCAAAGGATTTTACCAACCTCTCTACGACC 2336
QY 547 TGCACCTGCGCAGGAGCTGTTGATGACCTTGAATGAGCTCTTTGCGCGGTTTGACAAGCTG 606

Db 2337 TTGTCTGCTCAGGAGCTGGTCAGGATGCTCAACGAACCTCTTTGGCAGATTCGACCGGCTG 2396
Qy 607 GCTGGGAGAAATCACTGCTCAGGATCAAGATCTTTGGGGACTGTCTACTACTGTGTGTCA 666
Db 2397 GCCCATGACATCACTGTCTTCGATTTAAATCTCGGGGACTGCTACTACTGTGTGTCT 2456
Qy 667 GGGCTGCCGGAGGCCGGCGGACCATGCCCACTGCTGTGTGGAGATGGGGTAGACATG 726
Db 2457 GGAATGCTGAGCCCGCGCGGACACGCTCATTTGCTGTGTGAAATGGGCTCAGCATG 2516
Qy 727 ATTGAGGCCATCTCGCTGGTACGTGACAGGTGTGAATGTGAACATGCGCGTGGGC 786
Db 2517 ATCAAAACTATACAGGTTTGTGAGATCCAGAACGAAGCACGATGTTGACATCCGAATTGGA 2576
Qy 787 ATCCACAGCGGCGCGTGCACCTGGCGGTCTTGGCTTGGGAAATGSCAGTTTCGATGTG 846
Db 2577 ATCCATTACAGTTCTGTGCTATGTGGTGTGTGGCCCTGAGAAATGGCAGTTTGAATGC 2636
Qy 847 TGGTCCAATGATGTACCCCTGGCCAAACCATGGAAGCAGGAAGCCGGCTGGCCGCATC 906
Db 2637 TGGTCTTGGGATGTGGACATAGCAACAAGCTTGAGTCTGGAGGAATCCCTGGGAGGATT 2696
Qy 907 CACATCACTCGGCAACACTGCAGTACCTGAACGGGACTACGAAGTGGAGCCAGGCCGT 966
Db 2697 CACATTTCTAAAGCCACCCCTGGATTGCTCAATGGTGACTATAACGTGGAAGAGGGTCAC 2756
Qy 967 GGTGCAAGCGCAACGCGTACCTCAAGGAGCAGCACATTGAGACTTTCTCTCAT 1019
Db 2757 GGGAAAGAGAGAACGAAATCTTGAGGAAGCATACATAGAGACCTATTGTAT 2809

Search completed: February 23, 2003, 07:48:52
Job time : 376.092 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 22:03:04 ; Search time 2279.13 Seconds
(without alignments)
12876.070 Million cell updates/sec

Title: US-09-750-240-3
Perfect score: 1812
Sequence: 1 gttacgtgtgtctggcat.....gcagcttctcgtggttc 1812

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	593.4	32.7	676	12	BE840188
2	540.2	29.8	581	13	BG993320
3	463.4	25.6	565	12	BG872335
4	442.4	24.4	525	13	BM090325
5	418.6	23.1	682	14	BQ180663
6	393.2	21.7	442	9	AI905602

C	7	393.2	21.7	466	9	AI905641
C	8	392.8	21.7	453	12	BE838164
C	9	387.8	21.4	417	12	BE840138
	10	377	20.8	939	13	BI873142
	11	372	20.5	1016	14	BQ881496
	12	361.8	20.0	625	12	BF369868
C	13	347.2	19.2	611	12	BG004182
C	14	345.8	19.1	673	14	BQ370134
C	15	342.4	18.9	367	10	BE001572
	16	332.2	18.3	1039	14	BM811640
	17	316.6	17.5	2661	11	BC028085
	18	311	17.2	567	13	BI739363
	19	296.8	16.4	1076	13	BM548851
	20	293.6	16.2	515	14	BQ370137
	21	289.4	16.0	944	9	AL558455
	22	285.4	15.8	770	13	BI562576
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	25	276.6	15.3	630	14	BQ442310
	26	271.2	15.0	813	12	BF582692
	27	260	14.3	729	13	BI823791
	28	247.8	13.7	627	10	BB616087
	29	243.4	13.4	834	14	BM963626
	30	238.6	13.2	721	10	BE546643
	31	232.4	12.8	1075	12	BF982389
	32	227	12.5	600	13	BI118754
	33	223	12.3	243	12	BF817426
	34	218.4	12.1	233	12	BF988269
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	36	216.6	12.0	377	9	AI914903
	37	209.8	11.6	517	12	BG731141
C	38	208.6	11.5	464	9	AA672242
	39	201.2	11.1	431	10	BB863676
	40	199.8	11.0	448	9	AI218521
C	41	196.2	10.8	583	10	BE504143
	42	190.8	10.5	575	12	BG295901
	43	182.8	10.1	554	13	BJ104077
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ALIGNMENTS

RESULT 1	BE840188	676 bp	linear	EST 22-SEP-2000
LOCUS	BE840188	QV0-FN0181-100800-335-d08	FN0181	Homo sapiens cdna, mRNA sequence.
DEFINITION	QV0-FN0181-100800-335-d08	FN0181	Homo sapiens	cdna, mRNA sequence.
ACCESSION	BE840188			
VERSION	BE840188.1	GI:10272566		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
REFERENCE	1 (bases 1 to 676)			
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsumura, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.			
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	97 (7)	3491-3496	(2000)
MEDLINE	20202663			
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-01q, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001			

Plate: 97 row: A column: 9 Seq primer: ATTAGGTGCACATATAG. Location/Qualifiers 1. 525 /organism="Bos taurus" /db_xref="taxon:9913" /clone_lib="MARC 3BOV" /tissue_type="pooled" /lab_host="DH10B" /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle." 112 a 162 c 133 g 117 t 1 others									
Query Match 24.4%; Score 442.4; DB 13; Length 525; Best Local Similarity 91.4%; Pred. No. 2.2e-95; Matches 480; Conservative 0; Mismatches 42; Indels 3; Gaps 1;									
QY	90	CCCTGTGTTCTTTGTATACATCGCATACAGCTCCCTCCCATCCGGATCGGGCTGCCGT	149						
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QY	150	CCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATCTTGGCTGGCAACTTAACCGTGG	209						
Db	61	CTTCAGCGGCTGGGCTCTCCACCTGCACTTTGGCTTGGCTGGCAGCTCAACGGTGG	120						
QY	210	TGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTCTCTGTCACCAACGT	269						
Db	121	TGAGGCTTCTCTGGAAGCAGCTTGGAGCAACATGCTGCTGTTCTCTGCAACATGT	180						
QY	270	CATTAGCATCTGCACACACTATCAGCAGAGGTGTCTCAGCGCCAGGCGCTTTTCAGGAG	329						
Db	181	CATTGGCATCTGCACACACTATCCGCTGAGGTGTCTCAGCGCCAGGCACTTTCAAGAG	240						
QY	330	CCGCAGTTACATCCAGCGCGGCTCCACCTGCAGCATGAGAAATCGGCAGGAGCGGT	389						
Db	241	CCGCGGTTACATCCAGCGCGGCTGACCTGCAGCATGAGAAACCGCAGCAGGAGCGGT	300						
QY	390	GTCTGTCTGCTGTTATGCCCGCAGCAGCTTGCCATGGAGATGAAAGAGACATCAACAAA	449						
Db	301	GTCTGTCTGCTGTTGCGCCAGCATGTTGCCATGGAGATGAAAGAGACATCAACAAA	360						
QY	450	AAAAGAAGAC---ATGTTCCACAAGATCTACATACAGAGCATGACAATGTACAGCATCCT	506						
Db	361	AAAAGAAGACATGATGTTTTCATTAAGATCTACATCCAGAACGACGACAATGTACAGCATCCT	420						
QY	507	GTTTGCAGACATTTGAGGGCTTACAGCGCTGCATCCAGTGCACCTCGCGCAGGAGTGGT	566						
Db	421	GTTTGGGACATTTGAAGGCTTACAGCGCTGCCGCTCCAGTGCACGCGCANGAGTGGT	480						
QY	567	CATGACCTGAATGAGCTCTTTCCCGGTTTGACAGCTGGCTGC 611							
Db	481	CATGACCTGAACGAGCTCTTTCCCGGTTTGACAGCTGGCTGC 525							
RESULT 5 B0180663 LOCUS DEFINITION UI-M-EX0-bxb-n-18-0-UI.r1 NIH_BMAP_EX0 Mus musculus cDNA clone IMAGE:5706065 5', mRNA sequence. ACCESSION VERSION KEYWORDS SOURCE ORGANISM B0180663 682 bp mRNA linear EST 30-APR-2002 B0180663 B0180663 B0180663.1 GI:20356155 EST. house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 682) NIH-MGC http://mgi.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)									
Contact: Robert Strausberg, Ph.D. Email: cgapps@mail.nih.gov Tissue procurement: Dr. James Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov This clone was contributed by the Brain Molecular Anatomy Project (BMAP) Seq primer: pYX-5. Location/Qualifiers 1. .682 /organism="Mus musculus" /strain="C57BL/6" /db_xref="taxon:10090" /clone="IMAGE:5706065" /clone_lib="NIH_BMAP_EX0" /tissue_type="whole brain" /dev_stage="embryo 15.5 dpc" /lab_host="DH10B (T1 phage resistant)" /note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail , is GTGCGTGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemlin chin, Ph.D., program coordinator." BASE COUNT 142 a 195 c 187 g 156 t ORIGIN Query Match 23.1%; Score 418.6; DB 14; Length 682; Best Local Similarity 77.9%; Pred. No. 1.2e-89; Matches 529; Conservative 0; Mismatches 146; Indels 4; Gaps 2;									
QY	146	CGTCTCTCAGCGGCTTCTCCACCTTGCATTTGATCTTTGGCTGGCACTTAACC	205						
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QY	206	GTGCTGATGCTTCTCTGGAACAGCTCGTGCCCAATGTGCTGTTCTCTGCACCA	265						
Db	61	CCAGGACCAAGTTTCTGCTGAAACAGCTTGTCTCCAATGTCTCTCTCTGCACCA	120						
QY	266	ACGTCAATAGCATCTGCACACACTATCCAGCAGAGTGTCTCAGCGCGGCTTTTCAGG	325						
Db	121	ACATTGTGGTGTGCACTCACTCCACGTGAGGTCTCCAGAGACAGCGCTTCCAGG	180						
QY	326	AGACCCGCGATTTACATCCAGGCGGCTCCACCTGTCAGCATGAGAATCGCAGCAGGC	385						
Db	181	AGACCCGCGAGTGTATCAGGCTCGGCTCCATTCACCGCGGAGAACACACAGCAGC	240						
QY	386	GGCTGCTGCTGCGGTATTTGCCCGCAGCAGCTTGCCTATGGAGATGAAGAAGACATCAAC	445						
Db	241	GTCTCTGCTGCTGCTCTTCCCGCTCATGTTGCCATGGAGATGAAGAAGCAGCATCAACG	300						
QY	446	CAAAAANAAGA---CATGTTCCACAAGATCTACATACAGAAGCATGACAATGTTCAGCA	502						
Db	301	CCNAGCAGGAGATATGATGTTCCACAAGATCTACATCCAGAAGCATGACAATGTGAGCA	360						
QY	503	TCTGTTTTCAGACATTTAGGGGCTTCCAGCAGCTGGCATCCCACTGCCAGTCCCGCAGCAGC	562						
Db	361	TCTGTTTTCAGACATCGAGGGCTTCCAGCAGCTGGCTTCCCACTGCCAGTGTACTGCCCAAGAC	420						
QY	563	TGTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAAATCACT	622						

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Db 421 TGGTCATGACCCCTCAATGAGCTCTTCGCCCGCTTTGACAAAGTTGGCTGCGGAGAACTCACT 480
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Db 481 GTTTACGGATTAAGATCTCGGGATGTTACTACTGCTGCTCGGGCTGCTCGAAGCCA 540
|||||
QY 683 GGGCCGACCATGCCCCTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGC 742
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QY 803 TGCACGTGCGGCTCTTTGG 821
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Db 561 T-AACTGCGGTGCTCTTGG 678
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RESULT 6
AI905602/c
LOCUS AI905602 442 bp mRNA linear EST 30-MAR-2000
DEFINITION CM-BT094-050299-173 BT094 Homo sapiens cdna, mRNA sequence.
ACCESSION AI905602
VERSION AI905602.1 GI:6495989
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 442)
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=CM&t2=CM-BT094-173.html
&t3=050299&t4=1)
Seq primer: puc 18 forward.
Location/Qualifiers
1..442
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT094"
/sex="female"
/dev_stage="Adult"
/Note="Organ: breast; Vector: puc18; Site:1; SmaI; Site:2;
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 102 a 116 c 136 g 88 t
ORIGIN

Query Match 21.7%; Score 393.2; DB 9; Length 442;

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Best Local Similarity 96.7%; Pred. No. 1.4e-83;
Matches 412; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY 1069 CTGCAGCGGACTCGGGCCAACTCCATGCAAGGC-TGATGCCGCGATGGTTCCGTGATCG 1127
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Db 432 CAGCAGCGGACTCGGGCCAACTCCATGCAAGGCCTTGATGCCGCGCTGGTTCCGTGATCG 373
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QY 1128 TGCCTTCTCCCGGACCAAGGACTCCAGGCCTTCGCCAGATGGGCATTGATATCCAG 1187
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Db 372 TGCCTTCTCCCGGACCAAGGACTCCAGGCCTTCGCCAGATGGGCATTGATATCCAG 313
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QY 1188 CAAACAGAACCGGGCCACCAAGATGCCCTGAACCTGAGGATGAGTGGATGCTTCT 1247
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Db 312 CAAACAGAACCGGGCCACCAAGATGCCCTGAACCTGAGGATGAGTGGATGCTTCT 253
|||||
QY 1248 GAGCGGTGCCATCGATGCCCGCAGCATTTGATCAGCTGCGGAAGGACCATGTGCGCGGTT 1307
|||||
Db 252 GAGCGGTGCCATCGATGCCCGCAGCATTTGATCAGCTGCGGAAGGACCATGTGCGCGGTT 193
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QY 1308 TTTGCTCACCTTCCAGAGAGAGGATTTTGAAGAAGTACTCCCGGAAGTGGATCCCG 1367
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Db 192 TCTGCTCACCTTCCAGAGAGAGGATCTTGAGAAGAAGTACTCCAAAAGGTGGATCCCG 133
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QY 1368 CTTCCGAGCCTTACGTTGCTGTGCCCTGTTGGTCTTCTGCTTCATCTGCTTCATCCAGCT 1427
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Db 132 CTTCCGAGCCTTACGTTGCTGTGCCCTGTTGGTCTTCTGCTTCATCTGCTTCATCCAGCT 73
|||||
QY 1428 TCTAATTTTCCACACATCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCT 1487
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Db 72 TCTCATCTTCCACACATCCACCTGATGCTTGGGATCTATGCCAGCATCTTCTCCGCTGCT 13
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QY 1488 GCTAAT 1493
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Db 12 GGAAAT 7
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RESULT 7
AI905641/c
LOCUS AI905641 466 bp mRNA linear EST 30-MAR-2000
DEFINITION CM-BT094-110299-173 BT094 Homo sapiens cdna, mRNA sequence.
ACCESSION AI905641
VERSION AI905641.1 GI:6496028
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 466)
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=CM&t2=CM-BT094-173.html
&t3=110299&t4=1)
Seq primer: puc 18 forward.
Location/Qualifiers
1..466
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/db_xref="taxon:9606"
/clone_lib="BT094"
/sex="female"
/dev_stage="Adult"
/Note="Organ: breast; Vector: puc18; Site:1; SmaI; Site:2;
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 102 a 116 c 136 g 88 t
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Query Match 21.7%; Score 393.2; DB 9; Length 442;

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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/sex="female"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 107 a 125 c 143 g 91 t
ORIGIN
Query Match 21.7%; Score 393.2; DB 9; Length 466;
Best Local Similarity 96.7%; Pred. No. 1.4e-83;
Matches 412; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
QY 1069 CTCACGCGACTCGGCGCAACTCCATCGAAGGCG-TGATGCCGCGATGGTTCCTGATCG 1127
Db 456 CAGCAGCGACTCGGCGCAACTCCATCGAAGGCGTTGATGCCGCGCTGGGTTCTCTGATCG 397
QY 1128 TGCTTCTCCGCGACCAAGACTCCAAAGGCTTCCGCCAGATGGGCAATTGATGATTCACG 1187
Db 396 TGCTTCTCCGCGACCAAGACTCCAAAGGCTTCCGCCAGATGGGCAATTGATGATTCACG 337
QY 1188 CAAAGACAACCGGGGACCCCAAGATGCCCTGAACCTGAGGATGAGTGGATGAGTTCCT 1247
Db 336 CAAAGACAACCGGGGACCCCAAGATGCCCTGAACCTGAGGATGAGTGGATGAGTTCCT 277
QY 1248 GAGCGGTGCATCGATGCCGCGAGCATTTGATCAGCTGCCGAGGACCATGTGCGCCGGTT 1307
Db 276 GAGCGGTGCATCGATGCCGCGAGCATTTGATCAGCTGCCGAGGACCATGTGCGCCGGTT 217
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QY 1368 CTTCGAGGCTAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1427
Db 156 CTTCGAGGCTAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 97
QY 1428 TCTAATTTTCCACACTCCACCTGATGCTTGGGATTTATGCGAGCATCTTCTGCTGCT 1487
Db 96 TCTCATCTTCCACACTCCACCTGATGCTTGGGATCTATGCCAGCATCTTCCCGCTGCT 37
QY 1488 GCTAAT 1493
Db 36 GGAAAT 31
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LOCUS BE838164 453 bp mRNA linear EST 22-SEP-2000
DEFINITION CM1-FN0105-200600-280-f02 FN0105 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE838164
VERSION BE838164.1 GI:10270542
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 453)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
```

20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM1-FN0105-200
600-280-f02&t3=2000-06-20&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 453.
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone_lib="FN0105"
/dev_stage="Adult"
/note="Organ: prostate_normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT 75 a 141 c 134 g 103 t
ORIGIN
Query Match 21.7%; Score 392.8; DB 12; Length 453;
Best Local Similarity 96.7%; Pred. No. 1.7e-83;
Matches 433; Conservative 0; Mismatches 12; Indels 3; Gaps 3;
QY 881 AGCAGAGACCGGGCTGGCGCATCCACATCACTCGGGCAACACTGCAGTACTCTGAACG 940
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QY 941 GGGACTACGAGTGGAGCGCGGCTGGGCAAGCGCAACGCTACCTCAAGGAGCAGC 1000
Db 393 GGGACTACGAGTGGAGCGCGGCTGGGCAAGCGCAACGCTACCTCAAGGAGCAGC 334
QY 1001 ACATTGAGACTTTTCCTCATCTCTGGGCGCCAGCAGAAAGAGAGAAAGGAGCATGC 1060
Db 333 ACATTGAGACTTTTCCTCATCTCTGGGCGCCAGCAGAAAGAGAGAGAGGAGCATGC 274
QY 1061 TGCCCAAGCTGCAGCGGACTCGGGCCAACTCCATGAAAGGGCTGATGCCCGGATGGTTTC 1120
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QY 1121 CTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAAGGCTTCGCCAGATGGGATTTGATG 1180
Db 213 CTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAAGGCTTCGCCAGATGGGATTTGATG 154
QY 1181 ATTCCAGCAAGAACACACCGGGGCAACCAAGATGCCCTGAACCTGAGGATGAGTGGATG 1240
Db 153 ATTCCAGCAAGAACACACCGGGGCAACCAAGATGCCCTGAACCTGAGGATGAGTGGATG 94
QY 1241 AGTTCCTGAGCCGTGCCATCGATGCGCGCAGCATTCAGTTCGCGAAGGAGGACCATGTGC 1300
Db 93 AGTTCCTGAGCCGTGCCATCGATGCGCGCAGCA-TGATCAGCTGCGGAAGGA-CATGTGC 36
QY 1301 GCCGGTTTTTGTCTACCTTCCAGAGAGA 1328
Db 35 GCC-GTTTCTGCTACCTTCCAGAGAGA 9
RESULT 9
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LOCUS BE840138 417 bp mRNA linear EST 22-SEP-2000
DEFINITION QV0-FN0181-280700-321-d07 FN0181 Homo sapiens cDNA, mRNA sequence.

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ACCESSION BE840138.1 GI:10272516
VERSION BE840138.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 417)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=st2-QV0-FN0181-280
700-321-d07st3-2000-07-28&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 415.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0181"
/dev_stage="Adult"
/note="Organ: prostate.normal; Vector: puc18; Site_1: SmaI
products derived from ORESTES PCR (U.S. Letters Patent
Application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT 88 a 119 c 124 g 86 t
ORIGIN
Query Match 21.4%; Score 387.8; DB 12; Length 417;
Best Local Similarity 97.8%; Pred. No. 2.6e-82;
Matches 404; Conservative 0; Mismatches 7; Indels 2; Gaps 1;
QY 1033 CAGAAACGGAAGAGGAGAGGATGCTGGCCAGCTGAGCGGATCGGGCCAACTCC 1092
Db 417 CAGAAACGGAAGAGGAGAGGATGCTGGCCAGCTGAGCGGATCGGGCCAACTCC 358
QY 1093 ATGGAAGGCTGATGCGCGCATGGGTTCTGATGCTGCTTCTCCCGGACCAAGCTCC 1152
Db 357 ATGGAAGGCTGATGCGCGCATGGGTTCTGATGCTGCTTCTCCCGGACCAAGCTCC 298
QY 1153 AAGGCCCTCCGCCAGATGGGCATGATGATCCAGCAAGACAAACCGGGGACCCCAAGAT 1212
Db 297 AAGGCCCTCCGCCAGATGGGCATGATGATCCAGCAAGACAAACCGGGGACCCCAAGAT 238
QY 1213 GCCTGAACCCCTGAGGATGAGGTGAGTTCCTGAGCCGCTGCGCATGATGCGCCGAGC 1272
Db 237 GCCTGAACCCCTGAGGATGAGGTGAGTTCCTGAGCCGCTGCGCATGATGCGCCGAGC 178
QY 1273 ATTGATCAGCTGCGGAGGACCATGCGCGGGTTTTTGTCTACCTTCACGATCCAGAGAGAT 1332
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QY 1393 CTGTTGCTCTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTC 1445
Db 57 CTGTTGCTCTCTGCTTCATCTGCTTCATC--GCTTCTCATCTTCCACACTC 7
RESULT 10
BI873142
LOCUS 603397792F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5401415 5',
DEFINITION mRNA sequence.
ACCESSION BI873142.1 GI:16046817
VERSION BI873142
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 939)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM12023 row: h column: 24
High quality sequence stop: 638.
FEATURES
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/db_xref="taxon:10090"
/clone="IMAGE:5401415"
/clone_lib="NIH_MGC_94"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 208 a 271 c 256 g 204 t
ORIGIN
Query Match 20.8%; Score 377; DB 13; Length 939;
Best Local Similarity 75.6%; Pred. No. 1.1e-79;
Matches 521; Conservative 0; Mismatches 160; Indels 8; Gaps 4;
QY 133 CGCATGCGGCTCGGCTCCAGCGGCTGCGGCTCTCCACCTTGCTTCATCTTGCC 192
Db 12 CGCATGAGGCTCGGCTGCTCAGCGGCTGCTTCTGCGGCTCTCCACCTTGCTCATCTCT 71
QY 193 TGGCAACTTAACCGTGTGATGCTTCTCTCTGGAAGCAGCTCGGTGGCAATGTGCTGTG 252
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QY 253 TTCTCTGCAACCACTGATGATCTGACACACTATCCAGCAGAGGTTGTTCTCAGGC 312
Db 132 TTCTCTGCAACCACTGATGATGCTGCACTCACTACCCAGCTGAGGTCTCCAGAGA 191
QY 313 CAGGCTTTTCAGGAGACCCCGAGTTACATCCAGCCCGGCTCCACCTGCAGCATGAGAT 372
Db 192 CAGGCTTTTCAGGAGACCCCGAGTTACATCCAGCTCGGCTCCATTCACGCGGGAAC 251
QY 373 CGGACGAGGAGCGGCTGCTGCTGCTATTGTCGCCCGCAGCAGCTTGCCATGGAGATGAAA 432

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Db	252	CAGCAACAGGAGCGTCTCTGCTCTGCTCTCCCGTCAATGTTGCCATGGAGATGAAA	311
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Db	312	GCAGACATCAACGCAAGCAGGAGGATATGATGTTCCACAAGATCTACATCCAGAAGCAT	371
Qy	490	GACAAATGTCAGCATCCCTGTTTTCAGACACATTCAGAGGCTTACCACCGCTGGCATCCAGTGC	549
Db	372	GACAATGTGACATCCCTGTTTTCGTCGATCATGAGGCTTCCACACCGCTGGCTCCCACTGT	431
Qy	550	ACTCGGAGGAGCTGGTCATCACCTGAATGAGCTCTTTGCCCGCTTTTGACAAGCTGGCT	609
Db	432	ACTGCCAAGAACTGGTCATGACCTCAATGAGCTCTTCGCCCGCTTTTGACAAGTTGGCT	491
Qy	610	GCGGAGAACTACTGCTGAGGATCAAGATCTTTGGGGGACTGTTTACTACTGTGTCTCAGGG	669
Db	492	GCGGAGAACTACTGTTTACGGATTAAAGATCTCTCGGGATGTTTACTACTGCTGCTCGGG	551
Qy	670	CTGCCGAGGCGCGCGGACCATGCCACATGCTGTGTGG - AGATGGGGGTAGACATGAT	728
Db	552	CTGCTGAAGCCAGAGCCGA - CATGCCACATGCTGCGTGAAGATGGGAATGGACATGAT	610
Qy	729	TGAGGCCATCTCGTGTGATGAGGTGACAGGTGTGAATGTG --- AACATGCGCGTGGG	785
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Qy	786	CATCACAGCGGCGCGTGCATCTCGCGGG 814	
Db	671	AATTCACAGCGGACGAGTACACCTGCG 699	
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ACCESSION	clone IMAGE:6182035 5', mRNA sequence.		
VERSION	BQ881496		
KEYWORDS	BQ881496.1 GI:22273504		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
COMMENT	1 (bases 1 to 1016) NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-femail.nih.gov Tissue Procurement: Dr. James R. Lupski cDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAMI3567 row: f column: 20 High quality sequence start: 31 High quality sequence stop: 645. Location/Qualifiers 1..1016 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="IMAGE:6182035" /tissue_type="dorsal root ganglion" /sex="male" /tissue_type="dorsal root ganglia" /dev_stage="adult, 36 yr" /lab_host="DH10B" /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors:		
FEATURES	source		

5'-TCGACCACCGGTCGG-3' and
5'-GACTAGTCTAGAGCGGAGCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies".

BASE COUNT 186 a 297 c 268 g 265 t
ORIGIN

Query Match 20.5%; Score 372; DB 14; Length 1016;
Best Local Similarity 98.7%; Pred. No. 1.8e-78;
Matches 375; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1433 TTTTCCACACTCCACCGCTGATGCTGGGATTTATGCCAGCATCTTCCTGCTGTGCTAA 1492
Db 42 TCTTCCACACTCCACCGCTGATGCTGGGATCTATGCCAGCATCTTCCTGCTGTGCTAA 101

QY 1493 TCACCGTCTCATCTGCTCTGTACTCTCTGTGTTCTCTCTCCCTAAGCCCTGCAAC 1552
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QY 1553 GTCTGTCCCGCAGCATTTCCGCTCACGGGCACATAGCACCGCATTTGGCATCTTTTCCG 1612
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Db 222 TCCTGTCTTGTGTTTACTTCTGCCATTGCCACATGTTCACTGTAAACACACCCCCATAC 281

QY 1673 GGAGCTGTGACGCCGGATGCTGAATTTAAACACCTGCTGACATCACTGCCCTGCCACCTGC 1732
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Db 342 AGCAGCTCAATTACTCTCTGGCCCTGGATGCTCCCTGTGTGAGGGCACCATGCCACCT 401

QY 1793 GCAGCTTTCCTGAGGTTGTC 1812
Db 402 GCAGCTTTCCTGAGTACTTC 421

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DEFINITION OY4-CN0122-250900-424-c07 GN0122 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF369868
VERSION BF369868.1 GI:11331893
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 625)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

Db 370 TCTTCCCGCTCATGTGGCATGGAGATCAAGCAGACATCAACGCCAAGCAGGAGGATA 311
QY 460 --ATGTTCCACAAGATCTACATACAGAAGCATGACAAATGTCAGCATCCTGTTTGGCAGACA 517
Db 310 TGATGTTCCATAAGATTTACATCCAGAATCATGACAACTGAGCATCCTGTTTGGCTGACA 251
QY 518 TTGAGGCGTTCCACAGCCTGGCAGTCCAGTGCACCTGCGCAGGAGCTGGTTCATGACCTGA 577
Db 250 TCGAGGCGTTCCACAGCCTGGCGTCCAGTGCACCTGCGCAGGAGCTGGTTCATGACCTGA 191
QY 578 ATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAGTCACTGCTGAGAGATCAAGA 637
Db 190 ACGAGCTCTTCGCGCGCTTTGACAAGCTGGCGCAGAGAACTCACTGTTACGTATTAA 131
QY 638 TCTTGGGGACTCTTACTACTGTCTCAGGGCTGCGGAGGCGCGCGGCGGAGCAGCATGCC 697
Db 130 TCTTGGGGATGTTATTACTGCGTCTCGGGGCTGCGTGAAGCAAGGCTGACACGCGCC 71
QY 698 ACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTGGTACG 749
Db 70 ACTGCTGTGTGGAGATGGGCAT--GACATGATCGA--GCCATCTGTTGGTCCG 21

RESULT 14
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DEFINITION BQ370134 QV4-GN0122-250900-424-a04 GN0122 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ370134.1 GI:21045648
VERSION BQ370134.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 673)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=QV4-GN0122-250900-424-a04&t3=2000-09-25&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 556.
Location/Qualifiers
1. .673
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0122"
/dev_stage="Adult"
/note="Organ: placenta_normal; Vector: puc18; Site:1: SmaI ; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No.196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were

FEATURES
source

BASE COUNT 144 a 171 c 214 g 144 t performed under low stringency conditions."
ORIGIN
Query Match 19.1%; Score 345.8; DB 14; Length 673;
Best Local Similarity 76.4%; Pred. No. 3.3e-72;
Matches 438; Conservative 0; Mismatches 132; Indels 3; Gaps 1;
QY 165 CPTCTCCACCTTCGATTTGATCTTGGCCTGGCAACTTAACCGTGGTGCCTTCCTCTCTG 224
Db 590 CTTGTCCGCTCCACCTGGCCATCGCCCTGCCACCAAGCCCGAGGACAGTTCCTGCT 531
QY 225 GAAGCAGCTCGGTGCCAATGTGCTGTCTCTCTGCACCAAGCTCATAGCATCTGCAC 284
Db 530 GAAGCAGCTGTCTCCAATGTTCTCATTTTCTCTGCACCAACATCGTGGTGTCTGCAC 471
QY 285 ACATATTCAGCAGAGAGTGTCTCAGCGCCAGGCTTTTCAGGAGACCCGCGAGTTACATCCA 344
Db 470 CCACTATCGGGCTGAGGTCTCCAGAGACAGAGGCTTTCCAGGAGACCCGAGAGTGCATCCA 411
QY 345 GGCCCGGCTCCACCTCGACATGAGAATCGGACAGGAGCGCTGCTGCTGTGCTGCT 404
Db 410 GGCCTGCTCCACTCGCAGCGGAGAACACGACAGAGAGAGGCTCTGCTGTCTGTCTCT 351
QY 405 GCCCAGCAGCTTGCCATGGAGATGAAGAAGACATCAACACAAAAAAGAACAC---AT 461
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QY 462 GTTCCACAGATCTACATACAGAGCATGACATGTCAAGTCTGTTTGCACACATTTGA 521
Db 290 GTTCCATAAGATTTACATCCAGAAACATGACAACTGAGCATCTCTGTTGCTGACATCGA 231
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LOCUS BE001572 PM2-BN0080-180400-004-g02 BN0080 Homo sapiens cDNA, mRNA sequence.
DEFINITION BE001572
ACCESSION BE001572
VERSION BE001572.1 GI:8261805
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 367)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics

Search completed: February 23, 2003, 04:21:09
Job time : 2292.13 secs

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Run on: February 22, 2003, 20:53:24 ; Search time 8776.51 Seconds
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11768.450 Million cell updates/sec
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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39: gb_vl.*	39: gb_vl.*	39	495.8	14.0	3261	6	AX457036	14.0	3261	AX457036 Sequence	AX457036	Sequence	AX457036 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS AR174473
DEFINITION Sequence 5 from patent US 6306830.
ACCESSION AR174473
VERSION AR174473.1 GI:17914793
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3549)
AUTHORS Hammond H.Kirk., Insel, P.A., Ping, P., Post, S.R. and Gao, M.
TITLE Gene therapy for congestive heart failure
JOURNAL Patent: US 6306830-A 5 23-OCT-2001;
FEATURES Location/Qualifiers

Pred. No. is the number of results predicted by chance to have a

[illegible]

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Db	3361	GTCCCGGACCGAATCC	AGGTCAGCCAGCGACCTGTACACAGGTTCTAGCTGCCAAGGGCTAC	3420		
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Db	3421	CAGCTGGAGTGTGAG	GGGGTGGTCAAGGTGAAGGGCAAGGGGGAGATGACCACCTACTTC	3480		
Qy	3481	CTCAATGGGGCCCCAG	CAGTAAACAGGGCCCCAGCCACAAATTCAGCTGAAGGGACCAAG	3540		
Db	3481	CTCAATGGGGCCCCAG	CAGTAAACAGGGCCCCAGCCACAAATTCAGCTGAAGGGACCAAG	3540		
Qy	3541	GTGGGCAC	3549			
Db	3541	GTGGGCAC	3549			
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DEFINITION	Sequence 5 from Patent WO0148164.					
ACCESSION	AX189761					
VERSION	AX189761.1		GI:15143135			
KEYWORDS	human.					
SOURCE	ORGANISM	'Homo sapiens				
REFERENCE		Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE		1 (bases 1 to 3549)				
JOURNAL		Gene therapy for congestive heart failure				
		Patent: WO 0148164-A 5 05-JUL-2001;				
		THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)				
FEATURES		Location/Qualifiers				
source		1. 3549				
BASE COUNT		699 a 1025 c 1061 g 764 t				
ORIGIN						
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Db	61	GAACGAATGGCAGAACG	TTTCGGCGCCGTGGCACTCGGGCAGGTGGCTCTGGACG	120		
Qy	121	CCCGCTATATGAGT	GTGCTCCGGGATGCAGAGCCACCCAGCCACCCCTGCGGGCCCC	180		
Db	121	CCCGCTATATGAGT	GTGCTCCGGGATGCAGAGCCACCCAGCCACCCCTGCGGGCCCC	180		
Qy	181	CCTCGGTGCCCT	TGGCAGGATGACCCCTTCATCCGAGGGCGGCCAGGCAAGGGCAAG	240		
Db	181	CCTCGGTGCCCT	TGGCAGGATGACCCCTTCATCCGAGGGCGGCCAGGCAAGGGCAAG	240		

QY 241 GAGCTGGGCTGGGCACTGGCCCTCGGGCTTCGAGCATACCGAGTGACAAACGACGG 300
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Db 1381 CGTGAGGTGACAGGTGTGAATGTGAACATGCGGTGGGATCCACAGCGGGCGCTGCAC 1440
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QY 1621 CTCAAGGAGCAGCACATTTGAGACTTTCTCTATCTCTGGGCGCCAGCCAGAAACGAAAGAG 1680
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Db 1801 ATGGGCTTGTGATTTCCAGCAAAAGAACACCGGGGACCAAGATGCCCTGAAACCTTGAG 1860
QY 1861 GATGAGGTGGATGAGTTCCTGAGCCGTCATCGATGTCGCCGAGCATGATCAGCTGCGG 1920
Db 1861 GATGAGGTGGATGAGTTCCTGAGCCGTCATCGATGTCGCCGAGCATGATCAGCTGCGG 1920
QY 1921 AAGGACCATGTGGCGGTTTGTGCTACCTTCCAGAGAGAGGATTTTCAGAGAAGTAC 1980
Db 1921 AAGGACCATGTGGCGGTTTGTGCTACCTTCCAGAGAGAGGATTTTCAGAGAAGTAC 1980
QY 1981 TCCCGAAGGTGGATCCCGCTTCGGAGCTAGTGTGCCCTGTGCCCTGTGTGCTTCTGTC 2040
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Db 2041 TTTATCTGCTTATCCAGCTTCTAATTTTCCACACTCCACCTGATGCTTGGGATTTAT 2100
QY 2101 GCAGCATCTTCTGCTGCTGCTAATCAGCTGCTGATCTGTGCTGTCTGTCTCTGCTGCT 2160
Db 2101 GCAGCATCTTCTGCTGCTGCTAATCAGCTGCTGATCTGTGCTGTCTGTCTCTGCTGCT 2160
QY 2161 TCTCTGTTCCCTTAAGGCCCTGCAACGTCTGTCCCGCAGCATTTGCGGCTCACGGGACAT 2220
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QY 2221 AGCAGCGAGTTGGGATCTTTTCCGCTGCTGTGTTTACTTCTGCCATTTGCCAACATG 2280
Db 2221 AGCAGCGAGTTGGGATCTTTTCCGCTGCTGTGTTTACTTCTGCCATTTGCCAACATG 2280
QY 2281 TTTACCTGTAAACACACACCCCATACGAGCTGTGACGCGCGGATGCTGAATTTAACACCT 2340
Db 2281 TTTACCTGTAAACACACACCCCATACGAGCTGTGACGCGCGGATGCTGAATTTAACACCT 2340
QY 2341 GGTGACATCACTGCTGCGCACCTGACAGCTCAATTTACTTCTTGGGCTTGGATGCTCCC 2400
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QY CTGAGTCTCTTGCCAGCTCTGTCTTCCACATCAGCAGCATCGGAAGTTGGCCATG 2520
Db CTGAGTCTCTTGCCAGCTCTGTCTTCCACATCAGCAGCATCGGAAGTTGGCCATG 2520
QY ATCTTTGTCTTGCGGCTCATCTATTTTGGTGTCTCTTCTGCTGGTCCCGCAGCGCCATC 2580
Db ATCTTTGTCTTGCGGCTCATCTATTTTGGTGTCTCTTCTGCTGGTCCCGCAGCGCCATC 2580
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QY GATGGCTGACGTCTCCAGCTGAGGAGGTGCGCTCAATATATGACCCCTGTGATT 2700
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QY GCATACACCGGAGGTGCTGCATACATCTGCCCAAGGACGTGGCGGCCACTTCTCTG 2880
Db GCATACACCGGAGGTGCTGCATACATCTGCCCAAGGACGTGGCGGCCACTTCTCTG 2880
QY GCCCGGAGCGCGCAATGATGAACCTACTATCAGTCGTGTGAGTGTGGTGTATTG 2940
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Db CAGCTGAGTGTGAGGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACCACTACTTC 3480
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|||||

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QY 3541 GTGGGCACT 3549
Db 3541 GTGGGCACT 3549
RESULT 3
AX189766 AX189766 3552 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 10 from Patent WO0148164.
DEFINITION AX189766
ACCESSION AX189766
VERSION AX189766.1 GI:15143139
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3552)
AUTHORS Hammond,H.K. and Gao,M.
TITLE Gene therapy for congestive heart failure
PATENT: WO 0148164-A 10 05-JUL-2001;
JOURNAL THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
FEATURES
Location/Qualifiers
source
1..3552
BASE COUNT 686 a 1037 c 1068 g 761 t
ORIGIN
Query Match 98.2%; Score 3484.8; DB 6; Length 3552;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 3517; Conservative 0; Mismatches 32; Indels 3; Gaps 1;
QY 1 ATGTCATGTTTAGTGGCTTCTGTCCTTAACTGATGAACGAAACAGCTGGGT 60
Db 1 ATGTCATGTTTAGTGGCTTCTGTCCTTAACTGATGAACGAAACAGCTGGGT 60
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QY 181 CCTCGGTGCCCTTGGCAGGATGACCCCTTATCCGAGGGCGCGCCAGGGCAAG 240
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QY 301 GCGGGGAGCGCTGAGGTGGCGCCGACCGGTGCCAGAGTGGGCGCATCTGCTGGCGC 360
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QY 361 CGTTTGTGAGGTGTTCCAGTCCAGAGTTCCTGTTCCGGCCAAAGCTGGAGCGCTGTAC 420
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QY 421 CAGCGGTACTTTTCCAGATGAACAGAGCAGCTGAGCTGTGGTGGCGGTGCTGTG 480
Db 421 CAGCGGTACTTTTCCAGATGAACAGAGCAGCTGAGCTGTGGTGGCGGTGCTGTG 480
QY 481 CTGCTCAGCGGTGCTGCTGGCTTTCAGAGCCGACCGCCCGCTTCAGCCCTGCCTAT 540
Db 481 CTGCTCAGCGGTGCTGCTGGCTTTCAGAGCCGACCGCCCGCTTCAGCCCTGCCTAT 540
QY 541 GTGCACTGTTGGCTGTGGCGCGCGCTGTGTTGTGGGGCTCATGTTGTGTAACCGG 600
Db 541 GTGCACTGTTGGCTGTGGCGCGCGCTGTGTTGTGGGGCTCATGTTGTGTAACCGG 600

Qy	601	CATAGCTTCGCCAGGACTCCATGTGGGTGGTGAAGTAACTGGTGGCTCTGGGGCTCCTGGCG	660
Db	601	CATAGCTTCGCCAGGACTCCATGTGGGTGGTGAAGTAACTGGTGGCTCTGGCGATCTCGCG	660
Qy	661	GCAGTGCAGGTTCGGGGCGCTTTCGCAGACAGCCGCGCAGCCCTCTGCGGGGCTCTGG	720
Db	661	GCAGTGCAGGTTCGGGGCGCTCTCGCAGACAGCCGCGCAGCCCTCTGCGGGGCTCTGG	720
Qy	721	TGCGCTCTGTTCTTTGTATACATCGCATACAGCTCTCTCCCATCCGATCCGGCATCGGGCTGCC	780
Db	721	TGCGCTCTGTTCTTTGTCTACATCGCCTACAGCTCTCTCCCATCCGATCGGGCTGCC	780
Qy	781	GTCCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATCTTGGCTTGGCACTTAAACCGT	840
Db	781	GTCCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATCTTGGCTTGGCACTTAAACCGT	840
Qy	841	GGTGATCCCTTCCTCTGGAGAGAGCTCGGTGCCAATGTGCTGCTTCCCTCTGCACCAAC	900
Db	841	GGTGATCCCTTCCTCTGGAAAGAGCTCGGTGCCAATGTGCTGCTTCCCTCTGCACCAAC	900
Qy	901	GTCATTAGCATCTGCACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCCTTTCAGGAG	960
Db	901	GTCATTAGCATCTGCACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCCTTTCAGGAG	960
Qy	961	ACCGCATCTTACATCCAGGCCCGGCTCCACTTGCAGCATGAGAAATCGCAGCAGGAGCGG	1020
Db	961	ACCGCGGTTTACATCCAGGCCCGGCTCCACTTGCAGCATGAGAAATCGCAGCAGGAGCGG	1020
Qy	1021	CTGCTGCTGTCGTTATGCCCCAGCAGTTCGCATGGAGATCAAGAGAGACATCAACACA	1080
Db	1021	CTGCTGCTGTCGTTATGCCCCAGCAGTTCGCATGGAGATCAAGAGAGACATCAACACA	1080
Qy	1081	AAAAAAGAAGAC---ATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAAGCATC	1137
Db	1081	AAAAAAGAAGCATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAAGCATC	1140
Qy	1138	CTGTTTTCAGACATTGAGGCTTCACCGCTGGCATCCCAAGTGCAGTGCAGTGCAGGAGCTG	1197
Db	1141	CTGTTTTCAGACATTGAGGCTTCACCGCTGGCATCCCAAGTGCAGTGCAGTGCAGGAGCTG	1200
Qy	1198	GTCATGACCTGTAATGAGTCTTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGC	1257
Db	1201	GTCATGACCTGTAATGAGTCTTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGC	1260
Qy	1258	CTGAGGATCAAGATCTTTGGGGAGCTTTACTACTGTGTGTCAGGGCTGCGGAGGCCCGG	1317
Db	1261	CTGAGGATCAAGATCTTTGGGGAGCTTTACTACTGTGTGTCAGGGCTGCGGAGGCCCGG	1320
Qy	1318	GCGGACCATCGCCACTGCTGTGTGGAGATGGGGGTAGACATGNTTAGGCCATCTCGCTG	1377
Db	1321	GCGGACCATCGCCACTGCTGTGTGGAGATGGGGGTAGACATGNTTAGGCCATCTCGCTG	1380
Qy	1378	GTCAGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGCGCGTG	1437
Db	1381	GTCAGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGCGCGTG	1440
Qy	1438	CAGTTCGGGCTCCTTGGCTTGGGAAATGGCAGTTTCGATGTGTGTCCATGTGTGACC	1497
Db	1441	CAGTTCGGGCTCCTTGGCTTGGGAAATGGCAGTTTCGATGTGTGTCCATGTGTGACC	1500
Qy	1498	CTGSCCAACACATGAAGCAGGAAGCGGGCTGSCCGCATCCACATCACTCTGGGGCAACA	1557
Db	1501	CTGSCCAACACATGAAGCAGGAAGCGGGCTGSCCGCATCCACATCACTCTGGGGCAACA	1560
Qy	1558	CTGCAGTACCTGAACGGGACTACGAAGTGGAGCCAGGCCGTGTGGCAGCGCAACGCG	1617
Db	1561	CTGCAGTACCTGAACGGGACTACGAAGTGGAGCGAGGCCGTGTGTGGCAGCGCAACGCG	1620
Qy	1618	TACCTCAAGGACAGCACATTGAGACTTTTCCTCATCTTGGGGCGCAGCCAGAAACGGAAA	1677
Db	1621	TACCTCAAGGACAGCACATTGAGACTTTTCCTCATCTTGGGGCGCAGCCAGAAACGGAAA	1680

Qy	1678	GAGGAGAAAGGCATGCTGGGCCAAAGCTGCGAGCGGACTCGGGCCCAACTCCATGGAAGGGCTG	1737
Db	1681		1740
Qy	1738	ATGCGCGGATGGGTTCTGATCGTGGCTTCTCCGGACCAAGGACTCCAAGGCGCTTCGCG	1797
Db	1741	ATGCGCGGCTGGGTTCTGATCGTGGCTTCTCCGGACCAAGGACTCCAAGGCGCTTCGCG	1800
Qy	1798	CAGATGGGCATTGATGATTCAGCAAAAGACAACCGGGGCACCAAGATGCCCTGAACCCCT	1857
Db	1801	CAGATGGGCATTGATGATTCAGCAAAAGACAACCGGGGCACCAAGATGCCCTGAACCCCT	1860
Qy	1858	GAGGATGAGGTGGATGAGTTCTTGAGCCGTGGCATCGATGCGCCGACGATTTGATCAGCTG	1917
Db	1861	GAGGATGAGGTGGATGAGTTCTTGAGCCGTGGCATCGATGCGCCGACGATTTGATCAGCTG	1920
Qy	1918	CGGAGGACCATGTGCGCCGGTTTTTGCTACCTTCCAGAGAGAGGATTTTTGAGAAAG	1977
Db	1921	CGGAGGACCATGTGCGCCGGTTTTTGCTACCTTCCAGAGAGAGGATTTTTGAGAAAG	1980
Qy	1978	TACTTCCGGAAGGTGGATCCCGCTTCGGAGCCTACGTTTGCTGTGCCCTGTGGCTTTC	2037
Db	1981	TACTTCCGGAAGGTGGATCCCGCTTCGGAGCCTACGTTTGCTGTGCCCTGTGGCTTTC	2040
Qy	2038	TGCTTCATCTGCTTCATPCCAAGCTTCTAAATTTTCCACACTCCACCCTGATGCTTTGGGATT	2097
Db	2041	TGCTTCATCTGCTTCATPCCAAGCTTCTAAATTTTCCACACTCCACCCTGATGCTTTGGGATC	2100
Qy	2098	TATGCCAGCATCTTCTGCTGCTGCTTAATCACCGTGTGTGATCTGTGCTGTGTACTCCTGT	2157
Db	2101	TATGCCAGCATCTTCTGCTGCTGCTTAATCACCGTGTGTGATCTGTGCTGTGTACTCCTGT	2160
Qy	2158	GGTTCTCTGTTCCCTAAGGCCCTGCAACGCTGTGCCGACGATTTGCCGCTCACGGGCA	2217
Db	2161	GGTTCTCTGTTCCCTAAGGCCCTGCAACGCTGTGCCGACGATTTGCCGCTCACGGGCA	2220
Qy	2218	CATAGCACCGAGTTGGCAFTTTTTCCGTCCTGCTGTGTGTACTTTCGCAATTTGCCAAC	2277
Db	2221	CATAGCACCGAGTTGGCAFTTTTTCCGTCCTGCTGTGTGTACTTTCGCAATTTGCCAAC	2280
Qy	2278	ATGTTACCTGTAAACACACCCCATACGAGCTGTGCAGCCCGGATGCTCAATTTAAACA	2337
Db	2281	ATGTTACCTGTAAACACACCCCATACGAGCTGTGCAGCCCGGATGCTCAATTTAAACA	2340
Qy	2338	CCTGCTGACATCACTGCTGCCACCTGCGACGAGCTCAATTACTCTCTGGGCTGGATGCT	2397
Db	2341	CCTGCTGACATCACTGCTGCCACCTGCGACGAGCTCAATTACTCTCTGGGCTGGATGCT	2400
Qy	2398	CCCCTGTGTAGGGCACCATGCCCCACTCGAGCTTTCCCTGAGGTGTCAATCGGAAACATG	2457
Db	2401	CCCCTGTGTAGGGCACCATGCCCCACTCGAGCTTTCCCTGAGTACTTCTATCGGAAACATG	2460
Qy	2458	CTGCTGAGTCTTTGGCCAGCTCTGTCTTCTTGCACATCAGCAGCATCGGGAAGTTGGCC	2517
Db	2461	CTGCTGAGTCTTTGGCCAGCTCTGTCTTCTTGCACATCAGCAGCATCGGGAAGTTGGCC	2520
Qy	2518	ATGATCTTTGTTTGGGGCTCATCTATTTTGGTGTGCTTCTCTGGGTCCCGACCGCC	2577
Db	2521	ATGATCTTTGTTTGGGGCTCATCTATTTTGGTGTGCTTCTCTGGGTCCCGACCGACC	2580
Qy	2578	ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC	2637
Db	2581	ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC	2640
Qy	2638	TTTGATGGGCTGACATGCTCCAGCTCAGGAGGGTGGGCCCTCAATATATGACCCCTGTG	2697
Db	2641	TTTGATGGGCTGACATGCTCCAGCTCAGGAGGGTGGGCCCTCAATATATGACCCCTGTG	2700
Qy	2698	ATTCCTGCTGTGTTTGGCGCTGGCGCTGTATCTGCAATGCTCAGCAGGTGGAATCGACTGCC	2757
Db	2701	ATTCCTGCTGTGTTTGGCGCTGGCGCTGTATCTGCAATGCTCAGCAGGTGGAATCGACTGCC	2760
Qy	2758	CGCTAAACTTCTCTGGAACTTACAGGCACACAGGGGAAAAAGAGGAGATGGGAGAGCTA	2817

Db 935 GAGCTGGGCTCGGGCAGTGGCCCTGGCTTCGAGATACCGAGGTGACACGACAGCG 994
QY 301 GCGGGACGGCTGAGTGGCGCCGACGCGGTGCCAGAGTGGCGATCCTCTGGCGC 360
Db 995 GCGGGACGGCTGAGTGGCGCCGACGCGGTGCCAGAGTGGCGATCCTCTGGCGC 1054
QY 361 CGTTTGGTGCAGGTTCAGTGAAGCAGTTCCTTCGGCCAAAGTGGAGGCCCTGTAC 420
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QY 481 CTGCTCACAGCGGTGCTGGCTTTCCAAAGCGCACCGCCGCTCAGCGCTGCTAT 540
Db 1175 CTGCTCACAGCGGTGCTGGCTTTCCAGCGCGCACCGCCGCTCAGCGCTGCTAT 1234
QY 541 GTGGCACTGTTGGCTGTGCCCGCCCTGTTGCTGGGGCTCATGTGTGTGTAAACCG 600
Db 1235 GTGGCACTGTTGGCTGTGCCCGCCCTGTTGCTGGGGCTCATGTGTGTGTAAACCG 1294
QY 601 CATAGCTTCGGCCAGACTCCATGTGGGTGGTGAAGTAAAGTGTGCTGGGCATCCTGGCG 660
Db 1295 CATAGCTTCGGCCAGACTCCATGTGGGTGGTGAAGTAAAGTGTGCTGGGCATCCTGGCG 1354
QY 661 GCAGTGCAGGTGGGGCGCTTCGCGAGCAGACCGCGCAGCCGCTCTCGGGGCTCTGG 720
Db 1355 GCAGTGCAGGTGGGGCGCTCTCGCAGCAGACCGCGCAGCCGCTCTCGGGGCTCTGG 1414
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QY 841 GGTGATGCCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTCTCTGCACCAAC 900
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QY 1081 AAAAAAGAGAC---ATGTTCCAGAGATCTACATACAGAGCATGACAATGTACGATC 1137
Db 1775 AAAAAAGAGACATGATGTTCCACAGATCTACATACAGAGCATGACAATGTACGATC 1834
QY 1138 CTGTTTGCAGACATTGAGGCTTCACAGCTTGGCATCCAGTGCAGTCTGCGCAGGAGCTG 1197
Db 1835 CTGTTTGCAGACATTGAGGCTTCACAGCTTGGCATCCAGTGCAGTCTGCGCAGGAGCTG 1894
QY 1198 GTCATGACCTGAATGAGCTCTTTGGCCGCTTTGACAAGCTGGCTCGGAGAAATCACTGC 1257
Db 1895 GTCATGACCTGAATGAGCTCTTTGGCCGCTTTGACAAGCTGGCTCGGAGAAATCACTGC 1954
QY 1258 CTGAGGATCAAGATCTTGGGGACTGTTACTGTGTGTCAGGCTGCGGAGGCCCGG 1317
Db 1955 CTGAGGATCAAGATCTTGGGGACTGTTACTGTGTGTCAGGCTGCGGAGGCCCGG 2014
QY 1318 GCGGACCATGCCCATGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG 1377
Db 2015 GCGGACCATGCCCATGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG 2074

QY 1378 GTACGTGAGGTGACAGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGCGCGTG 1437
Db 2075 GTACGTGAGGTGACAGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGCGCGTG 2134
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Db 2255 CTGCACTACTCTAAACGGGACTACGAAGTGGAGCCAGGCGGTGGTGGCAAGCAACGCG 2314
QY 1618 TACCTCAAGAGAGACATTTGAGACTTTCCTCATCTGGGGCCAGCCAGAAACGAAA 1677
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Db 2375 GAGGAGAAAGCATGCTGCCAGCTGCAGGACTCGGGCCAACTCCATGGAAGGCTG 2434
QY 1738 ATGCCCGCATGGGTTCCTGATCGTGCCTTCTCCCGACCAAGGACTCCAGGCTTTCCCG 1797
Db 2435 ATGCCCGCATGGGTTCCTGATCGTGCCTTCTCCCGACCAAGGACTCCAGGCTTTCCCG 2494
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Db 2495 CAGATGGGATTTGATGATTTCCAGCAAGACAACCGGGGCAACCAAGATGCCCTGAACCT 2554
QY 1858 GAGGATGAGTGCAGTTCCTGAGCGGTGCATCGATCGCCGAGCATGATGATGATGATG 1917
Db 2555 GAGGATGAGTGCAGTTCCTGAGCGGTGCATCGATCGCCGAGCATGATGATGATGATG 2614
QY 1918 CGGAAGGACCATGTGCGCGGTTTTTGTCACTCCAGAGAGAGGATTTTGAGAAAG 1977
Db 2615 CGGAAGGACCATGTGCGCGGTTTTTGTCACTCCAGAGAGAGGATCTTGAGAAAG 2674
QY 1978 TACTCCCGAAGGTGATCCCGCTTCGGAGCTAGTTCCTGCTGCTGCTGCTGCTGCTTTC 2037
Db 2675 TACTCCCGAAGGTGATCCCGCTTCGGAGCTAGTTCCTGCTGCTGCTGCTGCTGCTTTC 2734
QY 2038 TGCTTCATCTGCTTCATCCAGCTTCTAAATTTTCCACACTCCACCTGATGCTGGGAT 2097
Db 2735 TGCTTCATCTGCTTCATCCAGCTTCTCACTTCCACACTCCACCTGATGCTGGGATC 2794
QY 2098 TATGCCAGCATCTTCTGCTGCTGCTTAATCACCGTCTGATCTGCTGCTGCTGCTGCTG 2157
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QY 2158 GGTTCCTGTTCCCTAAGGCCCTGCAACGCTGTCCTCCGAGCATTTGCTGCTCACGGCA 2217
Db 2855 GGTTCCTGTTCCCTAAGGCCCTGCAACGCTGTCCTCCGAGCATTTGCTGCTCACGGCA 2914
QY 2218 CATAGCACGCGAGTTGGCATCTTTTCCGCTCTGTTGTGTTTACTTCTGCGATTGCCAAC 2277
Db 2915 CATAGCACGCGAGTTGGCATCTTTTCCGCTCTGTTGTGTTTACTTCTGCGATTGCCAAC 2974
QY 2278 ATGTTCCACCTGTAACACACACCCCATACGAGCTGTGCAGCCCGGATGCTGAATTTAACA 2337
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AUTHORS Hammond, H. K. and Gao, M.
TITLE Gene therapy for congestive heart failure
JOURNAL Patent: WO 0148164-A 12 05-JUL-2001;
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REFERENCE
AUTHORS Ishikawa,K., Nagase,T., Nakajima,D., Seki,N., Ohira,M.,
Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
TITLE Prediction of the coding sequences of unidentified human genes.
VIII. 78 new cDNA clones from brain which code for large proteins
in vitro
JOURNAL DNA Res. 4 (5), 307-313 (1997)
MEDLINE 98116655

9455477
2 (bases 1 to 5877)
Ohara,O.
Direct Submission
Submitted (06-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology, Yana 1532-3, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel: +81-438-52-3913,
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On May 9, 2002 this sequence version replaced gi:2887418.
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DOGADENCYC 4046 bp mRNA linear MAM 27-APR-1993

LOCUS Canis familiaris adenylyl cyclase type VI mRNA sequence.

DEFINITION M94968.1 GI:163896

ACCESSION adenylyl cyclase type VI.

VERSION Canis familiaris cardiac muscle cDNA to mRNA.

KEYWORDS Canis familiaris

SOURCE ORGANISM

REFERENCE. Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

AUTHORS 1. (bases 1 to 4046)

TITLE Katsushika, S., Chen, L., Kawabe, J., Nilakantan, R., Halnon, N.J., Homcy, C.J. and Ishikawa, Y.

CLoning and characterization of a sixth adenylyl cyclase isoform: types V and VI constitute a subgroup within the mammalian adenylyl cyclase family

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (18), 8774-8778 (1992)

MEDLINE 92409599

PUBMED 1528892

FEATURES Location/Qualifiers

source 1..4046

organism="Canis familiaris"

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BASE COUNT 743 a 1206 c 1254 g 843 t

ORIGIN

Query Match 84.4%; Score 2996.8; DB 4; Length 4046;

Best Local Similarity 91.0%; Pred. No. 0;

Matches 3233; Conservative 0; Mismatches 307; Indels 12; Gaps 4;

QY 1 ATGTCATGTTAGTGGCTCTCTGTCTTAAAGTGAAGTGAACGAAACAGCCCTGGGGT 60

Db 131 ATGTCGTTAGTGGCTCTCTGTCTCCCAAGTGAAGTGAACGAAACAGCCCTGGGGT 190

QY 61 GAACGCAATGGCAGAGCGTTTCGGCGGCTTGGCACTTCGGGCGAGTGGCTTCTGCACG 120

Db 191 GAACGCAATGGCAGAGCGT---CCAGCGCGGGAGCTCGGACAGTGGCTTCTGCACG 247

QY 121 CCCGCTATATGAGCTGCCTCCGGGATGCAGACCCAGCCACCCCTGCGGGCCCC 180

Db 248 CCCGCTATATGAGCTGCCTCCGGGATGCAGACCCCGCCAGTCCGCGCTCCC 307

QY 181 CCTCGTCCCTGGCAGGATGACGCTTCATCCGAGGGCGGGCCAGGCAAGGCAAG 240

Db 308 CCTCGTCCCTGGCAGGATGAGCCCTTCATCCGAGAGGGCGGGCCAGGCGCAG 367

QY 241 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACGACG 300

Db 368 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGACACTGAGG---CCATGTCAGC 424

QY 301 GCGGGGCGGCTGAGTGGGCGCGCGACGCGGTGCCAGAGTGGCGGATCTGCTGGGCG 360

Db 425 GTTGGGCGAGCTGAGTGGGCGCTGACGTGACCCCGGGAGTAGCGGATCTGCTGGGCG 484

QY 361 GGTTTGGTGCAGGTGTTCCAGTTCGAAGCAGTTCGTTCCGGCAAGCTCGGAGCGCTGTAC 420

Db 485 CGTCTGGCCAGGTGTTCCAGTTCGAAGCAGTTCGCTCGGCCAAGCTCGAGCGCTGTAC 544

QY 421 CAGCGGTACTTTTCCAGATGAACAGACGACCTGACGCTGCTGCTGGTGGCTGCTGGTG 480

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QY 481 CTGCTCAGCGGCTGCTGCTGGCTTTTCAAGCGGACCGCGCCCTCAGCTGCGCTAT 540

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ORGANISM			
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AUTHORS			
TITLE			
Cloning and characterization of a cardiac adenylyl cyclase			

JOURNAL FEATURES	Patent: US 5578481-A 1 26-NOV-1996;	Location/Qualifiers	
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BASE COUNT	743 a 1202 c 1257 g 844 t		
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Qy	361	CGTTTGTGTCAGGTGTTCCAGTCGAAGCAGTTCGCTTCGCGCAAGCTGGAGGCCCTGTAC	420
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Qy	601	CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAAGTAACTGGTGGTGGCATCCTGCGC	660
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Db 2042 CGGAAGGACCATGTGCGCGGCTTCTGCTCAGCTTCCAGAGAGAGATTTTGAAAAAGAAG 2101
QY 1978 TACTCCCGGAAGGTGATCCCGCTTTCGGAGGCTACGTTGCGCTGTGCCCTGTGTGGTCTTC 2037
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DEFINITION Sequence 716 from Patent WO0188188.
ACCESSION AX305965
VERSION AX305965.1 GI:17645322
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 Ishikawa,K., Asai,S., Takahashi,Y., Nagata,T. and Ishii,Y.
AUTHORS Method for examining ischemic conditions
TITLE Patent: WO 0188188-A 716 22-NOV-2001;
JOURNAL School Juridical Person Nihon University (JP)
FEATURES Location/Qualifiers
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/organism="Mus musculus"
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BASE COUNT 1214 a 1538 c 1673 g 1396 t
ORIGIN

Query Match 77.9%; Score 2765; DB 6; Length 5841;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 3095; Conservative 0; Mismatches 445; Indels 13; Gaps 5;

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RESULT 11

AR106659

LOCUS AR106659 4131 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 11 from patent US 6107076.

ACCESSION AR106659

VERSION AR106659.1 GI:12821189

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 4131)

AUTHORS Tang, W.-J. and Gilman, A.G.

TITLE Soluble mammalian adenylyl cyclase and uses therefor

JOURNAL Patent: US 6107076-A 11 22-AUG-2000;

FEATURES

Location/Qualifiers

source 1..4131

BASE COUNT 835 a 1190 c 1182 g 924 t

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Best Local Similarity 86.7%; Pred. No. 0;

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DB 2390 CCGTCCGATGTCAACCGCTGCCACCTACGACAGCTCAATTTACTTCTTGGGACTTGAAGCT 2449
QY 2398 CCCTGTGTGAGGGACCATGCCACCTTCAGCTTCTCCAGTGTCCATCGGGAACATG 2457
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DB 2510 CTGCTGAGTCTCTTGCCAGCTCCGCTTCTTCCACATCAGCAGCATTGGCAAGCTAGTT 2569
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QY 2758 CGCTTAACTTCTCTGGAACCTACAGGCAACAGGGGAAAAAGAGAGATGGAGGACTA 2817
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DB 2870 CAGGCTACAAACCGGCGGCTGCTGCATACATCTTCCCAAGGACGTGGCTGCCACTTC 2929
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DB 2930 CTGCCCCGAGGAGCGCGCAACGACGAGCTGTACTACCAATCTTCCGAGTCCGTGGCTGTC 2989
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DB 2990 ATGTTTTCCTTCCATTTGCCAATTTCTCTGAGTTCTATGTGTGAGCTGGAGGCGAACAATGAG 3049
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RESULT 12

RATADCYB
LOCUS 4131 bp mRNA linear ROD 27-APR-1993
DEFINITION Rattus norvegicus adenylyl cyclase type VI mRNA, complete cds.
ACCESSION M96160
VERSION M96160.1 GI:202718
KEYWORDS adenylylate cyclase; adenylyl cyclase type VI.
SOURCE Rattus norvegicus (strain Sprague-Dawley) adult liver, kidney, heart cDNA to mRNA.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE	Rattus.
AUTHORS	1 (bases 1 to 4131)
TITLE	Premont,R.T. Multiple mechanisms underlying desensitization of the liver adenylyl cyclase system. Structure and cAMP regulation of liver adenylyl cyclases Thesis (1992)
JOURNAL	2 (bases 1 to 4131)
REFERENCE	Premont,R.T., Chen,J., Ma,H.W., Ponnappalli,M. and Iyengar,R.
AUTHORS	Two members of a widely expressed subfamily of hormone-stimulated adenylyl cyclases
TITLE	Proc. Natl. Acad. Sci. U.S.A. 89 (20), 9809-9813 (1992)
JOURNAL	93028552
MEDLINE	1409703
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Query Match	77.5%; Score 2751.2; DB 10; Length 4131;
Best Local Similarity	86.7%; Pred. No. 0;
Matches 3080; Conservative	0; Mismatches 463; Indels 11; Gaps 4;
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QY 61	GAACGCAATGGGAGAACGCTTCGCGGCGCGCTGGCACTCGGGCAGGTGGCTTCGCGACG 120
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QY 121	CCCGGCTATAGAGTCGCTCCGGGATGACAGACCCAGCCACCCCTCGCGGGCCCC 180
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QY 181	CTCGGTCGCCCTGGCAGGATGAGCCCTTCATCCGAGAGGGCGGCCAGGGAAGGCAAG 240
Db 233	ACTCGGTGCCCTGGCAGGATGAAGCCTTCATCAGGAGGGCTGGCCCGGGAAGGGGTGTG 292
QY 241	GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGTGACAAACACACCGC 300
Db 293	GAGCTGGGGCTGCGGGTCACTGGGCTTCAGTGGCTTCGGTTCATGACACTGAGGTG---ACCACACCG 349
QY 301	GGCGGGAGCGCTGAGGTGGGCGCGGACGCGGTGCCAGGAGTGGGCGCATCTGCTGGCGC 360
Db 350	ATGGGGACAGCTGAAGTGGCAGCCGACACATCGCTCGAAGCGGTCCGCTCCTGCTGGCGAC 409
QY 361	CGTTTGTGTCAGGTGTTCCAGTCCGAAGCAGTTCGTTGCGGCAAGCTGGAGCGCTGTAC 420
Db 410	CGGTAGCGGAGGTGTTCCAGTCTAAGCAGTTCGCTCCGCAAGCTGGAGCGCTGTGTAC 469
QY 421	CAGCGGTACTTTTCCAGATGAACGACAGCAGCCTGAGCTGCTGGTGGCGGTGCTGTGTG 480
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Db 830	GTGCTAGTGCCTGGGTCTTTCACCTGCTTTCACCTGCTTATTTTGGCTGCTCATCAACAAT 889
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Db	1370	GCAGACCATCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTCAGAGCCATCTCCGCTG	1429
Qy	1378	GTACGTGAGGTGACAGAGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGCGCGGTG	1437
Db	1430	GTGCTGAGGTAAACGGGTGAATGTGAACATGCGCGTGGGCATCCACAGCGCGCGTGA	1489
Qy	1438	CACGTGCGGCTCCTTGCTTGGCTTGGGAAATGGCAGTTTCGATGTGTGTGCCAATGATGTGACC	1497
Db	1490	CACGTGCGGCTCCTTGCTTGGCTTGGGAAATGGCAGTTTGAATGTGTGTGCCAAGATGTGACC	1549
Qy	1498	CTGSCCAACACATGGAAGCAGAAAGCCGGGCTGGCCGATCCACATCACCTTCGSGCAACA	1557
Db	1550	CTGCCAAACACATGAGGCGGGGGCCGGGCGGCGCATCCACATCACCTTCGSGGCACA	1609
Qy	1558	CTGCAGTACCTGAACCGGGGACTACGAAGTGGAGCGAGCGCGTGTGGCAAGCGAAGCGG	1617
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Qy	1678	GAGGAGAAAGGCATGCTGGCCAAAGCTGCAGCGGACTCTGGGCGCAACTCCATCGAAAGGCGT	1737
Db	1730	GAGGAGAAAGGCATGCTGGTCAAGCTGCAGCGGAGCGCGGCGCACTCCATCGAAGACTG	1789
Qy	1738	ATGCCGCGATGGGTTCTGATCGTGCTTCTCCGAGCAAGGACTTCAAGGCCCTTCGCG	1797
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Qy	1798	CAGATGGGCATGATGATTCACAGCAAGACAACCGGGCCACCAAGATGCCCTCAACCCCT	1857
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Qy	1858	GAGGATGAGGTGATGATTCCTGAGCGGTGCCATCGATGCCCGCAGACTTGCATCAGCTG	1917
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Qy	1918	CGGAAGGACCATGTGGCGCGGTTTTTGTCTACCTTCCAGAGAGAGATTTTGAAGAAG	1977
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Qy	2098	TATGCCAGCATCTTCCTGCTGTCTTAATCACCGCTGCTGATCTGTGCTGTGCTACTCCTGT	2157
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Q	y	2638	TTTTGATGGCTGGACTGTCCAGCTCGAGGAGGGTGGCCCTCAAATATATGACCCCTGTG	2697
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D	b	2750	ATTCTCTCTGTGTTGGCCCTGGCAGCTGTATCTACAGCACAAACAGGTGGAATCTACGCC	2809
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Db 3590 CCAAGTGGGCACT 3603

RESULT 13

RATADC 6036 bp mRNA linear ROD 12-AUG-1994
LOCUS Rattus norvegicus adenylyl cyclase type VI mRNA, complete cds.
DEFINITION L01115
ACCESSION L01115

VERSION L01115.1 GI:202712
KEYWORDS adenylyl cyclase; adenylyl cyclase type VI.
SOURCE Rattus norvegicus hepatoma CDNA to mRNA.
ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Rattus.

1 (bases 1 to 6036)
REFERENCE 1 Krupinski, J., Lehman, T.C., Frankenfield, C.D., Zwaagstra, J.C. and
Watson, P.A.

TITLE Molecular diversity in the adenylyl cyclase family. Evidence for
eight forms of the enzyme and cloning of type VI

J. Biol. Chem. 267 (34), 24858-24862 (1992)
93077589
1332969

FEATURES

Location/Qualifiers

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6036

polyA_site

BASE COUNT 1223 a 1657 c 1750 g 1406 t

ORIGIN

Query Match 77.3%; Score 2743.2; DB 10; Length 6036;
Best Local Similarity 86.5%; Pred. No. 0;
Matches 3075; Conservative 0; Mismatches 468; Indels 11; Gaps 4;

QY 1 ATGTCATGGTTAGTGGCTTCTGGTCCCTAAAGTGTGATGAACGAAACAGCCTGGGT 60

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Db 199 ATGTCATGGTTAGTGGCTTCTGGTCCCAAGTGTGATGAACGAAACAGCCTGGGC 258

QY 61 GAACGCAATGGGCGAGAAAGCGCTTCGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
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Db 259 GAACGCAATGGGCGAGAAAGCG---CCACGCGCAGCGCGCGCGTGGCTTCTGCAGCG 315
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QY 121 CCGCGCTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCACCCCTGGCGGCCCC 180
|||||
Db 316 CCGCGCTATATGAGCTGCCCTCAAGAAATGTGGAGCCACCCAGCCACCTCTCTGCACTGC 375
|||||
QY 181 CTTGGTGGCCCTCGCAGGATGAGCGCTTCATCCGAGGCGCGCCAGGCAAGGGAAG 240
|||||
Db 376 ACTCGGTGCCCTCGCAGGATGAAGCTTTCATCAGGAGGGCTGGCCGGGAGGGGTGTG 435
|||||
QY 241 GAGCTGGGGTTCGGGGCAGTGGCCCTGGGCTTCAGAGATACCCAGGTGACAAACACAGCG 300
|||||
Db 436 AAGCTGGGGTTCGGGTTCAGTGGCTTGGGTTTGTATGACACTGAGGTG---ACCACACCG 492
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QY 301 GCGGGGAGCGTGAAGTGGGCGCGCGCGCGTGGCCAGGAGTGGCGGATCTCTGCTGGCG 360
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Db 493 ATGGGGAGCGTGAAGTGGGCGCGCGCGCGTGGCCAGGAGTGGCGTCTCTGCTGGCGAC 552
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QY 361 CGTTTGTGTCAGGTGTTCCAGTTCGAAGCAGTTCCTGTTGGGCGCAAGCTGGAGCGCTGTAC 420
|||||
Db 553 CGGCTAGCGCAGGTGTTCCAGTCTAAGCAGTTCGCTCCGCGCAAGCTGGAGCGCTGTAC 612
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QY 421 CAGCGGTACTTTTCCAGATGAACAGCAGCAGCCTGAGCGTGTGGTGGCGGTGCTGGTG 480
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Db 613 CAGCGGTACTTCTTCCAGATCAACAGCAGCAGCCTGAGCGTGTGCTATGGCGGTGCTTGTG 672
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QY 481 CTGCTCAGCGGTGCTGCTGGCTTTCCAGCCGCGCGCGCGCTTCAGCGCTGCGCTTAT 540
|||||
Db 673 CTCCTCATGGCTGTACTGTTGACCTTCCACCGCGCGCTGCGCTGCGCTGCGCTTAT 732
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QY 541 GTGGCACTGTTGGCTGTGCGCGCGCGCTGTTGTTGGGCTCATGTTGGTGTGTAAACCGG 600
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Db 733 GTGGCGCTGCTGACCTGTGCGCTCGCTCTTTTGTGGTACTCATGGTGTGTAAACCGA 792
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QY 601 CATAGCTTCCCGCAGGACTCCATGTGGGTGTGTAGTAACTGAGTGTGGGCTGCTGGGCG 660
|||||
Db 793 CATAGCTTCCCGCAGGACTCCATGTGGGTGTGTAGTAACTGAGTGTGGGCTGCTGGGCG 852
|||||
QY 661 GCAGTGAAGTTCGGGGGCTTTCGACAGCAGCGCGCGCGCGCTGCTGCGGGGCTCTGG 720
|||||
Db 853 GCGGTGAAGTTCGGGGGCTTTCGACGCAACCGCGCGCGCTGCTGAGGCGCTTGG 912
|||||
QY 721 TGCCTGTGTTTCTTGTATATACATACACGCTCTCTCCCATCCGATCCGAGTGGCGCTCC 780
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Db 913 TGCCCGGTGTTCTGCTCATACACGCTCTCTTCCCATTCGTTGCTGAGCGCGCC 972
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QY 781 GTCCTAGCGCGCTGGGCGCTCTCCACCTTGATTTGATCTTGGCGCTGCGCACTTAAACGT 840
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Db 973 GTGCTAGTGGCTGGGCTTTCACCGCTGATTTGATTTGGGCTGCGCATCTCAACAA 1032
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QY 841 GGTATGCTTCTCTGGAAGCAGCTCGTGGTGGCTGCTTACGTTGGTGGCTGCGCACTT 900
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Db 1033 GGTGACCGCTTCTTGTGAAGCAGCTCGTGGTGGCTTACGTTGGTGGCTTCTCTGTGCA 1092
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QY 901 GTCATGTAGCATCTGCACACATATCCAGCAGAGGTGTCTCAGCGCGCGCGCTTTCAGGAG 960
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QY 961 ACCCGCATTTACATCCAGCGCGCGCTCCACCTCGAGCATGAGAAATCGGCAGCAGGCGG 1020
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QY 1081 AAAAAAAGAAC---ATGTTCCCAAGATCTACATACAGAGAGATGACAAATGTGAGCATC 1137
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Db 1273 AAAAAAGAGAGATGATGTTTCCACAGATTTACATCCAGAGCATGACAAATGTGAGCATC 1332
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QY 1138 CTGTTTGCAGACATTTAGGGGCTTCCACAGCGCTGCGCATCCCATGCTGCGCAGGAGCTG 1197

D	b	1333	CTGTTTCCGCACATCGAGGCGTTCAACAGCCTGGCGTCCCAGTGCATGCCAGGAAGTGC	1392
Q	y	1198	GTCATGACCCTGAATGAGCTCTTTGGCCCGGTTTGACAAGCTGGGTGGGAGAATCACTGC	1257
D	b	1393	GTATGATACCTTGAATGAGCTCTTTGGCCCGGTTCGACAAGCTGGCTGGGAGAATCACTGT	1452
Q	y	1258	CTGAGGATCAAGATCTTTGGGGNACTGTTACTACTGTGTGTGTCAGGGCTGCCGGAGGCCGG	1317
D	b	1453	CTGAGGATCAAGATCTTTAGGAGACTGTTACTACTGTGTGTGTCGGGGCTGCCGGAGGCCGG	1512
Q	y	1318	GCCGACCATGCCACCTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG	1377
D	b	1513	GCAGACCATGCCNACTGCTGTGTGGAGATGGGGGTAGACATGATCGAGGCCATCTCGCTG	1572
Q	y	1378	GTACGTGAGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGCGCGTG	1437
D	b	1573	GTGCGTGAAGTAACGGGTGTAATGTGAAATGTGCAATGTGCGGTGGCATCCACAGCGGCGGTGA	1632
Q	y	1438	CACGTGCGCGCTCTTGCGTTGGCGAATAAGCGAGTTTCGATGTGTGTCCAATGATGTCAAC	1497
D	b	1633	CACGTGCGGTGTCTTGTTGGTCTGCGGAATAAGCGAGTTTGAATGTGTCCAAGATGTGACC	1592
Q	y	1498	CTGCCAACACATGGAAGCAGGAAGCCGGGTGCGCCATCCACATCACTCGGGCAACA	1557
D	b	1693	CTGCCAACACATGGAGCGGGGGCGGGCCGCGCACATCCACATCACTCGGGCCACA	1752
Q	y	1558	CTGCAGTACCTGAACGGGACTACGAAAGTGGAGCCAGGCCGTGTGTGCAAGCCGAACGGC	1617
D	b	1753	CTGCAGTACCTGAACGGGACTATGAGTGGAGCCAGGCCGTGGCGTAGCGCAACGGC	1812
Q	y	1618	TACCTAAGGAGCAGCACATTGAGACTTTCCTCATCTCTGGCGCCAGCCAGAAAACGGAAA	1677
D	b	1813	TACCTAAGCAGCAGTGCAATTGAGACCTTTCCTCATCTAGGAGCCAGCCAGAAAACGGAAA	1872
Q	y	1678	GAGAGAAAAGCATGCTGGCCAAAGTGCAGCGGACTCGGGCCAACTCCATGTGAAGGCGTG	1737
D	b	1873	GAGAGAAAAGCCATGCTGTGTCAAGTGTCAAGCGAGCGCGGGCCAACTCCATGTGAAGAGCAT	1932
Q	y	1738	ATGCGCGGATGGGTTCCTGATGTGCTCTCTCCCGGACCAAAGGACTCCAAGGCCCTCCGC	1797
D	b	1933	ATGCCCCGCTGGGTCTCTGACGTGCTTCTCCCGSACCAAGGACTCTAAGGCATTCGGA	1992
Q	y	1798	CAGATGGGCATTCATGATTTCCAGCAAGACACCGGGGACCCCAAGATGCGCTTGAACCT	1857
D	b	1993	CAGATGGGCATTCATGACTCTAGCAAGAGAACCGGGGTGCCCAAGATGCTCTGAACCT	2052
Q	y	1858	GAGATCAGGTGGATGAGTTCTGTAGCGCTGCCATCTGATGCCGACGATTTGATCACTG	1917
D	b	2053	GAGATCAGGTGGAGCAGTTTTCTGGCCGAGCCATCGATGCCGGAAGCATGACACAGCTG	2112
Q	y	1918	CGGAAGACCATGTGCGCGGTTTTTGCTCACTTCCAGAGAGAGGATTTTGAAGAAG	1977
D	b	2113	CGTAAGACCATGTGCGCGGTTCTTGCTCACTTCCAGAGGGAGGATCTCGAGAAGAAG	2172
Q	y	1978	TACTCCGGAAAGTGGATCCCCGCTTCGAGCGCTACGTTGCTGTGCCCTGTGGTCTTC	2037
D	b	2173	TATTACGGAAAGTAGACCCCTGGTTTCGGAGCGCTACGTCGCTGTGCCCTCTGGTTTC	2232
Q	y	2038	TGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCTGATCTTGGGATT	2097
D	b	2233	TGCTTCATCTGTTTATCCAGTTCTCTGATTTCCACACTCGGCCCTGATCTCGGATT	2292
Q	y	2098	TATGCCAGCATCTTCTGCTGCTTAATCAACCGTGCATCACTGTGCTGTGTACTCTCTGT	2157
D	b	2293	TATGCCGGGATCTTCTTTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2352
Q	y	2158	GGTTCTCTGCTTCCCTAAGGCCCTGCAACCTGTCTCCCGACGATTTGCCGCTCAGGGCA	2217
D	b	2353	GGGTCTTCTTCCCGCAACGCCCTGCAAGGCCCTGTCCCGAGTAGTGTCCCGCTCAGGGGT	2412
Q	y	2218	CATAGCACCCAGTTGGCATCTTTTCCGTCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT	2277

Db	2413	CACAGCAGCGCTGTTGGAGTCTTCTCGGTTTGTGCTTGTATCTCTGCCATCTCTGCCATTTGCCAAC	2477
Qy	2278	ATGTTCACTGTAAACACACACCCCATACGAGCGTGTGCAGCCCGGATGCTGAATTTAAACA	2337
Db	2473	ATGTTTCACTTCACACCCCATGAGGACCTGTGCGGCCCGATGCTGAACTTAAACA	2532
Qy	2338	CTTGCTGACATCACTGCTGCCACCTTCGACGAGCTCAATTTACTCTCTGGGCTTGATGCT	2397
Db	2533	CCGTCGAGTGTACCGGCTGTCACTTACGACAGATCAATTTACTCTCTGGGACTTGAAGCT	2592
Qy	2398	CCCTGTGTGAGGCGACCATGCCACCTTCGACGTTTCTTGAGGTCTCATCGGAAACATG	2457
Db	2593	CCCTGTGTGAGGCGACAGCACCCACCTGCAGTTTCCCTGAGTACTTTGTCTGGGAGTGTG	2652
Qy	2458	CTGTGTAGTCTCTTTGGCCAGCTCTGTCTCTCTGACATCAGACGATCGGGAAGTTGGCC	2517
Db	2653	CTGTGTAGTCTCTTTGGCCAGCTCCGCTCTCTCTCCACATCAGACGATTTGGGAAGCTAGTT	2712
Qy	2518	ATGATCTTTGTGTTGGGCTCACTATTTTGGTGTGCTTCTGCTGGGTCCCCACGCGCC	2577
Db	2713	ATGACCTTTGTCTTTGGGTTCACTTACTTGTCTTGTGCTTTTGTCTGGTCTCCCGACCC	2772
Qy	2578	ATCTTTGACAACTATGACCTACTGCTTTGGCGTCCATTTGGCTTTGGCTTTCTCAATGAGACC	2637
Db	2773	ATCTTTGACAACTATGATCTACTGCTTAGCTTCCATTTAGCTTGGCTTGGCTTCTCCAAATGAGACC	2832
Qy	2638	TTTGATGGCTGGACTCTCCAGCTGCAGGAGGTGGCCCTCAAAATATATCACCCCTGTG	2697
Db	2833	TTGATGGCTTGGACTGCCACGCGTAGGAGGGTAGCGCTCAAAATATGATCACCCCTGTG	2892
Qy	2698	ATTTCTGTGTTGTTGGCTTGGCGCTGATCTGTCATGCTACGAGGTGGAATCGACTGCC	2757
Db	2893	ATTTCTCTCGTTTTCGCCCTGGCACTGTATCTACAGGCACAAAGGTGGAATCTACCGCC	2952
Qy	2758	CGCTTAACTTCTCTCGAAACTACAGGCACAGGGGAAAGAGAGATGGAGAGCTA	2817
Db	2953	CGCTTGAATCTTCTTGTGGAACCTGCAGGCCACAGGGGAGAGGAGATGGAGAGTTG	3012
Qy	2818	CAGGCATACAACCAGGAGCTTGTGCATTAACATTTGCCCAAGAGCTGGCGGCCACTTC	2877
Db	3013	CAGGCTACAAGCGGCGCTGTCATTAACATCTTCTCCCAAGGACGTGGCTGCCACTTC	3072
Qy	2878	GTGCGCGGAGCGCCGCATGATGAATCTACTATCAGTCTGTGTAGTGTGTGGCTGT	2937
Db	3073	GTGCGCGGAGCGCCGCACGACGACTGTACTACAAATCTGCGAGTGTGTGGCTGTC	3132
Qy	2938	ATGTTTGCTCCATTGGCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAAACATGAG	2997
Db	3133	ATGTTTGCTCCATCGCAACTTCTCTGAGTTCTATGTGGAACTGGAGCGACAAATGAG	3192
Qy	2998	GGTCCGAGTGTGCGGCTGTCAACGAGATCATCGCTGACTTTGTATGAGATTATCAGC	3057
Db	3193	GGCGTGGAGTGCCTTGCACCTTCTCAATGAGATCATCGCGGACTTTTGATGAGATCATGAT	3252
Qy	3058	GAGGAGCGGTTCCGGCAGCTGGAAGAGATCAAGACGATTTGGTAGCACTACATGGCTGCC	3117
Db	3253	GAGGAGAGGTTTCCGGCAGCTGGAGAGATCAAGACCATCGGTAGCACTTTACATGGCGGCC	3312
Qy	3118	TCAGGGTGAACCGCACCTACGATCAGGTGGCGCGCTCCACATCACTGCCCTGGCT	3177
Db	3313	TCCGGCTTAATGCCAGCACTATGACCAAGTGGCGCGCTCGCACATCACCGCCCTGGCA	3372
Qy	3178	GACTACGCCATGTGCGGCTTATGGAGCAGATGAGACGATCAATGACGACTCTCTTCAACAT	3237
Db	3373	GACTACGCCATGTGCGGCTTATGGAGCAAAATGAACACATCAAGCAACACTCTTTCAACAC	3432
Qy	3238	TTCCAGATGAAGATTGGGCTGAACATTTGGGCCACGTCGTGGCAGGTGTATCGGGCTCGG	3297
Db	3433	TTCCAGATGAAGATTCGGGTTGAACATTTGGTTCGGGTTGTAGCAGGTGTCTTTGGGCGCGG	3492
Qy	3298	AAGCCACGATATGACATCTCGGGGGAACACAGTGAATGTCTCTAGTCTGATGACGACGACG	3357
Db	3493	AAGCCACGATATGACTCTCGGGGAACACGTTGAATGTGTCTTCCAGCGCTATGACAGACACA	3552

QY 919 CACTATCCAGCAGAGGTGTCTCAGCCGAGCCCTTTTCAGGAGACCCGCGATTCATATCCAG 978
Db 895 CACTACCCTGCTCAAGTGTCTCAGCGCAAGCCCTTTTCAGGAGACCCGAGGTTACATCCAG 954
QY 979 GCCCGGCTCCACCTCAGACATGAGATGCGCAGCAGAGGGCGTGTCTGTCGGGTATTG 1038
Db 955 GCCCGGCTGCACCTGCAGCATGAGAACCGTFCAGCAGGAACGGCTGTCTATCGGTGTTG 1014
QY 1039 CCCACGACGTTCCCATGGAGATGAAGAAGACATCAACACAAAAAAGAGAC---ATG 1095
Db 1015 CCCACGACGTTGCCATGGAGATGAAGAAGACATCAACACAAAAAAGAGACATGATG 1074
QY 1096 TTCCACAAGATCTACATACAGAAGCATGACAATGTTCAGACATCCTGTTTGAGACATTTGAG 1155
Db 1075 TTCCATAAGATCTACATCCAGAAGCATGATAATGTTCAGCATCCTGTTTGGGACATTTGAG 1134
QY 1156 GGCTTCACAGCCTGGATCCCATGCTGCGCAGGAGGTGTCTATGACCCCTGAATGAG 1215
Db 1135 GGCTTCACAGCCTGGCTCCCATGCTGCACTGCACAGGAAGTGTCTATGACCTTTGAATGAG 1194
QY 1216 CTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGCTGAGGATCAAGATCTTG 1275
Db 1195 CTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGCTGAGGATCAAGATCTTA 1254
QY 1276 GGGGACTGTTACTACTGTGTGTGTCAGGGCTGCCGGAGGCCCGGCCGACCATGCCACTGC 1335
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QY 1336 TGTGTGAGATGGGTAGACATGATTGAGGCCATCTCGCTGTACTGAGGTGACAGGT 1395
Db 1315 TGTGTGAGATGGGTAGACATGATCGAAGCCATCTCGCTGTGCTGAGGTAAACAGGT 1374
QY 1396 GTGAATGTGAACATGGCGTGGGCATCCACAGCGGGCGCTGCACGTGCGCGCTCTTGCC 1455
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QY 1456 TTCCGGAATGGCAGTTTCGATGTGTGTCGAATGATGTGACCTGGCCACACACATGGAA 1515
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QY 1696 GCCAAGCTGCAGCGGACTCGGGCCAACTCCATCGAAGGGCTGATGCCGCGATGGTTCCCT 1755
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QY 1876 TTCTTGAGCGGTGCCATCGATGCCCGCAGCATTTGATCAGTTCGGGAGGACCATGTGCCG 1935
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QY 1936 CGGTTTGTCTACCTTCACAGAGAGGATTTTGAAGAAGTACTCCCGGAAGGTGGAT 1995
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Db 1975 CCTCGCTTCGGAGCCCTACGTCGCGCTGTGCCCTCTCGTTTGTTCATCTGTTTATC 2034
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QY 2176 GCCCTCAACGCTGTCTCCGAGCATTTGTCGCTACGGGCACATAGCACCCGAGTTGGC 2235
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QY 2356 TGGCCTGTGAGCAGCTCAATTTACTCTCTGGGCTGGATGCTCCCTGTGTGAGGGCAAC 2415
Db 2335 TGGCAGCTACAACAGCTCAATTTACTCTCTGGGACTGGATGCTCCCTGTGTGAGGGCAC 2394
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RESULT 15
ARI74472
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DEFINITION Sequence 3 from patent US 6306830.
ACCESSION ARI74472
VERSION ARI74472.1 GI:17914792
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1812)
AUTHORS Hammond,H.Kirk., Insel,P.A., Ping,P., Post,S.R. and Gao,M.
TITLE Gene therapy for congestive heart failure
JOURNAL Patent: US 6306830-A 23-OCT-2001;
FEATURES
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1. 1812
/organism="unknown"
BASE COUNT 361 a 539 c 507 g 405 t
ORIGIN

Query Match 51.0%; Score 1808.4; DB 6; Length 1812;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 696 GCGCAGCCCTCTCGGGGCTCTGGTGCCTGTGTCTTTGTATACATCGCATACAGCT 755
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QY 756 CTTCCCATCCGATGGGGTGCCTGCTCAGCGGCTGGGCTCTCCACCTTGCATTT 815
Db 123 CTTCCCATCCGATGGGGTGCCTGCTCAGCGGCTGGGCTCTCCACCTTGCATTT 182
QY 816 GATCTGGCTTGGCAACTTAACCTGGTGTATGCTCTCTGGAAGCAGCTCGTGCCAA 875
Db 183 GATCTGGCTTGGCAACTTAACCTGGTGTATGCTCTCTGGAAGCAGCTCGTGCCAA 242
QY 876 TGTGCTGTCTCTGCACCAACGTCATTTAGCATCTGCACACTATCCAGCAGAGGT 935
Db 243 TGTGCTGTCTCTGCACCAACGTCATTTAGCATCTGCACACTATCCAGCAGAGGT 302
QY 936 GTCTCAGCGCCAGGCTTTTCAGGAGACCCGAGTTACATCCAGGCCCGGCTCCACCTGCA 995

Db 303 GTCTCAGCGCCAGCCCTTTTCAGGAGACCCGCGATTACATCCAGGCCCGCTCCACCTGCA 362
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QY 1056 GGAGATGAAGAAGACATCAACACAAAAAAGAAAGACATGTTCCACAAAGATCTACATACA 1115
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QY 1116 GAACATGACNAATGTACGATCCTGTTTGGCAGACATGAGGGCTTCACCAGCTGGGATC 1175
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QY 1176 CCAGTGCACCTGCGCAGGAGCTGGTCAAGACCTGAATGAGCTCTTTGGCCCGTTTGACAA 1235
Db 543 CCAGTGCACCTGCGCAGGAGCTGGTCAAGACCTGAATGAGCTCTTTGGCCCGTTTGACAA 602
QY 1236 GCTGGCTGCGGAGAAATCACTGCCCTGAGGATCAAGATCTTTGGGGACTGTTACTACTGTGT 1295
Db 603 GCTGGCTGCGGAGAAATCACTGCCCTGAGGATCAAGATCTTTGGGGACTGTTACTACTGTGT 662
QY 1296 GTCAGGCTGCCGAGGCCCGCGGCGGACCATGCCACTGCTGTGTGGAGATGGGGGTAGA 1355
Db 663 GTCAGGCTGCCGAGGCCCGCGGCGGACCATGCCACTGCTGTGTGGAGATGGGGGTAGA 722
QY 1356 CATGATTGAGCCCATCTCGCTGAGTACGTGACAGTGTGAATGTGAATGCAATGCGCGT 1415
Db 723 CATGATTGAGCCCATCTCGCTGAGTACGTGAGGTGACAGTGTGAATGTGAATGCGCGT 782
QY 1416 GGGCATCCACAGCGGGCGCTGACCTGCGGCTCTTTGGCTTGGGAAATGGCAGTTGCA 1475
Db 783 GGGCATCCACAGCGGGCGCTGACCTGCGGCTCTTTGGCTTGGGAAATGGCAGTTGCA 842
QY 1476 TGTGTGTCCAAATGATGTGACCTTGGCCAAACACATGGAAGCAGGAACCCGGGCTGGCG 1535
Db 843 TGTGTGTCCAAATGATGTGACCTTGGCCAAACACATGGAAGCAGGAACCCGGGCTGGCG 902
QY 1536 CATCCATCACTCGGCAACACTGCACTACCTGAACGGGACTACGAAGTGGAGCCAGG 1595
Db 903 CATCCATCACTCGGCAACACTGCACTACCTGAACGGGACTACGAAGTGGAGCCAGG 962
QY 1596 CCGTGGTGGCAAGCGCAACCGCTACCTCAAGGAGCAGCACATTTGAGACTTTCTCATCCT 1655
Db 963 CCGTGGTGGCAAGCGCAACCGCTACCTCAAGGAGCAGCACATTTGAGACTTTCTCATCCT 1022
QY 1656 GGGCCGAGCCAGAAACGGAAGAGGAGAAAGGATGCTGSCCAAGCTGCAGCGGACTCG 1715
Db 1023 GGGCCGAGCCAGAAACGGAAGAGGAGAAAGGATGCTGSCCAAGCTGCAGCGGACTCG 1082
QY 1716 GGCCAACTCCATGGAAGGCTGATGCCGCTGATGGTTCCTGATGCTGCTTCTCCCGGAC 1775
Db 1083 GGCCAACTCCATGGAAGGCTGATGCCGCTGATGGTTCCTGATGCTGCTTCTCCCGGAC 1142
QY 1776 CAAGGACTTCAAGGCTTCCGCCAGATGGGCTTGTGATTTCCAGCAAGAACAAACCGGG 1835
Db 1143 CAAGGACTTCAAGGCTTCCGCCAGATGGGCTTGTGATTTCCAGCAAGAACAAACCGGG 1202
QY 1836 CACCAAGATGCCCTGAACCTGAGGATGAGGTGGATGAGTTCCTGAGCCGCTGCCATCGA 1895
Db 1203 CACCAAGATGCCCTGAACCTGAGGATGAGGTGGATGAGTTCCTGAGCCGCTGCCATCGA 1262
QY 1896 TGCCCGCAGCATGTATGAGTGGGAGGACATGCTGGCGGCTTTTGTTCACCTTCCA 1955
Db 1263 TGCCCGCAGCATGTATGAGTGGGAGGACATGCTGGCGGCTTTTGTTCACCTTCCA 1322
QY 1956 GAGAGAGATTTTGAAGAAGTACTCCCGGAAGGTGGATCCCGCTTCGGAGGCTTACGT 2015
Db 1323 GAGAGAGATTTTGAAGAAGTACTCCCGGAAGGTGGATCCCGCTTCGGAGGCTTACGT 1382
QY 2016 TGCCTGTGCCCTGTGTGCTTCTGCTTCATCTGCTTCATCCAGCTTCTAAATTTCCCA 2075
Db 1383 TGCCTGTGCCCTGTGTGCTTCTGCTTCATCTGCTTCATCCAGCTTCTAAATTTCCCA 1442

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 20:52:08 ; Search time 655.392 Seconds
(without alignments)
12194.743 Million cell updates/sec

Title: US-09-750-240-5

Perfect score: 3549

Sequence: 1 atgtcatgtttagtgccct.....aaggaccaggtgggcact 3549

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3549	100.0	3549	22	Human cardiac aden
2	3484.8	98.2	3552	22	Human cardiac aden
3	3478.4	98.0	4942	20	Human type VI aden
4	3379.2	95.2	3582	22	Human modified car
5	2996.8	84.4	4046	14	Cardiac adenyl cycl
6	2765	77.9	5841	24	Mouse ischaemic co
7	2751.2	77.5	4131	21	Type VI adenyl cycl
8	1808.4	51.0	1812	22	Human partial card
9	1808.4	51.0	2127	19	Human adenyl cycl

10	1703.4	48.0	4523	20	AA000462	Human type V adeny
11	1690	47.6	4356	16	AA095540	Cardiac adenyl cycl
12	1688.4	47.6	4356	14	AA037543	Cardiac adenyl cycl
13	1648.2	46.4	3924	21	AAAS3922	Type V adenyl cycl
14	843	23.8	3137	24	AA028058	Human adenyl cycl
15	595	16.8	3978	21	AAAS3918	Human adenyl cycl
16	586	16.5	837	22	AA030177	DNA encoding rena
17	545	15.4	3811	24	AA028061	Human adenyl cycl
18	529.6	14.9	915	22	AAAS3023	DNA encoding rena
19	529.6	14.9	915	22	AAAS3023	DNA encoding nove
20	505.2	14.2	3518	22	AA026694	Human adenyl cycl
21	495.8	14.0	6470	24	AA031191	Human adenyl cycl
22	494.2	13.9	4011	22	AA006820	Human adenyl cycl
23	475.2	13.4	5873	24	AA031190	Human adenyl cycl
24	463.6	13.1	4601	21	AAAS3925	Type VIII adenyl cycl
25	460.2	13.0	3769	24	AA028057	Human adenyl cycl
26	459	12.9	4008	17	AA014528	Rat adenyl cycl
27	459	12.9	4008	21	AAAS3919	Adenyl cyclase t
28	449.4	12.7	4827	23	ABL07501	Drosophila melanog
29	446.6	12.6	3312	24	ABN89298	Human adenyl cycl
30	441.6	12.4	4533	21	AAAS3920	Type III adenyl cycl
31	433	12.2	5199	21	AAAS3924	Type VII adenyl cycl
32	428	12.1	3357	21	AAAS3921	Type IV adenyl cycl
33	412	11.6	4355	24	ABL39754	Human NS cDNA sequ
34	407.6	11.5	3505	24	AA034078	Human secreted pro
35	395.8	11.2	2601	21	AA039124	Human pancreatic c
36	393.2	11.1	1652	21	AAAS3926	Adenyl cyclase C
37	388.6	10.9	4080	22	AA016647	Human cDNA sequenc
38	382.2	10.2	7005	23	ABL15355	Drosophila melanog
39	343.8	9.7	3239	22	AA033100	Human secreted pro
40	295.2	8.3	314	22	AA008561	Human partial card
41	288.2	8.1	2092	17	AA014529	Human adenyl cycl
42	284.4	8.0	1180	22	AA046933	Human secreted pro
43	277	7.8	5046	23	ABL02755	Drosophila melanog
44	273.6	7.7	320	24	ABL00026	Human polynucleoti
45	267.6	7.5	5201	23	ABL29627	Drosophila melanog

ALIGNMENTS

RESULT 1

AA008563

ID AAD08563 standard; DNA; 3549 BP.

AC AAD08563;

XX

XX 04-SEP-2001 (first entry)

DT Human cardiac adenylcyclase VI (ACVI) isoform #1 DNA.

DE Human; cardiant; beta-adrenergic signalling protein; beta-ASP;

DE Human; cardiant; beta-adrenergic signalling protein; beta-ASP;

KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;

KW adenylcyclase; adenylate cyclase; CAMP synthetase;

KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;

KW cardiac adenylcyclase VI; ACVI isoform; beta-ASP transgene; ds.

XX Homo sapiens.

OS Homo sapiens.

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PA (REGC) UNIV CALIFORNIA.

XX
PI Hammond HK, Gao M;

XX
DR WPI: 2001-418260/44.

XX
DR P-PSDB; AAE04310.

XX
PT Novel polynucleotide encoding a modified adenylyl cyclase polypeptide
PT useful for enhancing cardiac function in mammalian hearts, and for
PT treating heart disease, especially congestive heart failure -

XX
PS Example 5; Page 122-129; 153pp; English.

XX
CC The present invention relates to methods and compositions for enhancing
CC cardiac function in mammalian hearts by inserting transgenes encoding
CC beta-adrenergic signalling proteins (beta-ASP) which increase
CC beta-adrenergic responsiveness within the myocardium using in vivo
CC gene therapy. The beta-ASPs of the invention include beta-adrenergic
CC receptors (beta-AR), adenylyl cyclases (also referred as adenylyl cyclase,
CC adenylylate cyclase and cAMP synthetase) and G-protein receptor kinase
CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
CC in mammalian hearts and for treating heart disease, especially
CC congestive heart failure. The present DNA sequence encodes human
CC cardiac adenylyl cyclase VI (ACVI) isoform which is used for generating
CC a third beta-ASP transgene, used in the exemplification
CC of the invention.

XX
SQ Sequence 3549 BP; 699 A; 1025 C; 1061 G; 764 T; 0 other;

Query Watch 100.0%; Score 3549; DB 22; Length 3549;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTATGTGCTCTTCTGTCCTTAAAGTGGATGAACGAAACAGCCTGGGGT 60
DB 1 ATGTCATGTTTATGTGCTCTTCTGTCCTTAAAGTGGATGAACGAAACAGCCTGGGGT 60
QY 61 GAACGCAATGGGCAGAACGGTTCGCGGCGCGTGGCACTCGCGGACGTGTCGTGACG 120
DB 61 GAACGCAATGGGCAGAACGGTTCGCGGCGCGTGGCACTCGCGGACGTGTCGTGACG 120
QY 121 CCCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCCTCGCGGCCCC 180
DB 121 CCCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCCTCGCGGCCCC 180
QY 181 CCTCGGTGCCCTGGCAGGATGACGCTTCATCCGAGGGCGGCCAGCAAGGCAAG 240
DB 181 CCTCGGTGCCCTGGCAGGATGACGCTTCATCCGAGGGCGGCCAGCAAGGCAAG 240
QY 241 GAGCTGGGGTGGGGCAGTGGCCCTGGGGTTCGAGGATACCGAGGTGACACGACGCG 300
DB 241 GAGCTGGGGTGGGGCAGTGGCCCTGGGGTTCGAGGATACCGAGGTGACACGACGCG 300
QY 301 GCGCGACCGCTAGCTGGCGCCGACGCGGTGCCAGAGGTGGCGATCCTGCTGGCG 360
DB 301 GCGCGACCGCTAGCTGGCGCCGACGCGGTGCCAGAGGTGGCGATCCTGCTGGCG 360
QY 361 CGTTTGGTGCAGGTGTTCCAGTCAAGCAGTTCCTGTCGCCCAAGCTGGAGCGCTGTAC 420
DB 361 CGTTTGGTGCAGGTGTTCCAGTCAAGCAGTTCCTGTCGCCCAAGCTGGAGCGCTGTAC 420
QY 421 CAGCGGTACTTTTCCAGATGAACACAGAGAGCGCTGACGCTGCTGGGGCTCATGGTGGTGGTG 480
DB 421 CAGCGGTACTTTTCCAGATGAACACAGAGAGCGCTGACGCTGCTGGGGCTCATGGTGGTGGTG 480
QY 481 CTGCTCACACCGCTGCTGGCTTTTCCAGCGGACCCGCCCTCAGCGTGGCTAT 540
DB 481 CTGCTCACACCGCTGCTGGCTTTTCCAGCGGACCCGCCCTCAGCGTGGCTAT 540
QY 541 GTGGCACTGTTGGCTGTGCGCGCGCTTCTGCTGGGGCTCATGGTGGTGGTAAACCGG 600
DB 541 GTGGCACTGTTGGCTGTGCGCGCGCTTCTGCTGGGGCTCATGGTGGTGGTAAACCGG 600

QY 601 CATAGCTTCGCGCAGGACTCCATGTGGTGGTGAAGTAACGTGTGTGGCATCTCTGGCG 660
DB 601 CATAGCTTCGCGCAGGACTCCATGTGGTGGTGAAGTAACGTGTGTGGCATCTCTGGCG 660
QY 661 GCAGTGCAGTTCGGGGCGCTTTTCGAGCAGACCCCGGAGCCCTCTCTGGGGCTCTGG 720
DB 661 GCAGTGCAGTTCGGGGCGCTTTTCGAGCAGACCCCGGAGCCCTCTCTGGGGCTCTGG 720
QY 721 TGCCTCTGTGTCTTTGTATACATGATACACGCTCTCTCCCATCCGATCCGCGGTGCC 780
DB 721 TGCCTCTGTGTCTTTGTATACATGATACACGCTCTCTCCCATCCGATCCGCGGTGCC 780
QY 781 GTCTCAGCGGCTGGGCGCTCTCCATTCGATTTGATTTGGCTGGCAACTTAACCGT 840
DB 781 GTCTCAGCGGCTGGGCGCTCTCCATTCGATTTGATTTGGCTGGCAACTTAACCGT 840
QY 841 GGTGATGCCCTTCTCTGGAAAGCAGCTCGGTGCAATGTGCTGTGTTCTCTGCACCAAC 900
DB 841 GGTGATGCCCTTCTCTGGAAAGCAGCTCGGTGCAATGTGCTGTGTTCTCTGCACCAAC 900
QY 901 GTCATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 960
DB 901 GTCATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 960
QY 961 ACCCGAGTTACATCCAGGCGCGCTCCACTGCAGCATGAGAAATCGGAGAGGCGG 1020
DB 961 ACCCGAGTTACATCCAGGCGCGCTCCACTGCAGCATGAGAAATCGGAGAGGCGG 1020
QY 1021 CTCTCTGCTGCTGCTATTGCCCCAGCAGTGGCCATGGAGATGAAGAGACATCAACACA 1080
DB 1021 CTCTCTGCTGCTGCTATTGCCCCAGCAGTGGCCATGGAGATGAAGAGACATCAACACA 1080
QY 1081 AAAAAAGAGACATGTTCCACAAGATCTACATACAGAAGCATGACAAATGTCAGCATCCTG 1140
DB 1081 AAAAAAGAGACATGTTCCACAAGATCTACATACAGAAGCATGACAAATGTCAGCATCCTG 1140
QY 1141 TTTTCAGACATTCAGGCTTCACAGCTGGCATCCAGTGCAGTGCAGTGCAGGAGCTGGTC 1200
DB 1141 TTTTCAGACATTCAGGCTTCACAGCTGGCATCCAGTGCAGTGCAGGAGCTGGTC 1200
QY 1201 ATCACCCTGAATCAGCTCTTTGGCCGTTTGAAGCTGGCTCGGAGAAATCACTGCTG 1260
DB 1201 ATCACCCTGAATCAGCTCTTTGGCCGTTTGAAGCTGGCTCGGAGAAATCACTGCTG 1260
QY 1261 AGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTGTCAGGCTGCGGAGGCCGGGCC 1320
DB 1261 AGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTGTCAGGCTGCGGAGGCCGGGCC 1320
QY 1321 GACCATGCCCATCTGCTGTGGAGATGGGGTAGACATGATGAGGCCATCTCGTGGTA 1380
DB 1321 GACCATGCCCATCTGCTGTGGAGATGGGGTAGACATGATGAGGCCATCTCGTGGTA 1380
QY 1381 CGTGAGGTGACAGTGTGAATGTAACATGCGGTGGCATCCACAGCGGCGGTGCAC 1440
DB 1381 CGTGAGGTGACAGTGTGAATGTAACATGCGGTGGCATCCACAGCGGCGGTGCAC 1440
QY 1441 TGGCGGCTCCTTGGCTTGGCGAAATGCGAGTGTGCTGTCCTCAATGATGACCCCTG 1500
DB 1441 TGGCGGCTCCTTGGCTTGGCGAAATGCGAGTGTGCTGTCCTCAATGATGACCCCTG 1500
QY 1501 GCCAACACATGAAGCAGAGAGCCGGGTGCGCATCCACATCATCTCGGGCAACACTG 1560
DB 1501 GCCAACACATGAAGCAGAGAGCCGGGTGCGCATCCACATCATCTCGGGCAACACTG 1560
QY 1561 CAGTACTCAACGGGACTACGAAGTGGAGCGGCTGGTGGCAAGCCACGCGGTAC 1620
DB 1561 CAGTACTCAACGGGACTACGAAGTGGAGCGGCTGGTGGCAAGCCACGCGGTAC 1620
QY 1621 CTCAGGAGCAGCACATTTGAGACTTTTCTCATCTCGGGCCAGCCAGAAACGGAAGAG 1680
DB 1621 CTCAGGAGCAGCACATTTGAGACTTTTCTCATCTCGGGCCAGCCAGAAACGGAAGAG 1680
QY 1681 GAGAAAGGATGCTGCCAAGCTGACGGACTCGGGCCAACTCCATGGAGGGCTGATG 1740

Db	1681		GAGAAAGGATGCTGCCAAGCTGCAGCGGACTCGGGCCAATCCATGGAAGGCGTGA	1740
Qy	1741	CCGCGATGGTTCCTGATCGTGCCTTCTCCGGACCAAGGACTCCAAGGCTTCCGCCAG	1800	
Db	1741	CCCGATGGTTCCTGATCGTGCCTTCTCCGGACCAAGGACTCCAAGGCTTCCGCCAG	1800	
Qy	1801	ATGGGCATTGATGATTCACAGCAAGACAAACCGGGGACCCCAAGATGCCCTGAACCCCTGAG	1860	
Db	1801	ATGGGCATTGATGATTCACAGCAAGACAAACCGGGGACCCCAAGATGCCCTGAACCCCTGAG	1860	
Qy	1861	GATGAGGTGGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTCGGG	1920	
Db	1861	GATGAGGTGGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTCGGG	1920	
Qy	1921	AAGGACCATGTGCGCGGTTTTTGCTCACTTCCACAGACAGAGATTTTGAGAAGAAGTAC	1980	
Db	1921	AAGGACCATGTGCGCGGTTTTTGCTCACTTCCACAGACAGAGATTTTGAGAAGAAGTAC	1980	
Qy	1981	TCCCGGAAGTGGATCCCGCGTTCGGAGCCTACGTTGCCCTGTGCCCTGTGTTCTCTGC	2040	
Db	1981	TCCCGGAAGTGGATCCCGCGTTCGGAGCCTACGTTGCCCTGTGCCCTGTGTTCTCTGC	2040	
Qy	2041	TTTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCCCTGATGCTTGGGATTTAT	2100	
Db	2041	TTTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCCCTGATGCTTGGGATTTAT	2100	
Qy	2101	GCCAGCATCTTCTGCTGCTGCTAATCAACCGTGCATCTGCTGCTGTGTTACTCCTCTGGT	2160	
Db	2101	GCCAGCATCTTCTGCTGCTGCTAATCAACCGTGCATCTGCTGCTGTGTTACTCCTCTGGT	2160	
Qy	2161	TCTCTGTTCCCTTAAGGCCCTGCAAGCTGTGTCGGCAGCATTTGCCCTCACGGGCACAT	2220	
Db	2161	TCTCTGTTCCCTTAAGGCCCTGCAAGCTGTGTCGGCAGCATTTGCCCTCACGGGCACAT	2220	
Qy	2221	AGCACCGCAGTTGGCATCTTTTCCGTCCTGCTTGTGTTTACTTCTGGCATTTGCCAAGATG	2280	
Db	2221	AGCACCGCAGTTGGCATCTTTTCCGTCCTGCTTGTGTTTACTTCTGGCATTTGCCAAGATG	2280	
Qy	2281	TTTCCACTGTAAACACACCCCATACGGAGCTGTGCAGCCGGATGCTGAATTTAAACACCT	2340	
Db	2281	TTTCCACTGTAAACACACCCCATACGGAGCTGTGCAGCCGGATGCTGAATTTAAACACCT	2340	
Qy	2341	GCTGACATCACTGCTGCCACCTGCAGCAGCTCAATTAATCTCTGGCCCTGGATGCTCCC	2400	
Db	2341	GCTGACATCACTGCTGCCACCTGCAGCAGCTCAATTAATCTCTGGCCCTGGATGCTCCC	2400	
Qy	2401	CTGTGTGAGGGCACCATTGCCACCTGCAGCTTTCCTGAGTGTCCATCGGGAACATGCTG	2460	
Db	2401	CTGTGTGAGGGCACCATTGCCACCTGCAGCTTTCCTGAGTGTCCATCGGGAACATGCTG	2460	
Qy	2461	CTGAGTCTCTTGCCAGCTCTCTTCTCTGCACATCAGCAGCATCGGGAAGTTGGCCCATG	2520	
Db	2461	CTGAGTCTCTTGCCAGCTCTCTTCTCTGCACATCAGCAGCATCGGGAAGTTGGCCCATG	2520	
Qy	2521	ATCTTTTGTCTTGCGGCTCATCTAATTTGGTGTGCTTCTGCTGGTGCCTCCCGACCGCCATC	2580	
Db	2521	ATCTTTTGTCTTGCGGCTCATCTAATTTGGTGTGCTTCTGCTGGTGCCTCCCGACCGCCATC	2580	
Qy	2581	TTTGACAACATGACCTACTGCTTGGCGTCCATGCGTTGGCTTCTTCCAAATGAGACCTTTT	2640	
Db	2581	TTTGACAACATGACCTACTGCTTGGCGTCCATGCGTTGGCTTCTTCCAAATGAGACCTTTT	2640	
Qy	2641	GATGGGCTGGACTGCTACACTCGCAGGAGGTGGCCCTCAAAATATATGACCCCTGTATT	2700	
Db	2641	GATGGGCTGGACTGCTACACTCGCAGGAGGTGGCCCTCAAAATATATGACCCCTGTATT	2700	
Qy	2701	CTGCTGGTGTGTCGCTGGCGTGTATCTGCAATGCTCAGCAGGTGGAATCGACTGCCCGC	2760	
Db	2701	CTGCTGGTGTGTCGCTGGCGTGTATCTGCAATGCTCAGCAGGTGGAATCGACTGCCCGC	2760	
Qy	2761	CTAAACTTCTCTGGAACCTACAGGCAACAGGGGAAAAAGAGAGATGGAGAGCTACAG	2820	

D	b	2761	CTAACTTCTCTGGAACTACAGGCAACAGGGGAAAAAGAGGAGATGGAGGACGTCACG	2820
Q	y	2821	GCATACAACCGGAGGCTGCTGCATAACTTCTGCCAAGAGACGTGGGGGCCCACTTCCGT	2880
D	b	2821		
D	b	2821	GCATACAACCGGAGGCTGCTGCATAACTTCTGCCAAGAGACGTGGCGGCCCACTTCCGT	2880
Q	y	2881	GCCGGGAGCGCCGAATGATGAATCTACTATCACTAGTCGCTGAGTGTGTGGCTGTTATG	2940
D	b	2881		
Q	y	2941	TTTGGCTTCCATTCGCCAACTTCTCTGAGTGTCTATGTGAGCTGGAGGCAACAATGAGGGT	3000
D	b	2941		
Q	y	3001	GCCGAGTGCCCTGGCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGCGAG	3060
D	b	3001		
Q	y	3061	GAGCGGTTCCGGCAGCTGGAAGAAGATCAAGACGATTGGTAGCACTACATGGCTGCCTCA	3120
D	b	3061		
Q	y	3121	GGCTGAACGCCAGCAGCTTACGATCAGGTGGCGCGCTCCACATCATCTGCCCTGGCTGAC	3180
D	b	3121		
Q	y	3181	TAGCCATGGCGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCCTCAACAATTTTC	3240
D	b	3181		
Q	y	3241	CAGATGAAGATTGGGCTGAACATGGGCCCAAGTCGTGGCAGGTGTCTAGTGGGCTCGGAAG	3300
D	b	3241		
Q	y	3301	CCACAGTATCACATCTGGGGGAACACAGTGAATGCTCTAGTCTGATGGACAGCACGGG	3360
D	b	3301		
Q	y	3361	GTCCCCGACCCGATCCAGGTGACACGGGACCTGTACCAGTTCTAGCTGCCAAGGGCTAC	3420
D	b	3361		
Q	y	3421	CAGCTGGAGTGTGAGGGGTGGTCAAGGTGAAGGCAAGGGGGAGATGACCACCTACTTTC	3480
D	b	3421		
Q	y	3481	CTCAATGGGGGGCCCCAGCAGTTAACAGGGCCCCAGCCACAATTCAGCTGAAGGACCAAG	3540
D	b	3481		
Q	y	3541	GTGGGCACT 3549	
D	b	3541		
Q	y	3541	GTGGGCACT 3549	
D	b	3541		
RESULT 2				
AAD08567				
ID	AAD08567 standard; DNA; 3552 BP.			
XX	AAD08567;			
AC	AAD08567;			
XX				
XX				
DT	04-SEP-2001 (first entry)			
XX				
DE	Human cardiac adenylyclase VI (ACVI) isoform #2 DNA.			
XX				
KW	Human; cardiant; beta-adrenergic signalling protein; beta-ASP;			
KW	myocardium; gene therapy; beta-adrenergic receptor; beta-AR;			
KW	adenylyclase; adenylylate cyclase; CAMP synthetase;			
KW	G-protein receptor kinase; GRK; heart disease; congestive heart failure;			
XX	cardiac adenylyclase VI; ACVI isoform; beta-ASP transgene; ds.			
XX				
OS	Homo sapiens.			
XX				

Key	Location/Qualifiers
CDS	1..3507
FT	/*tag= a
FT	/product= "Human cardiac adenylylase VI isoform #2"
FT	/EC_number= "4.6.1.1"
XX	
PN	W0200148164-A2.
XX	
PD	05-JUL-2001.
XX	
PF	26-DEC-2000; 2000WO-US35411.
XX	
PR	27-DEC-1999; 99US-0472667.
XX	
PA	(REGC) UNIV CALIFORNIA.
PI	Hammond HK, Gao M;
XX	
DR	WPI; 2001-418260/44.
DR	P-PSDB; AAE04311.
XX	
PT	Novel polynucleotide encoding a modified adenylylase polypeptide
PT	useful for enhancing cardiac function in mammalian hearts, and for
PT	treating heart disease, especially congestive heart failure -
XX	
PS	Claim 6; Page 134-140; 153pp; English.
XX	
CC	The present invention relates to methods and compositions for enhancing
CC	cardiac function in mammalian hearts by inserting transgenes encoding
CC	beta-adrenergic signalling proteins (beta-ASP) which increase
CC	beta-adrenergic responsiveness within the myocardium using in vivo
CC	gene therapy. The beta-ASPs of the invention include beta-adrenergic
CC	receptors (beta-AR), adenylylases (also referred as adenylylase
CC	adenylate cyclase and cAMP synthetase) and G-protein receptor kinase
CC	(GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
CC	in mammalian hearts and for treating heart disease, especially
CC	congestive heart failure. The present DNA sequence encodes human
CC	cardiac adenylylase VI (ACVI) isoform which is used for generating
CC	a fourth beta-ASP transgene, used in the exemplification
CC	of the invention.
XX	
XX	Sequence 3552 BP; 686 A; 1037 C; 1068 G; 761 T; 0 other;
Query Match	98.2%; Score 3484.8; DB 22; Length 3552;
Best Local Similarity	99.0%; Pred. No. 0;
Matches 3517; Conservative	0; Mismatches 32; Indels 3; Gaps
Oy	1 ATGTCATGTTTATAGTGCCCTCCTGGTCCCTAAAGTGGATGAACGGAACAGCCCTGGGGT 60
Db	
1 ATGTCATGTTTATAGTGCCCTCCTGGTCCCTAAAGTGGATGAACGGAACAGCCCTGGGGT 60	
Oy	61 GAACGCAATGGCGAGCAAGCGTTCCGCGCGCGTGGCACTCGGCGAGTGGCTTCTGCACG 120
Db	
61 GAACGCAATGGCGAGCAAGCGTTCCGCGCGCGTGGCACTCGGCGAGTGGCTTCTGCACG 120	
Oy	121 CCCCGCTATATAGCTGCCTCCCGGGATGCAGAGCCACCCAGCCACCCTCGGGGCC 180
Db	
121 CCCCGCTATATAGCTGCCTCCCGGGATGCAGAGCCACCCAGCCACCCTCGGGGCC 180	
Oy	181 CCTCGGTGCCCTTGGCAGGATGACGCTTTCATCCGAGGGGGCGGCCAGGCAAGGCAAG 240
Db	
181 CCTCGGTGCCCTTGGCAGGATGACGCTTTCATCCGAGGGGGCGGCCAGGCAAGGCAAG 240	
Oy	241 GAGCTGGGGTGGGGCAGTGGGCCCTGGGCTTCGAGGATACCGAGTGACACGACAGCG 300
Db	
241 GAGCTGGGGTGGGGCAGTGGGCCCTGGGCTTCGAGGATACCGAGTGACACGACAGCG 300	
Oy	301 GCGGGACGCGTCAAGTGGCGCCGACGCGGTGCCAGGAGTGGCGATCTCTGCTGGCG 360
Db	
301 GCGGGACGCGTCAAGTGGCGCCGACGCGGTGCCAGGAGTGGCGATCTCTGCTGGCG 360	
Oy	361 CGTTTGGTGCAGTGTTCAGTGCAGACAGTTCCTCGTTCGCGCAAGCTGAGCGCCTGTAC 420
Db	

AC AAX00461;
XX
DT 21-MAY-1999 (first entry)
XX
DE Human type VI adenylyl cyclase cDNA.
XX
KW Adenylyl cyclase type VI; human; hAC6; therapy; diagnosis; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 145..3651
FT /*tag= a
XX
XX
PN MO9901547-A1.
XX
PD 14-JAN-1999.
XX
PF 01-JUL-1998; 98WO-0513694.
XX
PR 01-JUL-1997; 97US-0886550.
PR 01-JUL-1997; 97US-0070904.
XX
PA (COR-) COR THERAPEUTICS INC.
XX
XX Tomlinson JA;
PI
XX WPI; 1999-106049/09.
DR P-PSDB; AAW30599.
DR
XX
XX
PT Newly isolated and purified human type VI adenylyl cyclase (hAC6)
PT polypeptide - useful for identifying potential therapeutic agents
PT that modulate hAC6 activity, and for the diagnosis of
PT hAC6-associated diseases and disorders
XX
XX Claim 3; Fig 1A-I; 42pp; English.
XX
XX This DNA sequence encodes human type VI adenylyl cyclase (hAC6, see
CC AAW30599); that is expressed mainly in the heart and brain. hAC6 has
CC a similar putative structure to other adenylyl cyclase isoforms
CC but, like type V, is distinguishable in that it has a larger
CC N-terminus and a relatively shorter C-terminus as it lacks the C2b
CC region. hAC6 cDNA was initially isolated from a human heart cDNA
CC library using an adenylyl cyclase PCR fragment as probe. It was
CC used to design primers that were used in a PCR-based RACE to obtain
CC the full-length cDNA sequence. The invention relates to the hAC6
CC gene, methods for the recombinant production of purified hAC6 and
CC the proteins made by these methods, antibodies against hAC6,
CC vectors, probes and host cells (especially HEK-293) transformed by
CC genes encoding polypeptides having hAC6 activity, along with
CC diagnostic and therapeutic uses for these various reagents. hAC6
CC can be used as a tool to screen for agonists and antagonists that
CC stimulate/inhibit hAC6. Such compounds have therapeutic utility
CC in treating diseases caused by aberrant activity of this enzyme,
CC and diseases whose symptoms can be ameliorated by stimulating or
CC inhibiting the activity of hAC6.
XX
SQ Sequence 4942 BP; 953 A; 1404 C; 1512 G; 1073 T; 0 other;
Query Match 98.0%; Score 3478.4; DB 20; Length 4942;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 3513; Conservative 0; Mismatches 36; Indels 3; Gaps 1;
QY 1 ATGTCATGGTTTATGGCCCTCCCTGGTCCCTAAAGTGGATGAACGGAAAAACAGCCTGGGGT 60
DB 145 ATGTCATGGTTTATGGCCCTCCCTGGTCCCTAAAGTGGATGAACGGAAAAACAGCCTGGGGT 204
QY 61 GAACGCAATGGGCGAGAGCGTTCCGGGCGCGGTGGGCACATCGGGCAGGTGGCTTCTGCACG 120
DB 205 GAACGCAATGGGCGAGAGCGTTCCGGGCGCGGTGGGCACATCGGGCAGGTGGCTTCTGCACG 264
QY 121 CCCCGCTATATGAGCTTGCCTCCGGGATGCAGACCCACCCCGCTGGGGGCCCC 180
DB 1345 GTCATGACCCCTGAATGAGCTCTTTTGGCCCGGTTTGACAAAGCTGGCTGGGAGAAATCACTGC 1404

DB 265 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCCCTGGGGCCCC 324
QY 181 CCTCGGTGCCCTGGCAGGATGACGCTTCATCCGAGGGGGCGGCCCCAGCAAGGCGCAAG 240
DB 325 CCTCGGTGCCCTGGCAGGATGACGCTTCATCCGAGGGGGCGGCCCCAGCAAGGCGCAAG 384
QY 241 GAGCTGGGGCTGCGGGCAGTGGCCCTCGAGGCTTCGAGGATACCGAGGTGACAACGACAGCG 300
DB 385 GAGCTGGGGCTGCGGGCAGTGGCCCTCGAGGATACCGAGGTGACAACGACAGCG 444
QY 301 GCGGGACGCTGAGTGGGCGCCGAGCGGGTGCACAGGAGTGGGCGATCCTGCTGGCGC 360
DB 445 GCGGGACGCTGAGTGGGCGCCGAGCGGGTGCACAGGAGTGGGAGATCCTGCTGGCGC 504
QY 361 CGTTTGGTGCAGCTGTTCCAGTGAAGCAGTTCGCTTCGCGCCAAAGCTTGGAGCGCCTGTAC 420
DB 505 CGTCTGGTGCAGGTGTTCCAGTGAAGCAGTTCGCTTCGCGCCAAAGCTTGGAGCAGCTGTAC 564
QY 421 CAGCGGTACTTTTCCAGATGAACAGAGCAGCCTGACGCTGCTGTGGTGGCGGTGCTGGT 480
DB 565 CAGCGGTACTTTTCCAGATGAACAGAGCAGCCTGACGCTGCTGTGGTGGCGGTGCTGGT 624
QY 481 CTGCTCACAGCGTGTGCTGGCTTTCCAAAGCGCAGCGCCGCCCTCAGCCTGCTGCTAT 540
DB 625 CTGCTCACAGCGTGTGCTGGCTTTTCCAGCGCGCACCCGCCCTCAGCCTGCTGCTAT 684
QY 541 GTGGCACTGTTGGCCTGTGCGCGCCGCTTTCGTCGGGCTCATGTGCTGTGTAACCGG 600
DB 685 GTGGCACTGTTGGCCTGTGCGCGCCGCTTTCGTCGGGCTCATGTGCTGTGTAACCGG 744
QY 601 CATPAGTTCGCGCAGGACTCCATGTGGTGGTGGTGAAGTGGTGGTGGGATCCTGGCG 660
DB 745 CATPAGTTCGCGCAGGACTCCATGTGGTGGTGGTGAAGTGGTGGGATCCTGGCG 804
QY 661 GCAGTGCAGGTGCGGGCGCTTTCCGACAGAGACCCCGCGAGCCCTCTCGGGGCTCTGG 720
DB 805 GCAGTGCAGGTGCGGGCGCTCTCGGACGAGACCCCGCGAGCCCTCTCGGGGCTCTGG 864
QY 721 TGCCCTGTGTTCTGTATACATCGCATACACGCTCCTCCCATCGCATCGCGGCTGCC 780
DB 865 TGCCCTGTGTTCTGTATACATCGCATACACGCTCCTCCCATCGCATCGCGGCTGCC 924
QY 781 GTCCCTCAGCGGCTGGGCTCTCCACCTTGTCATTTGATCTTGGCCTGGCAACTTAACCGT 840
DB 925 GTCCCTCAGCGGCTGGGCTCTCCACCTTGTCATTTGATCTTGGCCTGGCAACTTAACCGT 984
QY 841 GGTGATGCCCTTCTCTGGAAGCAGCTCGGTGGCAAGTGTGCTGTCTCTCTGCACCAAC 900
DB 985 GGTGATGCCCTTCTCTGGAAGCAGCTCGGTGGCAAGTGTGCTGTCTCTCTGCACCAAC 1044
QY 901 GTCATTTAGCATCTGCACACATATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 960
DB 1045 GTCATTTAGCATCTGCACACATATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 1104
QY 961 ACCCGCAGTTTACATCCAGGCGCGGCTCCACCTGCACATGAGAAATCGGACGAGAGCGG 1020
DB 1105 ACCCGCGGTTTACATCCAGGCGCGGCTCCACCTGCACATGAGAAATCGGACGAGAGCGG 1164
QY 1021 CTGCTGCTGTGCGTATTGCCCGCAGCAGCTTGCCATGAGATGAAGAAGACATCAACACA 1080
DB 1165 CTGCTGCTGTGCGTATTGCCCGCAGCAGCTTGCCATGAGATGAAGAAGACATCAACACA 1224
QY 1081 AAAAAAAGAGAC---ATGTTCCACAAGATCTACATACAGAAGCATGACAAATGTCAGCATC 1137
DB 1225 AAAAAAAGAGACATGATGTTCCACAAGATCTACATACAGAAGCATGACAAATGTCAGCATC 1284
QY 1138 CTGTTTGCAGACATTGAGGGCTTCCACAGCTGGCATCCAGTGCATCGGCGAGGAGCTG 1197
DB 1285 CTGTTTGCAGACATTGAGGGCTTCCACAGCTGGCATCCAGTGCATCGGCGAGGAGCTG 1344
QY 1198 GTCATGACCCCTGAATGAGCTCTTTTGGCCCGGTTTGACAAAGCTGGCTGGGAGAAATCACTGC 1257
DB 1345 GTCATGACCCCTGAATGAGCTCTTTTGGCCCGGTTTGACAAAGCTGGCTGGGAGAAATCACTGC 1404

Db	1042	 CTGCTGCTCTCGGTATTTGCCCCAGACAGCTTGCCATGGAGATGAAGAAGACATCAACACA	1101
QY	1081	AAAAAAGAAGC---ATGTTCCACAAGATCTACATACAGAAGCATGCAATGTTCAGCATC	1137
Db	1102	 AAAAAAGAAGACATGATGTTCCACAAGATCTATACATACAGAAGCATGACATGTTCAGCATC	1161
QY	1138	CTGTTTGCAGACATTGAGGGCTTCACCAAGCTGGCATCCCAAGTCGACTGGCAGGAGCTG	1197
Db	1162	CTGTTTGCAGACATTGAGGGCTTCACCAAGCTGGCATCCCAAGTCGACTGGCAGGAGCTG	1221
QY	1198	GTCAATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAAAGCTGGCTGGGAGAATCACTGC	1257
Db	1222	GTCAATGACCTTGAATGAGCTCTTTGCCCGGTTTGACAAAGCTGGCTGGGAGAATCACTGT	1281
QY	1258	CTGAGGATCAAGATCTTTGGGGACTGTTACTACTGTGTGTGTCAGGGCTGCCGAGGCGCCGG	1317
Db	1282	CTGAGGATCAAGATCTTAGGAGACTGTTACTACTCGGTGTGAGGGCTGCCGAGGCGCCGG	1341
QY	1318	GCGGACCATGCCCACTGCTGTGTGAGATGGGGTAGACATGATGAGGGCATCTCGCTG	1377
Db	1342	GCAGATCACGCCCACTGCTGTGTGAGATGGGGTAGACATGATGAGGGCATCTCGCTG	1401
QY	1378	GTACGTGAGGTGACAGGTGTAATGTGAACATGCCGCTGGGCATCCACAGCGGCGGCTG	1437
Db	1402	GTGCGTGAAGTAAACAGGTGTGAACGTGAACATGCGTGTGGCATCTCCACAGCGGACGTGTG	1461
QY	1438	CACCTGGCGGCTCCTTGGCTTGGGAAATGGCAGATTCGATGTGTGGTCCAAATGATGCACC	1497
Db	1462	CATTGGCGGCTCCTTGGCCACCGAAATGGCAGTTTGATGTCTGGTCAACGATGTGACC	1521
QY	1498	CTGGCCAAACCATGGAAGCAGGAAGCCGGCTGGCCGACATCCACATCACTCGGGCAACA	1557
Db	1522	CTGGCTAACCATGAGGCGCGGGGC--GGCCGGCGCATCCACATCACTCGGGCTACA	1578
QY	1558	CTGCAGTACTGAACGGGGACTACGAAGTGGAGCAGGCCGTGTGTGGCAAGCGCAACCGG	1617
Db	1579	CTGCAGTACTGAACGGGGACTATGAGGTGGAGCAGGCCGTGTGTGTGAACGCAATGCG	1638
QY	1618	TACTTCAAGGACGACACATTTGAGACTTCTCTATCTCTGGCGCCAGCCAGAAACGAAA	1677
Db	1639	TACCTCAAGAGCAGTGCATTTGAGACCTTCTCATCTTGGCGCCAGCCAAACAGGAAA	1698
QY	1678	GAGGAAAGGCATGCTGGCCAAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGCTG	1737
Db	1699	GAGGAAAGCCATGCTGSCCAAGCTTCAGCGGACACGGGCCAACTCCATGGAAGGACTG	1758
QY	1738	ATGCCCGATGGTTCCTGATCGTGCCCTCTCCCGGACCAAGGACTCCAAGGCCCTCCGC	1797
Db	1759	ATGCCCGGTGGTTCCTGACCGTCCCTCTCCCGGACCAAGGACTCTAAGGCATTCGCG	1818
QY	1798	CAGATGGCATTGATGATTCCAGCAAGACAACCGGGCACCCCAAGATGCCCTCAACCCCT	1857
Db	1819	CAGATGGCATTGATGATTCTAGCAAAACAAACCGGGGTGCCCAAGATGCTCTCAACCCCT	1878
QY	1858	GAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCATCTGATGCCCGCAGCATGTGATCAGCTG	1917
Db	1879	GAAGATGAGGTGGATGAGTTCCTGGCCCGAGCATCTGATGCCCGCAGCATGTGATCAGCTG	1938
QY	1918	CGAAGGCACATGTGGCGCGTTTTTGTCTACCTTCCAGAGAGAGGATTTTGAGAAGAAG	1977
Db	1939	CGAAGGCACATGTGCGCGGTTTTCTGCTCACTTCCAGAGAGAGGATCTTGAGAAGAAG	1998
QY	1978	TACTCCCGGAAGGTGGATCCCGCTTCGGAGCCTACGTTGCTGTGCCCTCTTGCTCTTC	2037
Db	1999	TACTCCCGGAAGGTGGATCCCGCTTCGGAGCCTACGTTGCTGTGCCCTCTTGCTCTTC	2058
QY	2038	TGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCCCTGATCTTGGGATT	2097
Db	2059	TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCACACTCCACCCCTGATCTTGGGATC	2118
QY	2098	TATGCCAGCATCTCTGCTGCTGCTTAATCAACCGTGCTGATCTGTGCTGTACTCCTGT	2157

QY 3238 TTCCAGATGAAGATTGGCTGAACATGGGCCAGTCTGGCAGGTGTCATCGGGCTCGG 3297
|||||
Db 3259 TTCCAGATGAAGATTGGCTGAACATGGGCCAGTCTGGCAGGTGTCATCGGGCTCGG 3318
|||||
QY 3298 AAGCCACAGTATGACATCTCGGGGAAACACAGTGAATGCTCTAGTCGTATGGACAGCAG 3357
|||||
Db 3319 AAGCCACAGTATGACATCTCGGGGAAACACAGTGAATGCTCTAGTCGTATGGACAGCAG 3378
|||||
QY 3358 GGGTCCCCCAGCAATCCAGGTGACACAGGACCTGTACCAGGTTCCTAGTGTCCAGGGC 3417
|||||
Db 3379 GGGTCCCCCAGCAATCCAGGTGACACAGGACCTGTACCAGGTTCCTAGTGTCCAGGGC 3438
|||||
QY 3418 TACCAGTGGAGTGTCTGAGGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACACACCTAC 3477
|||||
Db 3439 TACCAGTGGAGTGTCTGAGGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACACACCTAC 3498
|||||
QY 3478 TTCTCAATGGGGCCCCCAGGTAAACAGGGCCCCAGCCACAAATTTCAGTGAAGGGACC 3537
|||||
Db 3499 TTCTCAATGGGGCCCCCAGGTAAACAGGGCCCCAGCCACAAATTTCAGTGAAGGGACC 3558
|||||
QY 3538 AAGTGGGCACT 3549
|||||
Db 3559 AAGTGGGCACT 3570
|||||

RESULT 5

AAQ42525
ID AAQ42525 standard; DNA; 4046 BP.

XX AAQ42525;

XX 14-SEP-1993 (first entry)

XX Cardiac adenyl cyclase gene.

XX Regulation; cardiac function; heart; heart failure; ss.

XX Canis familiaris.

XX Key Location/Qualifiers
FT CDS 131..3627
FT /*tag= a

XX EP543137-A.

XX 26-MAY-1993.

XX 12-OCT-1992; 92EP-0117374.

XX 18-NOV-1991; 91US-0793961.

XX (AMCY) AMERICAN CYANAMID CO.

XX Ishikawa Y;

XX WPI; 1993-168873/21.

DR P-PSDB; AAR37309.

XX Purified DNA encoding cardiac adenyl cyclase - useful to screen
PT for cpds. which stimulate activity of the cyclase

XX Claim 1; Fig 2; 34pp; English.

XX A canine heart cDNA library was constructed in lambda gt10 and was
CC screened with a 970 bp *k*atI-HincII fragment from type I adenyl
CC cyclase cDNA probe (encodes the first cytoplasmic domain of adenyl
CC cyclase, which has significant homology to other previously known
CC types of adenyl cyclase). One positive clone, of 5.4 kb was obtd.
CC Positive colonies were subcloned into pUC18 and further subcloned
CC and sequenced bidirectionally. The 5.4 kb clone was used to
CC rescreen the library and on overlapping clone contg. the 5' end of
CC the gene was isolated. Together the two clones cover the complete

CC canine cardiac adenyl cyclase gene. The gene is suspected of
CC being involved in the regulation of cardiac function and it is thought
CC that decreased activity of adenyl cyclase in the heart may be a
CC major factor in the development of heart failure. Thus the adenyl
CC cyclase gene is useful to screen cpds. which stimulate the activity
CC of the cyclase.

XX
SQ Sequence 4046 BP; 743 A; 1206 C; 1254 G; 843 T; 0 other;

Query Match 84.4%; Score 2996.8; DB 14; Length 4046;

Best Local Similarity 91.0%; Pred. No. 0;

Matches 3233; Conservative 0; Mismatches 307; Indels 12; Gaps 4;

QY 1 ATGTCTATGTTTGTAGTGGCTCTCTGCTTAAAGTGGATCAACGAAACAGCTGGGGT 60
|||||

Db 131 ATGTCTGTTTGTAGTGGCTCTCTGCTTAAAGTGGATCAACGAAACAGCTGGGGT 190
|||||

QY 61 GAACGCAATGGGAGAGCGTTCCGGCGCCGTGGCACTCGGACAGGTGCTTCTGCACG 120
|||||

Db 191 GAACGCAATGGGAGAGCGT---CCACGCCCGGGACTCGGACCACTGGCTTCTGCACG 247
|||||

QY 121 CCCCGCTATATGAGTGCCTCCGGGATGCAGACCCAGCCACCCCTGCGGGCCCC 180
|||||

Db 248 CCCCGCTATATGAGTGCCTCCGGGATGCAGACCCAGCCACCCCTGCGGGCTCC 307
|||||

QY 181 CCTCGTGGCCCTGGCAGGATGACGGCTTCATCCGAGGGCGGCCAGGCAAG 240
|||||

Db 308 CCTCGTGGCCCTGGCAGGATGAGGCTTCATCCGAGAGCGGCCGAGGCAAG 367
|||||

QY 241 GAGCTGGGGCTCGGGAGTGGCCCTGGGTTCCAGAGTACCAGAGTGAACAAGACAGCG 300
|||||

Db 368 GAGCTGGGGCTCGGGAGTGGCCCTGGGTTCCAGAGTACTGAGG---CCATGTTCAGCG 424
|||||

QY 301 GCGGGACGCTGAGTGGCGCCGCGGAGTGGCCAGGAGTGGGATCCTGCTGGCGC 360
|||||

Db 425 GTTGGGACGCTGAGTGGCGCCGCGGAGTGGCCAGGAGTGGGATCCTGCTGGCGC 484
|||||

QY 361 CGTTTGTGTCAGTGTTCAGTGAAGCAGTTCCTGTCGCGCAAGTGGAGCCCTGTATC 420
|||||

Db 485 CGTCTGGCCCGAGTGTTCAGTGAAGCAGTTCCTGTCGCGCAAGTGGAGCCCTGTATC 544
|||||

QY 421 CAGCGTACTTTTCCAGATGAACAGAGAGCGCTGACGCTGCTGGTGGCGGTGCTGGTG 480
|||||

Db 545 CAGCGTACTTTTCCAGATGAACAGAGAGCGCTGACGCTGCTGGTGGCGGTGCTGGTG 604
|||||

QY 481 CTGCTCACAGCGTGTGCTGGCTTTCCAAAGCCGACCCCGCCCTCAGCTGCTGCTAT 540
|||||

Db 605 CTGCTCACAGCGTGTGCTGGCTTTCCAAAGCCGACCCCGCCCTCAGCTGCTGCTAT 664
|||||

QY 541 GTGGCACGTGTGGCTGTGCGCGCCGCTGTTCTGGGGCTCATGTTGTTGTTAAACCGG 600
|||||

Db 665 GTGGCCCTGTGGCTGTGCGCGCCGCTGTTCTGGGGCTCATGTTGTTGTTAAACCGG 724
|||||

QY 601 CATAGTTCGCGCAGGACTCCATGTGGTGGTGAAGTAACTGTTGTTGGGATCCTGGCG 660
|||||

Db 725 CACAGCTTTGCGCAGGACTCCATGTGGTGGTGAAGTAACTGTTGTTGGGATCCTGGCA 784
|||||

QY 661 GCAGTGCAGTTCGGGGCGCTTTTCGAGCAGACCCCGGAGCCCTCTGCGGGCTCTGG 720
|||||

Db 785 GCGGTTTCAGGTTGGGGTGGCTGGGAGCCCAACCCCGGAGCCCTCTGTTGGGCTCTGG 844
|||||

QY 721 TGGCCCTGTGTTTGTATACATACAGCTCTCTCCCATCCGATCGGGGTGCC 780
|||||

Db 845 TGGCCCTGTGTTTGTATACATACAGCTCTCTCCCATCCGATCGGGGTGCC 904
|||||

QY 781 GTCTTCAGCGGCTCGGGCTCTCCAGTTCATGATTTGGCTGGGCAACTTAACCGT 840
|||||

Db 905 GTCTTCAGTGGCTCGGGCTCTCCAGTTCATGATTTGGCTGGGCAACTTAACCGC 964
|||||

QY 841 GGTGATGCCTTCCTCTGGAGAGAGCTCGGTGCGCAAGTGTGCTGTTCTCTGCACCAAC 900
|||||

Db 965 GGTGACGCCCTCTCTGGAGAGAGCTCGGTGCGCAAGTGTGCTGTTCTCTGCACCAAC 1024
|||||

Qy 901 GTCAATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTACGCCAGGCGCTTTCCAGAG 960
Db 1025 GTCAATTGGCATCTGCACACACTATCCAGCAGAGGTGTCTACGCCAGGCGCTTTCCAGAG 1084
Qy 961 ACCCGCAGTATACATCCAGGCGCGGCTCCACCTGCAGCATGAGATCGGCACGAGAGCGG 1020
Db 1085 ACCCGCGGTTACATTCAGGCGCGGCTCCACCTGCAGATGAGAAACCGGCACGAGAGCGG 1144
Qy 1021 CTGCTGCTGTCGGTATGCCCCAGCAGCTTGCCATGAGATGAAAGAGACATCAACACA 1080
Db 1145 CTGCTGCTGTCGGTATGCCCCAGCAGCTTGCCATGAGATGAAAGAGATATCAACACA 1204
Qy 1081 AAAAAGAAGAC---ATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCCAGCATC 1137
Db 1205 AAGAAAGAAGACATGATGTTCCACAAGATCTACATCCAGAAGCATGACAATGTCCAGCATC 1264
Qy 1138 CTGTTTTCAGACATTTAGGGCTTCCACAGCCTGGCATCCAGTGCAGTGCSCAGAGAGTG 1197
Db 1265 CTGTTTTCAGACATTTAGGGCTTCCACAGCCTGGCGTCCAGTGCACCGCAGAGAGTG 1324
Qy 1198 GTCAATGACCCGTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAAATCACATGC 1257
Db 1325 GTCAATGACCCGTGAAGAGCTCTTCCCGCGGTTTGACAAGCTGGCTGCGGAGAAATCACATGC 1384
Qy 1258 CTGAGGATCAAGATCTTTGGGGACTGTTACTACTGTGTGTGTCAGGGCTGCCGAGAGCGCGG 1317
Db 1385 CTGAGGATCAAGATCTTTAGGGACTGTTACTACTGTGTGTGTCGGGCTGCCGAGAGCGCGG 1444
Qy 1318 GCCGACCATGCCACTGCTGTGTGAGATGGGGTGAACATGATTTGAGGCCATCTCGCTG 1377
Db 1445 GCAGACCATGCCACTGCTGTGTGAGATGGGGTGAACATGATCGAGGCCATCTCGCTG 1504
Qy 1378 CTACGTGAGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGCGCGTG 1437
Db 1505 GTGCGTGAAGTGACAGGTGTGAACATGCGCGTGGGCATCCACAGCGGCGCGTG 1564
Qy 1438 CACTGCGCGCTCTTGCGCTTCGGAATGCGAATGCGAGTTCGATGTGTGTCGCAATGATGTGACC 1497
Db 1565 CACTGTGCTGCTTGCGCTTCGGAATGCGAATGCGAGTTCGAGCTGTGCTCAATGAGCTGACT 1624
Qy 1498 CTGCCAACACATGGAAGCAGAGAGCGGCTGCGCGCATCCACATCACATCGCGGCAACA 1557
Db 1625 CTGCCAACACATGGAAGCGG---CCGCGCGCGCGCGCATCCACATCACCGCGCGCACG 1681
Qy 1558 CTGCAGTACCTGAACGGGACTAGGAAGTGAGCGAGCGCGCTGTGGCAAGCGCAACCGG 1617
Db 1682 CTGCAGTACCTGAACGGGACTAGGAAGTGAGCGCGCGCGCTGTGGCGAGCGGCAACCGG 1741
Qy 1618 TACCTCAAGGAGCAGCAGATGAGACTTTCCTCATCTGCGGCGCGCAGCCAGCAAGAGGAAA 1677
Db 1742 TACCTCAAGGAGCAGCAGATGAGACTTTCCTCATCTGCGGAGCGCAGCAGCAAGAGGAAA 1801
Qy 1678 GAGGAGAGGAGCATGTGCGCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGCGTG 1737
Db 1802 GAGGAGAGGAGCATGTGCGCAAGCTGCAGCGGAGCGGGGCCAACTCCATGGAAGGCGTG 1861
Qy 1738 ATGCCCGCATGGGTCTGATCGTCTTCCCGGACCAAGGACTCCAAGGCGCTTCGCG 1797
Db 1862 ATGCCCGCATGGGTCTGATCGTCTTCCCGGACCAAGGACTCCAAGGCTTTCGCG 1921
Qy 1798 CAGATGGGCATTTGATGATTCAGCAAGACAAACCGGGCAGCCAGATGCCCTGAACCCCT 1857
Db 1922 CAGATGGGCATTTGATGATTCAGCAAGACAAACCGGGGTGCCAAGATGCCCTGAACCCCT 1981
Qy 1858 GAGGATGAGGTGATGAGTTCCTGAGCGGTGCCATCGATGCCGCGCAGCATTTGATCAGCTG 1917
Db 1982 GAGGATGAGGTGATGAGTTCCTGGGCGGTGCCATCGATGCCGCGCAGCATCGATCAGCTA 2041
Qy 1918 CGGAAGGACCATGTGCGCGCGCTTTTGTCTCACCTTCCAGAGAGAGGATTTTGAAGAAG 1977
Db 2042 CGGAAGGACCATGTGCGCGCGCTTCTGCTCACCTTCCAGAGAGAGGATCTTGAAGAAG 2101
Qy 1978 TACTCCCGGAAGGTGGATCCCGCTTCGGAGCCTACGTTGCTGTGCGCTGTGCTCTTC 2037

Db 2102 TACTCAAGGAAGGTGACCCCGCTTCGGAGCCTACGTGGCGTGTGGCGTGTGGTCTTC 2161
Qy 2038 TGCCTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCTGATGCTTGGGATT 2097
Db 2162 TGCCTCATCTGCTTCATCCAGCTCCTGCTCTTCCACACTCAACCTGATGCTTGGGATC 2221
Qy 2098 TATGCGACATCTTCTGCTGCTAATACCGTGTGATCTGCTGTGCTGTGCTGTGCTGTGCTGT 2157
Db 2222 TACGCCAGTATCTTTGCTGTGCTGATCACCCTGCTGACCTGTGCGGTGTACTCTCTGT 2281
Qy 2158 GTTCTCTGTTCCCTAAGGCCCTGCAACCTGTGTCCCGCAGCAATTTGCTCCAGCGCA 2217
Db 2282 GGCCTCTCTTCCCAAGGCCCTGCGAGCTCTTCCCGCAGCATGCTCCGCTCTCGGCA 2341
Qy 2218 CATAGCACCGCAGTTGGCATCTTTTCCGCTCTGCTGTGTTTACTTCTGCGCATTTGCCAC 2277
Db 2342 CACAGCATGTGGTTGGCATTTTTCAGTCTTGTGTGTGTTCACCTTCCCTGCGCATCCCAAC 2401
Qy 2278 ATGTTCACTGTAAACACACACCCCATACGGAGCTGTGAGCCCGGATGCTGAATTTAACA 2337
Db 2402 ATGTTCACTGTAAACACACACCCCATCCGACCTGTGAGCCCGGATGCTGAATGTAAACA 2461
Qy 2338 CCTGCTGACATCACTGCTGCAACCTGTGAGCAGCTCAATTTACTTCTGGGCTGTGATGCT 2397
Db 2462 CCGCTGACATCACTGCTGCAACCTGTGAGCAGCTCAATTTACTTCTGGGCTGTGATGCT 2521
Qy 2398 CCGCTGCTGAGGCGACCATGCCACCTGCGAGCTTTTCTGAGGTGTCCATCGGGAACATG 2457
Db 2522 CCGCTGCTGAGGCGACCGCACCTTGCAGCTTCCCTGAGTACTCTGTTGGGAACATG 2581
Qy 2458 CTGCTGAGTCTCTTGGCCAGCTCTGCTTCTGCAATCAGCAGCATCGGGAAGTTGGCC 2517
Db 2582 CTGCTGAGTCTCTTGGCCAGCTCTGTTTCTGCAATCAGTAGCATCGGGAAGTTGGCC 2641
Qy 2518 ATGATCTTTGCTTGGGCTCACTATTTTGTGTGCTGCTGCTGGTCCCGCCAGCGCCG 2577
Db 2642 ATGATCTTTGCTTGGGCTCACTATTTTGTGTGCTGCTGCTGGGCCCCCGCCAGCACC 2701
Qy 2578 ATCTTTGACAACTATGACTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGAC 2637
Db 2702 ATCTTTGACAACTATGACTACTGCTTGGTGTCCATGGCTTGGCTTCTTCCAATGAGACC 2761
Qy 2638 TTTGATGGCTGAGCTGTCCAGCTGCAGGAGGCTGGCCCTCAAAATATATGACCCCTGTG 2697
Db 2762 TTTGATGGCTGAGCTGTCCAGCTGCAGGAGGCTGGCAGTGAATACATGACCCCTGTG 2821
Qy 2698 ATCTGCTGCTGCTTGGCGTGGCGTGTATCTGCAATGCTCAGCAGGTGGAATCGACTGCC 2757
Db 2822 ATCTGCTGCTGCTTGGCGTGGCGTGTATCTGCAACGCGCCAGCAGGTGGAATCACTGCA 2881
Qy 2758 CGCCTAAAATCTCTCGAAACTACAGGCAACAGGGGAAAAAGAGAGATGAGGAGCTA 2817
Db 2882 CGTCTGAGTCTCTCGAAACTGCGCAACGGGAGAGAGAGATGAGGAGCTC 2941
Qy 2818 CAGGCATACAAACCGAGGCTGCTGATCAACATTTCTGCCAAGAGGCTGGCGGCCACTTTC 2877
Db 2942 CAGGCTTACAAACCGAAGCTGCTGATCAACATTTCTGCTTAAGSAGTGTGCTGCCACTTC 3001
Qy 2878 CTGGCCCCGGGAGCGCGCAATGATGAATCTACTACTGCTGTGAGTGTGTGGCTGTGT 2937
Db 3002 CTGGCCCCGGGAGCGCGCAACGATGAGCTTACTACCAGTCTGTGTGAGTGTGTGGCGCTC 3061
Qy 2938 ATGTTTGGCTCCATTTGCCAACTTCTGAGTCTTATGTGGAGCTGAGGCAACAAATGAG 2997
Db 3062 ATGTTTGGCTCCATTTGCCAACTTTTCTGAGTCTTATGTGGAGCTGAGGCAACAAATGAG 3121
Qy 2998 GGTGCGGAGTGTGCTGCGCTGCTCAACGAGATCATCGCTGACTTTTCATGAGATTTATCAGC 3057
Db 3122 GGTGCTGAGTGTGCTGCGCTGCTCAACGAAATCATCGCGACTTTTGTGATGAGATCATCAGC 3181
Qy 3058 GAGGAGCGGTTCCGCGAGCTGGAAAGATCAAGACGATTTGTTAGCACCTTACATGCTGCC 3117

Db 3182 GAGAGCGGTTCCGGCAGCTGAGAAATCAAGACGATCGGTAGCAGTACATGGCTGCG 3241
QY 3118 TCAGGGCTGAACCCAGCACCTACGATCAGGTGGCGCTGCCACATCACTGCCCTGGCT 3177
Db 3242 TCGGGCTGAACCCAGCACCTACGATCAGGTGGCGCTGCCACATCACTGCCCTGGCC 3301
QY 3178 GACTAGCCCATGGCTCATGAGCAGATGAAGCAGATCAATGAGCAGCTCTTCAACAAT 3237
Db 3302 GACTATGCCATGGCTCATGAGCAGATGAACACATCAACGAGCAGCTCTTCAACAAC 3361
QY 3238 TTCAGATGAAGATTGGCTGAACATGAGCGCCAGTCTGTCAGGTGTATCGGGGCTCGG 3297
Db 3362 TTCAGATGAAGATTGGCTGAACATGAGCGCCAGTCTGTCAGCGCTCATTTGGGGCTCGG 3421
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QY 3418 TACCAGCTGAGTGTGAGGGGTGGTCAAGGTGAAGGCAAGGGGAGATGACCACTAC 3477
Db 3542 TACCAGCTGAGTGTGAGGGGTGGTCAAGGTGAAGGCAAGGGGAGATGACCACTAC 3601
QY 3478 TTCTCTCAATGGGGGCCCCAGCAGTTAAACAGGGCCCCAGCCACAAATTCAGCTGAAGGAGC 3537
Db 3602 TTCTCTCAATGGGGGCCCCAGCAGTTAGCAGAGCCAGCTACAGTTTCAGCTGCAGGACC 3661
QY 3538 AAGGTGGGCACT 3549
Db 3662 AAGGTGGGCACT 3673

RESULT 6
ABI99680
ID ABI99680 standard; cDNA; 5841 BP.
XX
AC ABI99680;
XX
XX 07-MAR-2002 (first entry)
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:716.
XX
XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX
OS Mus musculus.
XX
XX WO200188188-A2.
XX
XX 22-NOV-2001.
XX
XX 18-MAY-2001; 2001WO-JP04192.
XX
XX 18-MAY-2000; 2000JP-0145977.
XX
XX (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX
PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX
DR WPI; 2002-034733/04.
DR P-PSDB; ABB57257.
XX
PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or
PT by determining the expression profile of a gene group comprising these
PT genes -
XX
PS Claim 2; Page 1771-1780; 2690pp; English.
XX
XX The present invention describes a method for examining ischaemic

CC conditions, comprising measuring the expression levels of particular
CC genes (I) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (I). The method
CC is useful for examining the ischaemic condition (e.g. compressive
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC expression levels of particular genes (ABI99202 to ABI99912, encoding
CC the protein sequences in ABB57020 to ABB57374) or by determining the
CC expression profile of a gene group comprising these genes. The
CC expression levels or expression profiles produced by these genes are
CC used as an indicator when screening for ischaemic condition-improving
CC drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914
CC represent PCR primers for a mouse ischaemic condition related sequence,
CC which are used in the exemplification of the present invention.
XX
QY Sequence 5841 BP; 1214 A; 1558 C; 1673 G; 1396 T; 0 other;
Query Match 77.9%; Score 2765; DB 24; Length 5841;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 3095; Conservative 0; Mismatches 445; Indels 13; Gaps 5;
QY 1 ATGTCATGTTTGTAGTGGCCCTCTGGTCCCTAAAGTGGATGAACGAAACAGCTGGGGT 60
Db 96 ATGTCATGTTTGTAGTGGCCCTCTGGTCCCAAGTGGATGAACGAAACAGCTGGGG 155
QY 61 GAACGCAATGGGCAGAGCGTTCCCGCGCCCTGGCACTCGGCAGGTGCTTTCGACG 120
Db 156 GAACGCAATGGGCAGAGCG- - -CCCACGCCACGCGAATCGAGCAGTGGCTTTCGCA 212
QY 121 CCCCCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180
Db 213 CCTCGCTACATGAGTGCCTCAAGATTCGGAGGCCACCCAGCCCTCTCGAGCTCAC 272
QY 181 CCTCGGTGCCCTGGCAGGATGACGCTTCATCGGAGGGCGGCCAGCAAGGGCAAG 240
Db 273 ACTCGGTGCCCTGGCAGGATGAGCCTTCATCAGGAGGGCGGCCGCGAGGGGTGTG 332
QY 241 GAGCTGGGGCTGCGGGCAGTGGCCCTTCGAGGTACCGAGGTGACACAGCAGCG 300
Db 333 GAGCTGGGGCTGCGGTGAGTGGCTTTGAGCAGACACTGAGGTGACACACCGATG 392
QY 301 GCGGGACGCTGAGTGGCGCCCGCGGTCGCCAGGAGTGGCGCATCTGCTGGCG 360
Db 393 GGC- - -ACAGTGAAGTGGCAGCCGATACATCGCTCGGAGCGGTCCGTCTGCTGGC 449
QY 361 CGTTTGTGTCAGTGTTCAGTGAAGCAGTTCGCTTCGGCCAAAGTGGAGCGCTCTAC 420
Db 450 CGCTTGTGCGAGTGTTCAGTCTAAGCAGTTCGGCTCTGCCAAGCTGGAGCGGTGAC 509
QY 421 CAGCGTACTTTTCCAGATGAACACAGCAGCTGACGCTGTGTGTGGGTGCTGTGTG 480
Db 510 CAGCGTACTTCTCCAGATGAACACAGCAGCTCAGCTGTCTCATGCGGTGCTGTGTG 569
QY 481 CTGCTCACAGCGGTGCTGGCTTTCCAAAGCCGACCCCGCCCTCAGCGCTGCTAT 540
Db 570 CTGCTCATGCTGTACTGTGTGACTTTCCACGCTGCGGCTGCCAGCCTCAGCCTGCTTAC 629
QY 541 GTGCGACTGTGGCTGTGCGCGCCCTCTGCTGGGGCTCATGTGTGTGTGTGTAAACCG 600
Db 630 GTGCGCTGTGACCTGTGCTCTGCTCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 689
QY 601 CATAGCTTCGCCAGGACTCCTCATGTGGTGTGAGTAACTGTGTGTGGCATCTCGGGC 660
Db 690 CACAGCTTCGCCAGGACTCCTCATGTGGTGTGAGTATGTGTGTGTGTGTGTGTGTGT 749
QY 661 GCAGTCAGTGGGGCGCTTTTCGAGCAGACCCCGCGAGCCCTCTGCGGGCTCTGTG 720
Db 750 GCGGTGCAAGTGGGGTGGCTGGCAGCCCAATCCACACAGCCCTCTCGGGCGGCTTTGG 809
QY 721 TGCCCTGTGTCTTTGTATACATCGCATACACGCTCTCTCCCATCCGATCGGGGTGCC 780
Db 810 TGCCCGGTGTCTTCGTCTACATCACCTACACTCTCTCTCTCTCTCTCTCTCTCTCT 869
QY 781 GTCTCTCAGCGGCTGGGCTCTCCACCTTGCACTTTGACTTTGGCTGGCAACTTAACCGT 840

Db 870 GTACTCAGCGCCTGGCGCTCTCTACTCTGCAATTTGATTTTGGCTGCGACCTCAACAGC 929
QY 841 GGTGATGCTTCCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTTCTCTCTGACCAAC 900
Db 930 AGCAGCCCTTCCCTTTGGAAGCAGCTCGGTGCTAACGTGGTGTCTCTCTCTGACCAAT 989
QY 901 GTCAATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 960
Db 990 GCCATGGTGTCTGCACACACTACCTTGTGAAGTGTCTCAGCGCCAAAGCTTTTCAGGAG 1049
QY 961 ACCCGCAGTTTACATCCAGGCGCGGCTCCACTGCAGCATGAGATCGGCACGAGAGGG 1020
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QY 1021 CTGCTGTCTGCGTATTGGCCCGACAGCTTGCCTATGAGATGAAGAAGACATCAACACA 1080
Db 1110 CTGCTGTCTGCGTATTGGCCCGACAGCTTGCCTATGAGATGAAGAAGACATCAACACA 1169
QY 1081 AAAAAAGAAC ---ATGTTTCCACAAGATCTACATACAGAACGATGACAATGTTCAGCATC 1137
Db 1170 AAAAAAGGACATGATGTTCCATAAGATCTACATCCAGAACGATGATAATGTTCAGCATC 1229
QY 1138 CTGTTTGCAGACATGAGGGTTCCACAGCCTGCGATCCCGAGTGCATGCGCCAGGAGCTG 1197
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QY 1198 GTCATGACCTGAAATGAGCTTTCGCCGTTTCACAGCTGCGTGGCGGAATCACTGC 1257
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QY 1258 CTGAGGATCAAGATCTTTGGGAGCTGTACTACTGTGTGTCAGGCGTCCCGAGGCGCGG 1317
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QY 1378 GTACGTGAGGTGACAGGTGTAATGTGAACATGCGCGTGGGCATCCACAGGGCGCGCTG 1437
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Db 1707 TACCTCAAGGAGCAGTGCATTTAGACCTTCTCATACTTGGCGCAGCAGCAAGAAACGGAAA 1766
QY 1678 GAGGAGAAAGCATCTGGCCCAAGCTGCAGCGGACTCGGGCCCACTCCATGGAAGGGCTG 1737
Db 1767 GAGGAGAAAGCATCTGGCCCAAGCTTCAGCGGACACGGGCGCACTCCATGGAAGGACTG 1826
QY 1738 ATGCCGGATGGGTTCTGATGTCGCTTCTCCCGACCAAGGACTCCAGGCGCTTCGCG 1797
Db 1827 ATGCCCGCTGGGTTCTGACGCTGCGCTTCTCCGGAGCAAGGACTCTTAAGGCAATTCGCG 1886
QY 1798 CAGATGGGCATTTGATTTCCAGCAAGAACACACCGGGGACCCCAAGATGCGCTGAACCT 1857
Db 1887 CAGATGGGCATTTGATTTCTAGCAAGAACACACCGGGGTGCCAGATGCTCTGNAACCT 1946
QY 1858 GAGGATGAGGTGAGTTCTCTGAGCGGTGCCATCGATGCCGCGAGCATTTGATCAGCTG 1917
Db 1917 GAGGATGAGGTGAGTTCTCTGAGCGGTGCCATCGATGCCGCGAGCATTTGATCAGCTG 1917

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QY 2278 ATGTTTCACTGTAAACACACACCCCATACGAGCTGTGAGCGCCGATGCTGATTAACA 2337
Db 2367 ATGTTTCACTGTAAACACACCCCATACGAGCTGTGAGCGCCGATGCTGATTAACA 2426
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Qy 1056 GGAGATGAAGAAGACATCAACACAAAAAAGAAAGACATGTTCCACAAAGATCTACATACA 1115
Db 423 GGAGATGAAGAAGACATCAACACAAAAAAGAAAGACATGTTCCACAAAGATCTACATACA 482
Qy 1116 GAAGCATGACAAATGTACAGCATCTGTTTGGCAGACATTCAGGGCTTCACAGCCTGGCATC 1175
Db 483 GAAGCATGACAAATGTACAGCATCTGTTTGGCAGACATTCAGGGCTTCACAGCCTGGCATC 542
Qy 1176 CCAGTGCACATCGCGAGAGCTGGTCAATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAA 1235
Db 543 CCAGTGCACATCGCGAGAGCTGGTCAATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAA 602
Qy 1236 GCTGGCTGCGAGAAATCACTGCCCTGAGGATCAAGATCTTTGGGGGACTGTTACTACTGTGT 1295
Db 603 GCTGGCTGCGAGAAATCACTGCCCTGAGGATCAAGATCTTTGGGGGACTGTTACTACTGTGT 662
Qy 1296 GTCAGGGCTGCGGAGGCGCGGCGACCATGCCACTGCTGTGTGGAGATGGGGGTAGA 1355
Db 663 GTCAGGGCTGCGGAGGCGCGGCGACCATGCCACTGCTGTGTGGAGATGGGGGTAGA 722
Qy 1356 CATGATTGAGGCCATCTCGCTGTGATGAGGTGACAGGTGTGAATGTGAACATGCGCGGT 1415
Db 723 CATGATTGAGGCCATCTCGCTGTGATGAGGTGACAGGTGTGAATGTGAACATGCGCGGT 782
Qy 1416 GGGCATCCACAGCGCGCGTGCACCTGGCGGCTCTTTGGCTTGGGAAATGGCAGTTTCA 1475
Db 783 GGGCATCCACAGCGCGCGTGCACCTGGCGGCTCTTTGGCTTGGGAAATGGCAGTTTCA 842
Qy 1476 TGTGTGTCTCAATGATGTGACCTTGGCCAAACCACATGGAAGCAGGAGCGGGCTGGCGG 1535
Db 843 TGTGTGTCTCAATGATGTGACCTTGGCCAAACCACATGGAAGCAGGAGCGGGCTGGCGG 902
Qy 1536 CATCCACATCACTCGGGCAACACTGTCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGG 1595
Db 903 CATCCACATCACTCGGGCAACACTGTCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGG 962
Qy 1596 CCGTGGTGGCAGCGCAGCGTACCTCAAGGAGCAGCACATTTGAGACTTTTCTCATCTCT 1655
Db 963 CCGTGGTGGCAGCGCAGCGTACCTCAAGGAGCAGCACATTTGAGACTTTTCTCATCTCT 1022
Qy 1656 GGGCGCCAGCCAGAAACGGAAGAGGAGGATGCTGGCCAAAGCTGCAGCGGACTCG 1715
Db 1023 GGGCGCCAGCCAGAAACGGAAGAGGAGGATGCTGGCCAAAGCTGCAGCGGACTCG 1082
Qy 1716 GGCCAACTCCATGAAGGGCTGATGCCCGATGGGTTCCTGATCGTCTTCTCCCGGAC 1775
Db 1083 GGCCAACTCCATGAAGGGCTGATGCCCGATGGGTTCCTGATCGTCTTCTCCCGGAC 1142
Qy 1776 CAAGGACTCCAGGCTTCCCGCAGATGGGCATTTGATGATTTCCAGCAAGACACCGGGG 1835
Db 1143 CAAGGACTCCAGGCTTCCCGCAGATGGGCATTTGATGATTTCCAGCAAGACACCGGGG 1202
Qy 1836 CACCAAGATGCCCTGAACCTTGAGGATGAGTGGATTCCTTGAGCCGTGCCATCGA 1895
Db 1203 CACCAAGATGCCCTGAACCTTGAGGATGAGTGGATTCCTTGAGCCGTGCCATCGA 1262
Qy 1896 TGCCCGCAGCATGATCAGCTGCGGAAGGACCATGTGCGCGCGGTTTTTGTCACTTCCA 1955
Db 1263 TGCCCGCAGCATGATCAGCTGCGGAAGGACCATGTGCGCGCGGTTTTTGTCACTTCCA 1322
Qy 1956 GAGAGAGATTTTGAAGAGAGTACTCCCGAAGGTGATCCCGCTTCGGAGCCTAGCT 2015
Db 1323 GAGAGAGATTTTGAAGAGAGTACTCCCGAAGGTGATCCCGCTTCGGAGCCTAGCT 1382
Qy 2016 TGCCCTGCCCTGTTGGTCTTCTGCTTCATCTGCTTCAATCCAGCTTCTAAATTTTCCACA 2075
Db 1383 TGCCCTGCCCTGTTGGTCTTCTGCTTCATCTGCTTCAATCCAGCTTCTAAATTTTCCACA 1442
Qy 2076 CTCCACCCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTTAATCAGCGTCT 2135
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Db 1443 CTCCACCCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTTAATCAGCGTCT 1502
Qy 2136 GATCTGTGCTGTGACTCTCTGTGGTTCCTGTTCCTTAAGGCCCTGCACAGCTCTGTCCG 2195
Db 1503 GATCTGTGCTGTGACTCTCTGTGGTTCCTGTTCCTTAAGGCCCTGCACAGCTCTGTCCG 1562
Qy 2196 CAGCATTTCTCGCTCACGGGCACATAGCAGCGCAGTTGGCATCTTTTCCGCTCTGCTGT 2255
Db 1563 CAGCATTTCTCGCTCACGGGCACATAGCAGCGCAGTTGGCATCTTTTCCGCTCTGCTGT 1622
Qy 2256 GTTTACTTCTGCAATGCCCACATGTTTCACTGTAAACACACACCCCATACGAGAGTGTGC 2315
Db 1623 GTTTACTTCTGCAATGCCCACATGTTTCACTGTAAACACACACCCCATACGAGAGTGTGC 1682
Qy 2316 AGCCCGGATGCTGAATTTAAACACCTGTGACATCACTGCTGCCACCTGCACGACGCTCAA 2375
Db 1683 AGCCCGGATGCTGAATTTAAACACCTGTGACATCACTGCTGCCACCTGCACGACGCTCAA 1742
Qy 2376 TTACTTCTTGGGCCCTGGATGCTCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTCC 2435
Db 1743 TTACTTCTTGGGCCCTGGATGCTCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTCC 1802
Qy 2436 TGAGGTGTCC 2445
Db 1803 TGAGGTGTTC 1812

RESULT 9
AAV23246
ID AAV23246 standard; cDNA; 2127 BP.
XX
AC AAV23246;
XX
DT 17-JUL-1998 (first entry)
XX
DE Human adenylylase isoform VI encoding cDNA.
XX
KW Human; adenylylase VI; AC-VI; beta-adrenergic signalling protein;
transgene; gene therapy; congestive heart failure; cardiac function;
adenovirus; ss.
XX
OS Homo sapiens.
XX
FH Key 1..2127 Location/Qualifiers
CDS /tag= a
FT /product= "adenylylase isoform VI"
FT /transl_except= (pos:229..231,aa:Xaa)
FT /transl_except= (pos:315..317,aa:Xaa)
FT /note= "no stop codon given; Xaa = unknown"
FT misc_difference 315
FT /*tag= b
FT /*note= "n indicates a gap of about 0.5 kb"

WO9810085-A2.
PN
PD 12-MAR-1998.
XX
XX 05-SEP-1997; 97MO-US15610.
PF
PR 16-JUN-1997; 97US-0048933.
PR 05-SEP-1996; 96US-0708661.
XX
XX (COLL-) COLLATERAL THERAPEUTICS.
XX (REGC ) UNIV CALIFORNIA.
PI Gao M, Hammond HK, Insel PA, Ping P, Post SR;
XX
XX WPI: 1998-193633/17.
DR P-FSDB; AAW53345.
XX
XX Vectors containing transgene(s) encoding beta-adrenergic signalling
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proteins - useful for gene therapy of congestive heart failure

Claim 60; Fig 12A; 114pp; English.

The present sequence encodes human adenylylcyclase isoform VI (AC-VI) from the present invention. The present invention describes a recombinant replication-defective viral particle (I) comprising a gene encoding a beta-adrenergic signalling protein (beta-ASP) operably linked to a promoter. Also described are: (1) a recombinant pro-viral plasmid (Ia) comprising a gene encoding a beta-ASP, as above, operably linked to a promoter and further comprising a replication-defective viral genome; (2) a (mammalian) cell transfected with (I) or (Ia); (3) an isolated polynucleotide comprising a sequence encoding a human adenylylcyclase isoform VI (AC-VI), or a variant having AC activity; (4) a human AC-VI encoded by (3); (5) an isolated polynucleotide sequence which hybridises at high stringency to (3); and (6) a vector comprising the polynucleotide of (3). (I) can be used to form a filtered adenovirus particle preparation. (I) is used to enhance cardiac function in mammals.

XX Sequence 2127 BP; 421 A; 637 C; 615 G; 452 T; 2 other;

Query Match 51.0%; Score 1808.4; DB 19; Length 2127;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	636	TAACGTGGTGTCTGGGCATCTCGCGCAGTGCAGGTGCGGGGCGCTTTCGACGACAGCC	695
DB	318	TAACGTGGTGTCTGGGCATCTCGCGCAGTGCAGGTGCGGGGCGCTTTCGACGACAGCC	377
QY	696	GCGCAGCCCTCTGCGGGCCTCTGGTGCCTGTGTTCTTTGTATACATCGCATACAGCCT	755
DB	378	GCGCAGCCCTCTGCGGGCCTCTGGTGCCTGTGTTCTTTGTATACATCGCATACAGCCT	437
QY	756	CTTCCCATCCGATCGGGCTGCGGCTCCAGCGGCTGCGGCTCTCCACCTTGCAATTT	815
DB	438	CTTCCCATCCGATCGGGCTGCGGCTCCAGCGGCTGCGGCTCTCCACCTTGCAATTT	497
QY	816	GATCTTGGCTGGCACTTAACCGTGTGTATGCTTCTCTGGAAGCAGCTCGGTGCAAA	875
DB	498	GATCTTGGCTGGCACTTAACCGTGTGTATGCTTCTCTGGAAGCAGCTCGGTGCAAA	557
QY	876	TGTGCTGCTTCTCTGCAACCAAGTCAATAGCATCTGCACACATATCCAGCAGAGT	935
DB	558	TGTGCTGCTTCTCTGCAACCAAGTCAATAGCATCTGCACACATATCCAGCAGAGT	617
QY	936	GTCTCAGCGCAGGCGCTTTCAGGAGACCCCGCAGTTACATCCAGGCCGGCTCCACCTGCA	995
DB	618	GTCTCAGCGCAGGCGCTTTCAGGAGACCCCGCAGTTACATCCAGGCCGGCTCCACCTGCA	677
QY	996	GCATGAGAATCGGCAGCAGGCGGCTGCTGCTGTGCGTATTCGCCAGCAGCCTTGCCAT	1055
DB	678	GCATGAGAATCGGCAGCAGGCGGCTGCTGCTGTGCGTATTCGCCAGCAGCCTTGCCAT	737
QY	1056	GGAGATGAAGAGACATCAACCAAAAGAGACATGTTCCACAAGATCTACATACA	1115
DB	738	GGAGATGAAGAGACATCAACCAAAAGAGACATGTTCCACAAGATCTACATACA	797
QY	1116	GAAGCATGAACATCTCAGCATCTGTTTGCAGACATTTAGGGCTTCCAGCAGCCTGGCATC	1175
DB	798	GAAGCATGAACATCTCAGCATCTGTTTGCAGACATTTAGGGCTTCCAGCAGCCTGGCATC	857
QY	1176	CCAGTGACATCGGCAGGAGCTGTGATGACCTTGAATGAGCTCTTTGCCCGGTTTGACAA	1235
DB	858	CCAGTGACATCGGCAGGAGCTGTGATGACCTTGAATGAGCTCTTTGCCCGGTTTGACAA	917
QY	1236	GCTGGCTGCGGAGAAATCACTGCTGAGGATCAAGATCTTTGGGGAGCTGTTACTGTGT	1295
DB	918	GCTGGCTGCGGAGAAATCACTGCTGAGGATCAAGATCTTTGGGGAGCTGTTACTGTGT	977
QY	1296	GTACGGCTGCGGAGGCGCGGCGGACCATGCCACTGCTGTGTGGAGATGGGGTAGA	1355
DB	978	GTACGGCTGCGGAGGCGCGGCGGACCATGCCACTGCTGTGTGGAGATGGGGTAGA	1037

QY	1356	CATGATTGAGGCCATCTCGCTGTGTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGT	1415
DB	1038	CATGATTGAGGCCATCTCGCTGTGTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGT	1097
QY	1416	GGGCATCCACAGCGGGCGCGTGCACCTCGCGGCTCTTTGGCTTGGGAAATGGCATTCGA	1475
DB	1098	GGGCATCCACAGCGGGCGCGTGCACCTCGCGGCTCTTTGGCTTGGGAAATGGCATTCGA	1157
QY	1476	TGTGTGTTCAATGATGTGACCCCTGGCCAAACCCACATGGAAGCAGGAAGCGGGCTGCGCG	1535
DB	1158	TGTGTGTTCAATGATGTGACCCCTGGCCAAACCCACATGGAAGCAGGAAGCGGGCTGCGCG	1217
QY	1536	CATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGACCTACGAAGTGGAGCCAGG	1595
DB	1218	CATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGACCTACGAAGTGGAGCCAGG	1277
QY	1596	CCGTGTGGCAAGCGCAACCGGTACCTCAAGGAGCAGACATTTGAGACTTTCTTCATCCT	1655
DB	1278	CCGTGTGGCAAGCGCAACCGGTACCTCAAGGAGCAGACATTTGAGACTTTCTTCATCCT	1337
QY	1656	GGCGCCAGCCAGAAACGAAAGAGAGAGGATGCTGSCCAAGCTGCAGCGGACTCG	1715
DB	1338	GGCGCCAGCCAGAAACGAAAGAGAGAGGATGCTGSCCAAGCTGCAGCGGACTCG	1397
QY	1716	GGCCAACTCCATGGAAGGGCTGATGCGCGGATGGGTTCTCTGATCGTCCCTTCTCCCGGAC	1775
DB	1398	GGCCAACTCCATGGAAGGGCTGATGCGCGGATGGGTTCTCTGATCGTCCCTTCTCCCGGAC	1457
QY	1776	CAAGGACTCCAAAGCCTTCCGCCAGATGGGATTTGATGATTTCCAGCAAGACACCGGGG	1835
DB	1458	CAAGGACTCCAAAGCCTTCCGCCAGATGGGATTTGATGATTTCCAGCAAGACACCGGGG	1517
QY	1836	CACCAAGATGCCCTGAACCTTGAGGATGAGGTGAGTTCTGAGCGGTGCATTCGA	1895
DB	1518	CACCAAGATGCCCTGAACCTTGAGGATGAGGTGAGTTCTGAGCGGTGCATTCGA	1577
QY	1896	TGCCCGCAGCATTTGATCAGCTGCGGAAGACCATGTGCGCGGTTTTTGTCACTTTCCA	1955
DB	1578	TGCCCGCAGCATTTGATCAGCTGCGGAAGACCATGTGCGCGGTTTTTGTCACTTTCCA	1637
QY	1956	GAGAGAGATTTTGAGAAGAAGTACTCCCGAAGGTGGATCCCGCTTCGGAGCCTACGT	2015
DB	1638	GAGAGAGATTTTGAGAAGAAGTACTCCCGAAGGTGGATCCCGCTTCGGAGCCTACGT	1697
QY	2016	TGCTGTGCCCTGTTGGTCTTCTGCTTCACTGCTTCATCCAGCTTCTAAATTTCCACACA	2075
DB	1698	TGCTGTGCCCTGTTGGTCTTCTGCTTCACTGCTTCATCCAGCTTCTAAATTTCCACACA	1757
QY	2076	CTCCACCTGATGCTGGGATTTATGCCAGCATCTTCTGCTGCTGCTAATCAGCGTGT	2135
DB	1758	CTCCACCTGATGCTGGGATTTATGCCAGCATCTTCTGCTGCTGCTAATCAGCGTGT	1817
QY	2136	GATCTGTGCTGTGATCTCTGTTGTTCCCTTAAGGCCCTGCAACGCTGTGTCGG	2195
DB	1818	GATCTGTGCTGTGATCTCTGTTGTTCCCTTAAGGCCCTGCAACGCTGTGTCGG	1877
QY	2196	CAGCATTTGTCGCTCAGCGGCACATAGCAGCATTTGGCATCTTTTCCGCTGCTGTGT	2255
DB	1878	CAGCATTTGTCGCTCAGCGGCACATAGCAGCATTTGGCATCTTTTCCGCTGCTGTGT	1937
QY	2256	GTTTACTTCTGCCATTTGCCAACATGTTACCTGTAAACACACACCCCATACGGAGCTGTG	2315
DB	1938	GTTTACTTCTGCCATTTGCCAACATGTTACCTGTAAACACACACCCCATACGGAGCTGTG	1997
QY	2316	AGCCCGGATGCTGAATTTAACCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCAA	2375
DB	1998	AGCCCGGATGCTGAATTTAACCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCAA	2057
QY	2376	TTACTCTCTGGGCTGTGATGCTCCCTGTGTGAGGGCAGCATGCCACTGCGAGCTTTC	2435
DB	2058	TTACTCTCTGGGCTGTGATGCTCCCTGTGTGAGGGCAGCATGCCACTGCGAGCTTTC	2117

[illegible]

[illegible]

[illegible][illegible]

PD 03-MAR-1993.
XX PF 27-AUG-1992; 92EP-0114637.
XX PR 29-AUG-1991; 91US-0751460.
XX PA (AMCY) AMERICAN CYANAMID CO.
XX PI Ishikawa Y, Konski AF;
XX WPI; 1993-068688/09.
DR P-PSDB; AAR32882.
XX PT Isolated nucleic acid mol. encoding Cardiac adenyllyl cyclase type
XX PT V - useful for determining and modifying cardiac function
XX PS Claim 1; Page 15-27; 38pp; English.
XX CC Left ventricular tissue of canine heart was used as a source of mRNA.
CC A cDNA library was prep'd. in lambda gt10 phage. A 970 bp Aat-HincII
CC fragment from type I adenyllyl cyclase cDNA was used as probe. The
CC clones isolated were used to obtain cDNA encoding CACV. This probe
CC may also be used to screen a human cardiac cDNA library to obtain
CC the cDNA encoding human CACV. CACV, its analogues and antibodies
CC are useful in therapy or diagnostic assays, e.g. in modifying and
CC determining cardiac function. A decrease in CACV content of the
CC heart contributes to impaired cAMP prodn. and in heart failure. The
CC CACV can also be used to screen for cpds. which stimulate or inhibit
CC the activity of the cyclase.
XX SQ Sequence 4356 BP; 837 A; 1367 C; 1377 G; 775 T; 0 other;
Query Match 47.6%; Score 1688.4; DB 14; Length 4356;
Best Local Similarity 70.1%; Pred. No. 0;
Matches 2347; Conservative 0; Mismatches 981; Indels 20; Gaps 5;
QY 165 CACCCCTCGGGGCCCCCTCGGTGCCCTGGCAGGATGACGCCCTTCATCCGGAGGGCGG 224
DB 165 CACCCCTCGGGGCCCCCTCGGTGCCCTGGCAGGATGACGCCCTTCATCCGGAGGGCGG 224
DB 346 CGCCCTCGGGGCGGCG 405
QY 225 CCGAGGCAAGGGCAAGAGCTGGGGCTGGGGCAGTGGCCCTGGGCTTCGAGGATACGGA 284
DB 225 CCGAGGCAAGGGCAAGAGCTGGGGCTGGGGCAGTGGCCCTGGGCTTCGAGGATACGGA 284
DB 406 CTCGGTGGAGCTGGGCTGGAGCGAGCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 465
QY 285 GGTGACACGACAGCGGGCGGCGGCTGAGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 342
DB 285 GGTGACACGACAGCGGGCGGCGGCTGAGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 342
DB 466 GGCCGAGCG 525
QY 343 GGGGATCTCTGCTGGCGCGGCTTGGTGCAGGTGTTCCAGTGCAGACGATTCCTGTCGGCC 402
DB 343 GGGGATCTCTGCTGGCGCGGCTTGGTGCAGGTGTTCCAGTGCAGACGATTCCTGTCGGCC 402
DB 526 CCGCGCGCTCTGCTGGCGCGGCTCTGCAGATCTTCGCTCCAGAAAGTTCCTGTCGGAC 585
QY 403 AAGCTGAGCGCTGTACCGAGCGTACTTTTCAGATGAACAGAGCAGCGCTCACCGTG 462
DB 403 AAGCTGAGCGCTGTACCGAGCGTACTTTTCAGATGAACAGAGCAGCGCTCACCGTG 462
DB 586 AAGCTGAGCGCTGTACCGAGCGTACTTTTCGCTGCTGATGCTGGCTTCCAGCGCGCGGCC 645
QY 463 CTGTCGCGGTGCTGGTCTCTCACAGCGCTGCTGGCTGCTTCCAAAGCGCGCACCGCC 522
DB 463 CTGTCGCGGTGCTGGTCTCTCACAGCGCTGCTGGCTGCTTCCAAAGCGCGCACCGCC 522
DB 646 CTATGCGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 705
QY 523 CGCCCTCAGCGCTGCTATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 582
DB 523 CGCCCTCAGCGCTGCTATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 582
DB 706 CCGTGGCGGTGCGCCACCTGGCGCTGCTGGCGCGCGGCTGCTGGGCTCATCTGTCATG 765
QY 583 ATGTTGTTGTGTACCGGCATAGCTTCGGCAGACGCTTCATGTTGGTGGTGAATACGTG 642
DB 583 ATGTTGTTGTGTACCGGCATAGCTTCGGCAGACGCTTCATGTTGGTGGTGAATACGTG 642
DB 766 GCGTGTCTGCAACCGCGCGCTTCCACAGGACACATGTTGGCTGGCTGGCTGGCTGGCT 825
QY 643 GTGCTGGGATCTCTGGCGGAGTGCAGTGGGGCGCTTTCGAGCAGAGACCGCGGAGC 702
DB 643 GTGCTGGGATCTCTGGCGGAGTGCAGTGGGGCGCTTTCGAGCAGAGACCGCGGAGC 702
DB 826 CTATTCGCGGTGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 885
QY 703 CCCTCTCGGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 762

DB 886 GCCTCCGAGGCGCTCTGCTGGACCGTCTTCTCATCTACACCATACACGCTGCTGCC 945
QY 763 ATCCGATGCGGGCTGCGCTCTCAGCGCGCTGGCGCTCTCCACCTTCGATTCGTTG 822
DB 946 GTGGCATGCGGGGCGCGCTCTCAGCGGAGTGCTCTGTCGGCGCTGCTCCTGCGCATC 1005
QY 823 GCCTGGCAACTTAACCGTGGTGATGCCCTCTCTGGAAGCAGCTCGGTGCCAATGCTG 882
DB 1006 GCCTGCGCGCAACGCCAGCCGCTCTGCTCAAGCAGCTGCTCTCAATGCTCTC 1065
QY 883 CTGTTCTCTGCACCAACGCTCATAGCATCTGCACACACTATCCAGCAGAGAGTGTCTCAG 942
DB 1056 ATTTTCTCTGCACCAACATGCTGGTGTCTGTACCCACTACCCGCTGAGGTCTCCAG 1125
QY 943 CGCCAGGCGCTTTCAGGAGACCGCGAGTTACATCCAGCCCGCTCCACCTGCAGCATGAG 1002
DB 1126 AGCAGGCGCTTCCAGAGACCGCGGAGTGCATCCAGGACGCTCCATCCGCAAGCGGAG 1185
QY 1003 AATCGCAGCAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1062
DB 1186 AACCAGCAACAGGAGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1245
QY 1063 AAAGAAGACATCAACACAAAAAAGAAGA---CATGTTTCCACAGATCTACATACAGAG 1119
DB 1246 AAGCAGACATCAATGCCAAGCAGGAGATATGATGTTTCCATAAGATTTACATCCAGAAA 1305
QY 1120 CATGACATGTCAGCATCCTGTTTGCACACATGAGGCTTCCACAGCTGCGCATCCCGAG 1179
DB 1306 CATGACAACTGAGCATCCTGTTTGTGACATCGAGGCTTCCACAGCTTGCATCCCGAG 1365
QY 1180 TGCACCTGCGCAGGAGCTGCTGATGACCTGAATGAGCTTGTGCGCGGTTTGCACAGCTG 1239
DB 1366 TGCACCTGCGCAGGAGCTGCTGATGACCTGAATGAGCTTGTGCGCGGTTTGCACAGCTG 1425
QY 1240 GCTCGGAGATCACTGCTGCTGAGGATCAAGATCTTGGGGGAGCTGTTACTACTGTGTG 1299
DB 1426 GCTCGGAGATCACTGTTTACGTTTAAAGATCTTGGGGGAGTGTATTAATGCTGCTCT 1485
QY 1300 GGGTCTCGGAGGCG 1359
DB 1486 GGGTCTCGTGAAGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1545
QY 1360 ATTGAGGCGATCTCTGCTGCTGAGTGCAGGCTGTAATGTAATGTAATGTAATGTAATG 1419
DB 1546 ATTGAGGCGATCTCTGCTGCTGAGTGCAGGCTGTAATGTAATGTAATGTAATGTAATG 1605
QY 1420 ATCCACAGCGGCGCTGCTGCTGAGTGCAGGCTGTAATGTAATGTAATGTAATGTAATG 1479
DB 1606 ATTACAGCGGCGAGTACACTGCGGTGCTCTCAGGAAGTGGCAGTTCGACGCTC 1665
QY 1480 TGGTCCATGATGTGACCTTGGCCAAACACATGGAAGCAGGAGCGCGCTGCGCGCATC 1539
DB 1656 TGGTCTAATGAGTCACTGCTGCGCAACCATATGGAAGCTGGAAGCAGGCTGCGCGCATC 1725
QY 1540 CACATCACTCGGCAACACTGCGAGTACCTGAACCGGAGCTACGAGTGGAGCGAGCGCT 1599
DB 1726 CCAATCAACAGGCGACACTCAGCTACCTGAACGCTGACTAGAGTGGAGCGAGCGCTG 1785
QY 1600 GGTGCAAGCGCGCTGCTGCTGAGGAGCAGTACGAGTGGAGCTTCTCTCATCTCTGGG 1659
DB 1786 GGGGCGAGCGCAACGCTTCTCAGGAGCAGTATCGAGACCTTCTCTCATCTCTGCGC 1845
QY 1660 GCCAGCAGAAACGGAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1719
DB 1846 TGCACCCAGAGAGCGGAG 1905
QY 1720 AACTCCATGGAAGGCTGATGCTGCGGATGGTTCCTGATGCTGCTCTCTCCCGGAGCAAG 1779
DB 1906 AACTCCATGGAAGGCTGATGCTGCGGATGGTTCCTGATGCTGCTCTCTCCCGGAGCAAG 1965
QY 1780 GACTCCAAAGGCTTCCCGCAGATGGGCTGATGATTCAGCAAGAGAGAGAGAGAGAGAG 1837

Db 1966 GGAGGCACACCGTGTCCCAAGGAGATGAAGCGCATGGGCTTCGAAGACCCCAAGGACAAG 2025
QY 1838 -----CCCAAGATGCCCTGAACCCCTGAGGATCAGGTGATGAGTTCCTGAGCCCGTGCCATC 1893
Db 2026 AACGCCACGAAAGTGCRAACCCCTGAGGATGAAGTGAATTCCTGGGCGCGCCATTC 2085
QY 1894 GATGCGCGCAGCATGATGATGCGGGAAGGACCATGTCGCGCGGTTTTCCTGATCACCCTC 1953
Db 2086 GAGGCCAGGAGCATCGACAGGCTCGGTCGGAGCAGCATCGCGCAAGTTCCTCCTGACCTTC 2145
QY 1954 CAGAGAGAGATTTTGAGAGAGAGTACTCCCGGAAGTGTGATCCCGCTTCGGAGCCTAC 2013
Db 2146 AGGAGCCTGACCTTAGAAAAGAGTACTCCAAGCAGTGTGATGACCATTCGCTGCGCTAC 2205
QY 2014 GTTGCCCTGTGCCCTGTGTGCTTCTGCTTCATCTGCTTCATCCAGCTTCCTAAATTTTCCCA 2073
Db 2206 GTGCAATGTCCTCGCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2265
QY 2074 CACTCCACCCTGATGCTTGGGATTTATGCGAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTG 2133
Db 2266 CACTCCGCTGTCATGTTGAGTTCCTTACTTGACCTGTTTCTGCTGCTGCTGCTGCTGCTGCTG 2325
QY 2134 CTGATCTGCTGTGTACTCTCTGCTGCTCTCTGCTTCTCTTCTTCTTCTTCTTCTTCTTCTT 2193
Db 2326 TTTGTGCTCGATCTTATCTCTGCTGGAAGCTCTTCTCCGGGCGGCTTCCAGAGCCTCTCG 2385
QY 2194 CGCAGCATTTGTCGGCTCACCGGCACATPAGCACCGCAGTTGGCATCTTTCCTGCTCTGCTT 2253
Db 2386 AGNAGATCTGCGCTCCAGACCAACAGCACCTGTGCGGGGTGTCCACCATCACCTG 2445
QY 2254 GTGTTTACTTCTGCCATPTGCCAATGTTTACCTGTTAACACACACCCGCCATACGAGGAGT 2313
Db 2446 GTGTTCTGTCGGCTTTCGTCACATGTTTCACTGTGAATCCGAGGACCTGTTGGGCTG 2505
QY 2314 GCAGCCGGATGCTGAATTTAAACCTGCTGACATCACTGCTGCCACCT-----CGAG 2367
Db 2506 CTGGCGGACGAGCACACATCAGACACAGCCGGGTCAACCGGTGCCACGTGGCGGGGTG 2565
QY 2368 CAGTCAATTACTCTCTGGGCGCTGGATGCTCCCGCTGTGTGAGGCGACCATGCCACCTG 2427
Db 2566 GCGGCCAACCCTAGCCTGGCGGACGAGCAGGGCTTCTGCGGCACGCCCTGGCCCGAGCTG 2625
QY 2428 AGCTTTCTCAGGTGTCATCGGGAACATGCTGCTGAGTCTTCTTGGCCAGCTCTGTGCTTC 2487
Db 2626 AACTTCCCGAGTACTTCACTACAGGTGCTGCTCAGCCTGCTGCTGCTGCTGCTGCTGCTGCT 2685
QY 2488 CTCACATCAGCAGCATCGGSAAGTTGGCCATGATCTTCTTGGGGCTCATCTATTG 2547
Db 2686 CTCGATCAGCTGCATCGGGAAGCTGGTCTCATGCTGGCCATTTGAGCTCATATA---C 2742
QY 2548 GTGCTGCTTCTGCTGGTCCCGCAGCGCCATCTTTGACAACTATGACCTACTGCTTGGC 2607
Db 2743 GTGCTGCTGCTGAGGTGCCCGGGTCACACTGTTTGACAACGCTGACCTGCTGGTCAAC 2802
QY 2608 GTCCATGGCTTGGCTTCTTCCATGAGACCTTTGATGGGTGAGCTGTCAGCTGCAAGG 2667
Db 2803 GCCAACGCCATAGACTTCAACAACAACAACGGGACCTTCGAGTGCCTGAGCAGCGCAAC 2862
QY 2668 AGGTGGCCCTCAAAATATATGACCCCTGTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCT 2727
Db 2863 AAGTGGCGCTGAAGGTGTGAGCCCATCATCTCCGCTCTCTGCTGCTGCTGCTGCTGCTGCT 2922
QY 2728 CTCGATGCTCAGCAGGTGGAATGAGCTGCCCGCTTAACTTCTCTGGAACATACAGGCA 2787
Db 2923 CTCGATGCCAGCAAGTGGAGTCCACCGCCGCTCGACTTCTCTGGAACATGCGAGGCC 2982
QY 2788 ACAGGGAAAAGAGAGATGGAGAGCTACAGGCATACAAACCGAGGCTGCTGCTGCTGCT 2847
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QY 2848 ATTCTGCCAAGGACGTGGCGGCCACTTCTTGGCCGGGAGCGCCGCAATGATGACTC 2907
Db 3043 ATCTTCCCCAAGACGTGGCTGCCACTTCTTGGCCGCTGAGCGACGCAACGAGGACTC 3102

QY 2908 TACTATCAGTCGTGTGAGTGTGGCTGTATGTATTGTTTCTCCATTGCAACTTCTCTGAG 2967
Db 3103 TACTACCAGTCGTGCGAGTGGTGGCTGTCATGTTGCGCTCCATCGCAACTTCTCCGAG 3162
QY 2968 TTTATGTGAGCTGGAGGCAACAATGAGGTCGCCAGTGCCCTGCGGCTGCTCAACGAG 3027
Db 3163 TTTACGTGAGCTTGAGGCCACAATGAGGTCGAGTGCCTGCGCTGCTCAATGAG 3222
QY 3028 ATCATCCTGACTTTTGTGATGAGATTATCAGCGAGGAGCGGTTCCGCGAGCTGGAAGAATC 3087
Db 3223 ATCATCCTGACTTTTGTGATGAGATCATCAGCGAGGATCGGTTTACGCGAGCTGGAAGAATC 3282
QY 3088 AAGACCATTTGATAGCACCCTACATGGCTGCCTCAGGGCTGAACGCCAGCCTACGATCAG 3147
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Db 3343 GTGGCGAAGACCCACATCAAGGCCCTGGCTGACTTTTCCCATGAAGCTCATGGACCAATG 3402
QY 3208 AAGCACATCAATGAGCACTCCTTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGC 3267
Db 3403 AAGTACATCAATGAGCACTCCTTCAACAATTTCCAGATGAAGATCGGGCTCAACATCGG 3462
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Db 3463 CCCGTGTCGCGCGGGTGTATCGGGGCTCGCAAGCTCAGTACGACATCTGGGCAATACG 3522
QY 3328 GTGAATGTCCTGATGCTATGAGCAGACACGGGGTTCGCCAGCAATCCAGGTGACCAAG 3387
Db 3523 GTGAATGTGCCAGCCGATGGACAGACCGGCTGCGGACCGCATCCAGTCCACCAG 3582
QY 3388 GACCTGTACCAGGTCTTAGCTGCCAAGGCTACACGCTGGAGTCTCAGGGGTGCTCAAG 3447
Db 3583 GACATGTACCAGGTGTTGGCTGCCAACACAGTACCAGCTGGAGTGCAGGGGTGCTGCTCAAG 3642
QY 3448 GTGAAGGCGAAGGGGAGATGACCACCTACTTCTCTCAATGGGGGCC 3495
Db 3643 GTCAAGGCGAAGGCGAGATGATGACCTACTTCTCTCAACGTTGGGCC 3690

RESULT 13
AAAS3922
ID AAAS3922 standard; cDNA; 3924 BP.
XX
AC AAAS3922;
XX
DT 03-JAN-2001 (first entry)
XX
DE Type V adenyllyl cyclase coding sequence.
DE
XX Adenyllyl cyclase; type I; type II; recombinant; enzyme; CAMP;
KW cyclic AMP; adenosine monophosphate; screening; stimulation;
KW inhibition; treatment; cholera; pituitary tumour; heart failure;
KW ischaemia; endocrine disorder; cell necrosis;
KW pseudohypoparathyroidism; endocrine deficiency; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 3..3329
FT /*tag= a
FT /product= Type V adenyllyl cyclase
XX
PN US6107076-A.
XX
PD 22-AUG-2000.
XX
PF 04-OCT-1996; 96US-0726214.
XX
PR 04-OCT-1995; 95US-0005498.
XX

(TEXA) UNIV TEXAS SYSTEM.

Gillman AG, Tang W;

WFI: 2000-578539/54.

P-PSDB: AAB02009.

Novel soluble mammalian polypeptide composition comprising adenylyl cyclase activity for screening stimulators and inhibitors of adenylyl cyclase, is activated by Gsalpha

Disclosure: Columns 65-70; 73pp; English.

A recombinant adenylyl cyclase is described which lacks membrane bound domains. Separation and purification of the recombinant enzyme is much easier compared with wild type enzymes and the recombinant enzyme is more stable than the wild type enzyme which allows easier screening of compounds that stimulate and inhibit Adenylyl cyclase activity. The recombinant adenylyl cyclase comprises a chimera of adenylyl cyclase C.1 and C.2 domains linked covalently. The domains may be linked by a linker peptide. The recombinant adenylyl cyclase is useful for screening inhibitors and stimulators of adenylyl cyclase activity. Inhibitors of the enzyme are useful for treating cholera, pituitary tumors, heart failure, ischaemia, endocrine disorders and cell necrosis. Stimulators of adenylyl cyclase are useful for treating pseudohypoparathyroidism and other endocrine deficiencies.

Sequence 3924 BP; 860 A; 1103 C; 1110 G; 851 T; 0 other;

Query Match 46.4%; Score 1648.2; DB 21; Length 3924;

Best Local Similarity 71.4%; Pred. No. 0;

Matches 2265; Conservative 0; Mismatches 873; Indels 33; Gaps 6;

QY 345 GCGATCTGCTGGCGCGTTGGTGCAGGTTCCTCCAGTCGAGCAGTTCGCTGGGCCAA 404
DB 128 GGGCGCTGCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 187
QY 405 GCTGAGCGCTGTACAGCGGTACTTTTCCAGATGAACAGAGCAGCCTGACGCTGCT 464
DB 188 ACTGAGCGCTGTACAGCGCTATTTCTCCGCTGAAACAGAGCAGCCTACCATGCT 247
QY 465 GGTGGCGGTGCTGTGCTGCTACAGCGGTGCTGCTGGCTTCCAGCGGACCGCGCG 524
DB 248 CATGGCGGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 307
QY 525 CCCTCAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 584
DB 308 GCTCCAGGTAGTCTACCTGGCGGTGCTGGAGCTGCTGGCGGTGCTGCTGCTGCTGCT 367
QY 585 GGTGGTGTGAACCGGCATAGCTTCCGCGAGGACTCCATGTGGGTGCTGCTGCTGCTGCT 644
DB 368 TGTGCTCTGACCGTGCAGCCTTCCAGGAGGACCATGCGCCTGGCCTGCTGCTGCTGCT 427
QY 645 GCTGGGCATCTGCGCGAGTGCAGGTGCGGGGCGCTTTCGACGACCGCGCGAGCC 704
DB 428 CATTCAGTGTGCTGCGCGTCCAGGTAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 487
QY 705 CTCTGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 764
DB 488 CTCCGAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
QY 765 CCGCATGGGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 824
DB 548 GCGCATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 607
QY 825 CTGCAACTTAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 884
DB 608 TCTGCACACCAACGCCCGGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 667
QY 885 GTTCTCTGCAACAGCTCATAGCATCTGCACACACTATCCAGAGAGGTGCTGCTGCTGCT 944
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DB 908 TGACAATGTAGCATCTGTTTGTGATCATCGAAGCTTCACTAGCTGGCATCCAGTG 967
QY 1182 CACTGCGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1241
DB 968 TACTGCCCAAGAACTGGTTCATGACCTCAACGAGCTCTTCGCCGCTTTGACAAGTTGCG 1027
QY 1242 TGGGAGAACTGCTGCTGAGGATCAAGATCTTGGGGACTGTTACTACTGCTGCTGCTGCTGCT 1301
DB 1028 TGGGAGAACTGCTTACGATTAAGATCTCGGGATGTTACTACTGCTGCTGCTGCTGCTGCTGCT 1087
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QY 1422 CCAGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1481
DB 1208 TCACAGCGGAGAGTACACTGCGGTGCTTGGGCTTCAGAAAGTGGCAATTCGAGCTGCTG 1267
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QY 1830 CCGGGGACCCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1889
DB 1622 CAGAATGCCAGGAAGTGCACACCTGAGGATGAGTGGACGAGTTCCTGGGTCGAGC 1681
QY 1890 CATCGATGCCCGCAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1949
DB 1682 CATCGATGCCAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1741
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[illegible]

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Qy	3204	GATCAAGCACATCAATGAGCACCTCTTCAACAATTTCCAGATGAAGATTGGGCTCAACAT	3263
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Qy	3264	GGGCCCACTCGTGCGCAGGTGTCACTGGGGCTCGGAAGCCACAGTATGACATCTGGGGGAA	3323
Db	3056	TGGACCTGTAGTGGCTGGGCTCATTTGGGCTCGCAGCCTCAGTATGACATCTGGGGCAA	3115
Qy	3324	CACAGTGAATGTCTTAGTCGTATGACAGCAGCGGGGTTCCCGACCGAATCCAGGTGAC	3383
Db	3116	TACAGTAAATGTGCCAGGCCGTATGCACAGCACTGGGGTGCTGTGACCGCATCCAGGTTAC	3175
Qy	3384	CACGACCTCTACCAGGTTCTAGCTGCCAAGGCTACCAGCTGGAGTGTCCAGGGGTGGT	3443
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Qy	3444	CAAGGTCAAGGCAAGGGGAGATACCACTACTTCTCAATGGGGGCC	3494
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XX	KW	Human; adenyl and guanylyl cyclase; ADGUC-2; cardiovascular disorder	
XX	KW	angina pectoris; myocardial infarction; vision disorder; keratitis;	
XX	KW	iritis; cataract; neurological disorder; epilepsy; Alzheimer's disease	
XX	KW	Pick's disease; stroke; mental disorder; mood and anxiety disorder;	
XX	KW	reproductive disorder; infertility; endometriosis; impotence; asthma;	
XX	KW	smooth muscle disorder; migraine; bacterial infection; gene therapy;	
XX	OS	transgenic animal; vaccine; enzyme; ss.	
XX	XX	Homo sapiens.	
XX	FH	Key	
XX	FT	Location/Qualifiers	
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XX	PF	26-JUN-2001; 2001WO-US20491.	
XX	PR	29-JUN-2000; 2000US-215476P.	
XX	PR	04-AUG-2000; 2000US-223545P.	
XX	PR	31-AUG-2000; 2000US-229876P.	
XX	PR	22-SEP-2000; 2000US-234838P.	
XX	PR	29-SEP-2000; 2000US-236483P.	
XX	PA	(INCY-) INCYTE GENOMICS INC.	
XX	PI	Gandhi AR, Tribouley C, Ding L, Lu DAM, Lee EA, Yue H, Yang J;	
XX	PI	Baughn MR, Thornton M, Yao MG, Wallia NK, Tang YT, Elliott VS;	
XX	PI	Lu Y;	
XX	DR	WPI; 2002-154740/20.	
XX	DR	P-PSDB; AAEL17130.	

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Db 1099 CTCCTGGGAAGTTTGGAGAGCTGGCCACAGAAACCACTCCGCCGCATCAAGATCCTG 1158
Qy 1276 GGGAGCTGTTTACTACTGTGTGACAGGCTGCCGAGGCGCGGCGGCGACCATGCGCCACTGC 1335
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Qy 1336 TGTGTGAGATGGGGGTAGACATGATTTAGGCCCATCTCGCTGGTGTACGTGAGGTTGACAGGT 1395
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Qy 1396 GTGAATGTGAACATGCGCTGGGATCCACAGCGGCGGCGTGCACGTGGCGCTCTTGGC 1455
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Db 1399 GCTCGCGGCTTGCCTGGGAAGTTTCAATCAACAAGACACCTTGGCTGGCTGCTGAATGGT 1458
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Qy 1876 TTCTGAGCCGTGCCATCGATGCCCGCAGCATTTGATCAGCTGCGGAAGGACCATGTGGC 1935
Db 1743 ACTCAGAAACCGCTGCTTTCTCTACA----- 1770
Qy 1936 CGGTTTTTGTCTCACTTCCAGAGAGAGATTTTTGAGAAGAAGTACTCCCGGAAGGTGGAT 1995
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Qy 1996 CCCCGCTTCGGAGCCTAGTTGCCGTGCCCTGTGGTTCCTTCTGCTTCATCTGCTTCATC 2055
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Qy 2356 TCCACCTGCAAGAGCTCAATTAATCTCTGCGCCTGGATGCTGCCCTGTGAGGCGCAC 2415
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Qy 2416 ATGCCCACTGAGCTTTCTGAGGTGCCATCGGGAACATGCTGCTGCTGCTGCTGCTGCTG 2475
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Qy 2476 AGCTGTGCTTCTGACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGCTGCTGGG 2535
Db 2287 GCGCCCATGCCCTGCTGCGGCTCTGGGCAACCTCCCGCTGCCATATCTCTGCGG 2346
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Db 2347 GTCTCTCTTGGCCAAAATGATCTGCTGCCGTGCTCACACCTCTCATCTCTGCTC 2406
Qy 2596 CTACTGCTTGGGCTCCATGGCTTGGCTTCTTCCAAATGACATTTGATGGGCTGGAGCTG 2655
Db 2407 CTGAGCTCAGCG-----GGTACAGGAAGCCATG 2436
Qy 2656 CCAGCTCAGGAGGGTGGCCCTCAATATATGACCCCTGTGATCTGCTGGTGTGG 2715
Db 2437 GGGCCGCTGCCATCTCAGGGCGCAGCTTCGAGCGCATATGGCCATCTGCTATCTCG 2496
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Db 2497 TGCAGCTGGCCCTGCACGCCCGCAGGTGGATGTCAAGCTGCGGCTGGACTACCTCTG 2556
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Qy 2896 AATGATGAACCTCTACTATCAGTCTGTGAGTGTGTGGCTGTATGTTGGCTTCCATTGCC 2955
Db 2677 AACATGGACCTGTATTACAGTCACTCGCAGGTGGGGTGTGCTGCTGCTGCTGCTGCTG 2736
Qy 2956 AACTTCTCTGAGTCTATGTGAGCTGGAGCAACATGAGGTTGCCAGTGCCTGCGG 3015
Db 2737 AACTTCAATGACTTCTACATCGAGTGGATGGCAACATGGGGTGGATGTCTACGC 2796
Qy 3016 CTGCTCAACGAGATCATCGCTGACTTTGATGAGATTAATCAGGAGGCGGTTCCGGCAG 3075
Db 2797 CTTCTGATGAGATCATCGCTGACTTTGATGAGCTCATGGCAAGAGACTTTTACAGGAC 2856
Qy 3076 CTGGAAGAAGTCAAGAGCATGGTATGACACCTACATGCTGCTGCTGCTGCTGCTGCTG 3132
Db 2857 CTAGAGAAGTCAAGACCATTTGGGAGCAGTACATGGCTGTGTGGGCTGGCGCCACT 2916
Qy 3133 -----AGCACCTAGCATCAGTGGCGGCTCCACATCACTGCGCTGGCTGACTACGCC 3186
Db 2917 GCTGGGACCAAGGCTAAGAAGTGCATCTCTCCACCTCAGCAGCTTGGCAGATTTGCC 2976
Qy 3187 ATCGGCTCATGAGCAGATGAAGCAGATCAATGAGCATCTCTTCAACAATTTCCAGATG 3246
Db 2977 ATCGAGATGTTTGTGCTCTGCTGATGAGATCAACTACCAGTCTTATAACGACTTTGTGCTC 3036

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QY 3247 AAGATTGGCTGACATGGGCCAGTCGTGGCAGGTGTCTCGGGGCTCGGAAGCCACAG 3306
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3037 CGTGTGGCATCAATGTGGCCCGTGGTGGTGGATGATCGGGGCTCGCAGGCCGAG 3096
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3307 TATGACATCTGGGGAAACACAGTCAATGTCTCTAGTCGTATGGACAGCAGGGGGTCCCC 3366
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3097 TATGACATTTGGGGAAACACAGTCAATGTGGCCAGTCGGATGGACAGTACCGGCGTCCAG 3156
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QY 3367 GACCGAATCCAGGTGACACCGGACCTGTACCAGGTTCCTAGCTGCCAAGGGCTACAGCTG 3426
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QY 3157 GGCAGGATCCAGGTCACAGAGGAAGTTCACCGGCTGTGCGGGGGGTTCCTACCGCTTC 3216
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QY 3277 GGCAGGACC 3285

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Search completed: February 22, 2003, 22:29:16
 Job time : 687.392 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 22:08:18 ; Search time 116.945 Seconds
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9306.902 Million cell updates/sec

Title: US-09-750-240-5

Perfect score: 3549

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Gapop 10.0 , Capext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3549	100.0	3549	4	US-09-008-097-5
2	3478.4	98.0	4942	4	US-09-474-076-1
3	2990.4	84.3	4046	1	US-07-793-961A-1
4	2990.4	84.3	4046	1	US-08-240-357-1
5	2751.2	77.5	4131	3	US-08-726-214-11
6	1808.4	51.0	1812	4	US-09-008-097-3
7	1703.4	48.0	4523	4	US-09-473-716-1
8	1648.2	46.4	3924	3	US-08-726-214-9
9	595	16.8	3978	3	US-08-726-214-1
10	505.2	14.2	3518	4	US-09-412-210-2
11	463.6	13.1	4601	3	US-08-726-214-15
12	459	12.9	4008	3	US-08-307-896-5
13	459	12.9	4008	3	US-08-726-214-3
14	459	12.9	4008	5	PCT-US95-11808-5
15	441.6	12.4	4533	3	US-08-726-214-5
16	433	12.2	5199	3	US-08-726-214-13
17	428	12.1	3357	3	US-08-726-214-7
18	393.2	11.1	1652	4	US-08-726-214-17
19	295.2	8.3	314	4	US-09-008-097-1
20	288.2	8.1	2092	3	US-08-307-896-6
21	288.2	8.1	2092	5	PCT-US95-11808-6
22	216.8	6.1	4473	3	US-08-894-173-1
23	216.8	6.1	4473	4	US-09-398-193-1
24	209.4	5.9	4985	4	US-09-473-717-1
25	207.8	5.9	5515	4	US-09-398-193-98
26	73	2.1	7218	1	US-08-232-463-14
27	64.4	1.8	1259	2	US-08-997-080-123

28 64.4 1.8 1259 2 US-08-997-362-123 Sequence 123, App

29 64.4 1.8 1259 4 US-09-095-855-123 Sequence 123, App

30 64.4 1.8 1259 4 US-09-324-542-123 Sequence 123, App

31 64.4 1.8 1259 4 US-09-205-426-123 Sequence 123, App

32 64.4 1.8 2013 2 US-08-997-080-176 Sequence 176, App

33 64.4 1.8 2013 2 US-08-997-362-176 Sequence 176, App

34 64.4 1.8 2013 4 US-09-095-855-176 Sequence 176, App

35 64.4 1.8 2013 4 US-09-324-542-176 Sequence 176, App

36 64.4 1.8 2013 4 US-09-205-426-176 Sequence 176, App

37 64.4 1.8 2172 2 US-08-997-080-173 Sequence 173, App

38 64.4 1.8 2172 2 US-08-997-362-173 Sequence 173, App

39 64.4 1.8 2172 4 US-09-095-855-173 Sequence 173, App

40 64.4 1.8 2172 4 US-09-324-542-173 Sequence 173, App

41 64.4 1.8 2172 4 US-09-205-426-173 Sequence 173, App

42 54.4 1.5 3243 2 US-08-231-193A-44 Sequence 44, Appl

43 54.4 1.5 3243 2 US-08-486-273A-44 Sequence 44, Appl

44 54.4 1.5 3243 3 US-08-480-474-44 Sequence 44, Appl

45 54.4 1.5 3243 3 US-08-940-086A-44 Sequence 44, Appl

ALIGNMENTS

RESULT 1

US-09-008-097-5

; Sequence 5, Application US/09008097

; Patent No. 6306830

; GENERAL INFORMATION:

; APPLICANT: Hammond, H. Kirk

; APPLICANT: Insel, Paul A.

; APPLICANT: Ping, Peipei

; APPLICANT: Post, Steven R.

; APPLICANT: Gao, Meihua

; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE

; TITLE OF INVENTION: HEART FAILURE

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 PAGE MILL ROAD

; CITY: PALO ALTO

; STATE: CA

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/008.097

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Dylan, Tyler M

; REGISTRATION NUMBER: 37,612

; REFERENCE/DOCKET NUMBER: 22000-20567.21

; TELEPHONE: 650-813-5600

; TELEFAX: 650-494-0792

; TELEX: 706141

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3549 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: Coding Sequence

; LOCATION: 1...3501

; OTHER INFORMATION:

US-09-008-097-5

Query Match 100.0%; Score 3549; DB 4; Length 3549;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3549; Conservative 0; Mismatches 0; Gaps 0;

QY	1	ATGTCATGTTT	AGTGGCCCT	CCCTGGTCCCT	TAAAGTGGAT	GAAGGAAAC	CAGCCTGGGGT	60
DB	1	ATGTCATGTTT	AGTGGCCCT	CCCTGGTCCCT	TAAAGTGGAT	GAAGGAAAC	CAGCCTGGGGT	60
QY	61	GAAGCAATGG	CAGAACGCT	TCGGCGCGCT	TGGCACTCG	CGCAGTGGCT	TCTGCACG	120
DB	61	GAAGCAATGG	CAGAACGCT	TCGGCGCGCT	TGGCACTCG	CGCAGTGGCT	TCTGCACG	120
QY	121	CCCCGCTAT	ATAGCTGCC	TCCGGATG	CAGAGCCACC	AGCCGCC	CCCTGGGGCCCC	180
DB	121	CCCCGCTAT	ATAGCTGCC	TCCGGATG	CAGAGCCACC	AGCCGCC	CCCTGGGGCCCC	180
QY	181	CCTCGGTGC	CCCCCTGG	CAGGATG	AGCGCTTCA	TCCGGAGGG	CGGCCAGGCAAG	240
DB	181	CCTCGGTGC	CCCCCTGG	CAGGATG	AGCGCTTCA	TCCGGAGGG	CGGCCAGGCAAG	240
QY	241	GAGCTGGGG	CTGGGGCAG	TGGCCCTTC	GAGGATACC	GAGGTGACA	ACGACAGCG	300
DB	241	GAGCTGGGG	CTGGGGCAG	TGGCCCTTC	GAGGATACC	GAGGTGACA	ACGACAGCG	300
QY	301	GGCGGACGC	TGAGTGGC	CGCCGAC	CGCGGTGCC	CAGAGTGGG	CGATCCTTGGCGC	360
DB	301	GGCGGACGC	TGAGTGGC	CGCCGAC	CGCGGTGCC	CAGAGTGGG	CGATCCTTGGCGC	360
QY	361	CGTTTGGTG	AGCTGTTCC	AGTGAAC	CAGAGCCT	TGACGCTGCT	TGGCGGTGCTGGTG	420
DB	361	CGTTTGGTG	AGCTGTTCC	AGTGAAC	CAGAGCCT	TGACGCTGCT	TGGCGGTGCTGGTG	420
QY	421	CAGCGTACT	TTTTCCAGAT	GAACAGAG	CAGCCTGAC	CGCTGCTGCT	TGGCGGTGCTGGTG	480
DB	421	CAGCGTACT	TTTTCCAGAT	GAACAGAG	CAGCCTGAC	CGCTGCTGCT	TGGCGGTGCTGGTG	480
QY	481	CTGCTCAG	CGGTGCTG	CTGGCTTT	TCCAAAGCG	CACCGCCG	CCCTCAGCCTGCTAT	540
DB	481	CTGCTCAG	CGGTGCTG	CTGGCTTT	TCCAAAGCG	CACCGCCG	CCCTCAGCCTGCTAT	540
QY	541	GTGGCACTG	TGGCTGTC	CGCGCGCT	CTGCTGGG	GGCTCATG	TGTTGTAACCGG	600
DB	541	GTGGCACTG	TGGCTGTC	CGCGCGCT	CTGCTGGG	GGCTCATG	TGTTGTAACCGG	600
QY	601	CATAGCTTC	CGCCAGGAC	TCCATG	TGGTGGT	GAGTAAAG	TGGTGGTGGCATCCTTGGCG	660
DB	601	CATAGCTTC	CGCCAGGAC	TCCATG	TGGTGGT	GAGTAAAG	TGGTGGTGGCATCCTTGGCG	660
QY	661	GCAGTCAG	GTGGGGCGG	TTTCG	CAGCAGAC	CGCCGCG	CCCTCTGGGGCCCTCTGG	720
DB	661	GCAGTCAG	GTGGGGCGG	TTTCG	CAGCAGAC	CGCCGCG	CCCTCTGGGGCCCTCTGG	720
QY	721	TGCGCTGTG	TTCTATAT	ATATGCA	TACACGCT	CTCTCCCAT	CCGATGCGGGCTGCC	780
DB	721	TGCGCTGTG	TTCTATAT	ATATGCA	TACACGCT	CTCTCCCAT	CCGATGCGGGCTGCC	780
QY	781	GTCTCAGG	CGGCTGCG	CCCTC	CCACCTTGC	ATTGATCTT	GGCCCTGGCAACTTAACCGT	840
DB	781	GTCTCAGG	CGGCTGCG	CCCTC	CCACCTTGC	ATTGATCTT	GGCCCTGGCAACTTAACCGT	840
QY	841	GGTGATGCC	TTCTCTCG	GAAGAGCT	CGGTGGC	CAATGTG	TCTCTGCACCAAC	900
DB	841	GGTGATGCC	TTCTCTCG	GAAGAGCT	CGGTGGC	CAATGTG	TCTCTGCACCAAC	900
QY	901	GTCAATTAG	CATGTCAC	ACTATCC	AGCAGAGG	TCTCTC	CAGCCAGGCTTTCAGGAG	960
DB	901	GTCAATTAG	CATGTCAC	ACTATCC	AGCAGAGG	TCTCTC	CAGCCAGGCTTTCAGGAG	960
QY	961	ACCCGAGTT	ACATCCAG	CGCCGGCT	TCCACCTGC	AGCATGAG	AAATCGGACGAGGCGG	1020
DB	961	ACCCGAGTT	ACATCCAG	CGCCGGCT	TCCACCTGC	AGCATGAG	AAATCGGACGAGGCGG	1020

QY 181 CCTGGTGCCTTGGCAGGATGACGCTTCATCCGGAGGGCGGCCAGCAAGGGCAAG 240
Db CCTCGTGCCTTGGCAGGATGACGCTTCATCCGAGGGCGGCCAGCAAGGGCAAG 384
QY 241 GAGCTGGGCTCGGGCAGTGGCCCTTGGGCTTCGAGGATACCGAGGTGACAAACGACAGCG 300
Db GAGCTGGGCTCGGGCAGTGGCCCTTGGGCTTCGAGGATACCGAGGTGACAAACGACAGCG 444
QY 301 GGGGGACGGCTGAGGTGGCGCCCGAGCGGTGCCAGGAGTGGCGCATCCTGCTGGCGC 360
Db GGGGGACGGCTGAGGTGGCGCCCGAGCGGTGCCAGGAGTGGCGCATCCTGCTGGCGC 504
QY 361 CGTTTGTGAGGTGTTCCAGTGAACAGAGTTCGTTTGGCCAAAGCTGGAGCGCCTGTAC 420
Db CGTTTGTGAGGTGTTCCAGTGAACAGAGTTCGTTTGGCCAAAGCTGGAGCACCTGTAC 564
QY 421 CAGCGTACTTTTCCAGATGAACACAGCAGCCTGACGCTGCTGTGGTGGCGGTGCTGGTG 480
Db CAGCGTACTTTTCCAGATGAACACAGCAGCCTGACGCTGCTGTGGTGGCGGTGCTGGTG 624
QY 481 CTGCTCACAGCGGTGCTGGCTTTTCCAAAGCCGACACCCCGCCCTCAGCCTGCCCTAT 540
Db CTGCTCACAGCGGTGCTGGCTTTTCCAAAGCCGACACCCCGCCCTCAGCCTGCCCTAT 684
QY 541 GTGGCACTGTTGGCCTGTGCGCGCGCCCTGTTCGTGGGGCTCAATGTGGTGTGTAAACGG 600
Db GTGGCACTGTTGGCCTGTGCGCGCGCCCTGTTCGTGGGGCTCAATGTGGTGTGTAAACGG 744
QY 601 CATAGCTTCCGCGAGGACTCATGTGGTGGTGAATGAACGTGTGCTGGGCATCCTGGCG 660
Db CATAGCTTCCGCGAGGACTCATGTGGTGGTGAATGAACGTGTGCTGGGCATCCTGGCG 804
QY 661 GCAGTCAGGTGCGGGCGCTTTCGACAGCAGACCCGCGCAGCCCTCTGCGGGCTCTGG 720
Db GCAGTCAGGTGCGGGCGCTTTCGACAGCAGACCCGCGCAGCCCTCTGCGGGCTCTGG 864
QY 721 TGGCCTGTGTTCTTGTATACATCGCATACAGGTCTCTCCCATCCGCATCGGGGCTGCC 780
Db TGGCCTGTGTTCTTGTATACATCGCATACAGGTCTCTCCCATCCGCATCGGGGCTGCC 924
QY 781 GTCTCACGCGCCTGGGCTCTCCACCTTGATTTGATCTGGCTGGCAACTTAAACCGT 840
Db GTCTCACGCGCCTGGGCTCTCCACCTTGATTTGATCTGGCTGGCAACTTAAACCGT 984
QY 841 GGTGATGCCCTCTCTGGAAGCAGCTCGGTGGCAATGTGCTGTGTTCTCTGCAACCAAC 900
Db GGTGATGCCCTCTCTGGAAGCAGCTCGGTGGCAATGTGCTGTGTTCTCTGCAACCAAC 1044
QY 901 GTCAATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTCAGGAG 960
Db GTCAATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTCAGGAG 1104
QY 961 ACCCGAGTTACATCCAGGCGCGCTCCACCTGCAGCATGAGAAATCGGACGAGGAGCGG 1020
Db ACCCGAGTTACATCCAGGCGCGCTCCACCTGCAGCATGAGAAATCGGACGAGGAGCGG 1164
QY 1021 CTGCTGCTGCGGTATTTGCCCGCAGCAGTTCGCAATGGAGATGAAAGAGACATCAACACA 1080
Db CTGCTGCTGCGGTATTTGCCCGCAGCAGTTCGCAATGGAGATGAAAGAGACATCAACACA 1224
QY 1081 AAAAAAGAACAC---ATGTTTCCACAGATCTACATACAGAAAGATGACAATGTCAAGATC 1137
Db AAAAAAGAACACATGATGTTTCCACAGATCTACATACAGAAAGATGACAATGTCAAGATC 1284
QY 1138 CTGTTTGCACACATGAGGGCTTCCACAGCCTGGCATCCGAGTGCAGTGCAGGAGCTG 1197
Db CTGTTTGCACACATGAGGGCTTCCACAGCCTGGCATCCGAGTGCAGTGCAGGAGCTG 1344
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QY 1258 CTGAGGATCAAGATCTTGGGGGACTGTACTACTGTGTGTCAGGGCTGCGGAGGCCCGG 1317

Db 1405 CTGAGGATCAAGATCTTGGGGACTGTACTACTGTGTGTCAGGGCTGCCGAGGCCCGG 1464
QY 1318 GCGACCATGCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCCCTG 1377
Db GCGACCATGCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCCCTG 1524
QY 1378 GTAGTGTGAGTGTACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGCGCGTG 1437
Db GTAGTGTGAGTGTACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGCGCGTG 1584
QY 1438 CACTGCGCGCTCCTTGGCTTTCGGGAAATGGCAGTTCGATGTGTGTCATGATGTGACC 1497
Db CACTGCGCGCTCCTTGGCTTTCGGGAAATGGCAGTTCGATGTGTGTCATGATGTGACC 1644
QY 1498 CTGGCCAAACACATGGAAGCAGGAAGCCGGCTGGCGCGCATCCACATCACTCGGGCAACA 1557
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QY 1558 CTGCAGTACCTGAACGGGACTACGAAGTGGAGCGCGCTGGTGGCAAGCGCAACGCG 1617
Db CTGCAGTACCTGAACGGGACTACGAAGTGGAGCGCGCTGGTGGCGAGCGCAACGCG 1764
QY 1618 TACCTCAAGGAGCAGCAGTTCGATGAGCTTTCCTCATCTCGGGCGCCAGCCAGAAACGAAA 1677
Db TACCTCAAGGAGCAGCAGTTCGATGAGCTTTCCTCATCTCGGGCGCCAGCCAGAAACGAAA 1824
QY 1678 GAGGAGAAAGCATGCTGGCCAAAGCTGACGGGACTCGGGCCCACTCCATGGAAGGGCTG 1737
Db GAGGAGAAAGCATGCTGGCCAAAGCTGACGGGACTCGGGCCCACTCCATGGAAGGGCTG 1884
QY 1738 ATCGCGGATGGTTCCTGATGCTGCTTCTCCGCGACCAAGGACTCCAAGGCTTCCCG 1797
Db ATCGCGGATGGTTCCTGATGCTGCTTCTCCGCGACCAAGGACTCCAAGGCTTCCCG 1944
QY 1798 CAGATGGGCATTGATGATTCAGCAAAAGACAAACCGGGGACCCCAAGATGCCCTGAACCT 1857
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QY 1858 GAGGATCAGGTGATGATGCTGAGCGGTGCCATCGATGCCCGCAGCATGATGATCAGCTG 1917
Db GAGGATCAGGTGATGATGCTGAGCGGTGCCATCGATGCCCGCAGCATGATGATCAGCTG 2064
QY 1918 CGAAGACCATGTGCGCGGTTTTTCTGCTCACCTTCCAGAGAGAGATTTTGAAGAAG 1977
Db CGAAGACCATGTGCGCGGTTTTTCTGCTCACCTTCCAGAGAGAGATTTTGAAGAAG 2124
QY 1978 TACTCCCGAAGTGGATCCCGCTTCGAGCGCTTACGCTGCTGCTGCTGCTGCTC 2037
Db TACTCCCGAAGTGGATCCCGCTTCGAGCGCTTACGCTGCTGCTGCTGCTGCTC 2184
QY 2038 TGCTTCACTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCTGATGCTTGGGAT 2097
Db TGCTTCACTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCTGATGCTTGGGAT 2244
QY 2098 TATGCCAGCATCTCTGCTGCTGCTAATCACCGTGTGATGCTGCTGCTGCTGCTGCT 2157
Db TATGCCAGCATCTCTGCTGCTGCTAATCACCGTGTGATGCTGCTGCTGCTGCTGCTGCT 2304
QY 2158 GGTTCCTGTTCCCTAAGGCCCTGCAACGCTGTGTCGCGCAGCATTTGCCGCTCAGGGCA 2217
Db GGTTCCTGTTCCCTAAGGCCCTGCAACGCTGTGTCGCGCAGCATTTGCCGCTCAGGGCA 2364
QY 2218 CATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2277
Db CATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2424
QY 2278 ATGTTCACCTGTAAACACACCCCATACGAGCTGTGACGCCGAGTGTGAATTTAAAC 2337
Db ATGTTCACCTGTAAACACACCCCATACGAGCTGTGACGCCGAGTGTGAATTTAAAC 2484
QY 2338 CTTGCTGACATCACTGCTGCCACAGCTCAATTTACTCTCTGCGGCTGGATGCT 2397

Db 2485 CCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCAATTACTCTCTGGGCTGSGATGCT 2544
Qy 2398 CCCCTGTGTGAGGACACCATGCCCCACCTGCAGCTTTCTCTGAGGTGTCCATCGGGAACATG 2457
Db 2545 CCCCTGTGTGAGGACACCATGCCCCACCTGCAGCTTTCTCTGAGTACTTCACTCGGGAACATG 2604
Qy 2458 CTGCTGAGTCTCTTGGGCCAGCTCTGTCTTCTGTCACATCAAGCAGCATCGGGAAGTTGGCC 2517
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Qy 2578 ATCTTTTGACAACTATGACCTACTCTTGGGGTCCATGGCTTGGCTTCTTCCAATGAGACC 2637
Db 2725 ATCTTTTGACAACTATGACCTACTCTTGGGGTCCATGGCTTGGCTTCTTCCAATGAGACC 2784
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Qy 2698 ATTCTGCTGTGTGTTGGCTGGCCCTGTATCTGCATCTCAGCAGGTGGAATCGACTGCC 2757
Db 2845 ATTCTGCTGTGTGTTGGCTGGCCCTGTATCTGCATCTCAGCAGGTGGAATCGACTGCC 2904
Qy 2758 CGCTAAACTTCTCTGGAACACTACAGGCAACAGGGGAAAGAGAGATGGAGAGCTA 2817
Db 2905 CGCTAGACTTCTCTGGAACACTACAGGCAACAGGGGAGAGAGATGGAGAGCTA 2964
Qy 2818 CAGGCATACACCGGAGGCTGCTGCATTAACATTTCTGCCCAAGGACGTGGGGGCCACTTC 2877
Db 2965 CAGGCATACACCGGAGGCTGCTGCATTAACATTTCTGCCCAAGGACGTGGGGGCCACTTC 3024
Qy 2878 CTGCCCCGGAGCGCCCAATGATGAATCTCTGAGTCTTCTATGAGTGTGAGTGTGCTGTT 2937
Db 3025 CTGCCCCGGAGCGCCCAATGATGAATCTCTGAGTGTGAGTGTGAGTGTGCTGTT 3084
Qy 2938 ATGTTTGCTCCATTGCCAATCTCTGAGTCTTCTATGTGAGCTGGAGGCAACAAATGAG 2997
Db 3085 ATGTTTGCTCCATTGCCAATCTCTGAGTCTTCTATGTGAGCTGGAGGCAACAAATGAG 3144
Qy 2998 GGTCCGAGTCCCTGGCGTCTCAAGAGATCATCTGCTGATCTTGTGATGAGATTATCAGC 3057
Db 3145 GGTCTGAGTCCCTGGCGTCTCAAGAGATCATCTGCTGATCTTGTGATGAGATTATCAGC 3204
Qy 3058 GAGGAGCGTTCGGGAGCTGGAAGAGATCAAGAGATTTGTAGCAGCTACATGCTGCC 3117
Db 3205 GAGGAGCGTTCGGGAGCTGGAAGAGATCAAGAGATTTGTAGCAGCTACATGCTGCC 3264
Qy 3118 TCAGGGTGAACGCCAGCACCCTACGATCAGTGGGGCGGCTCCACATCACTGCGCTGGCT 3177
Db 3265 TCAGGGTGAACGCCAGCACCCTACGATCAGTGGGGCGGCTCCACATCACTGCGCTGGCT 3324
Qy 3178 GACTACGCCATGCGGCTCATGAGCAGATGAAGCACATCAATGAGCAGCTCTTCAACAAT 3237
Db 3325 GACTACGCCATGCGGCTCATGAGCAGATGAAGCACATCAATGAGCAGCTCTTCAACAAT 3384
Qy 3238 TTCCAGATGAAGATTGGGCTGAACATGGGCCAGCTCGTGGCAGTGTCTATCGGGGCTCGG 3297
Db 3385 TTCCAGATGAAGATTGGGCTGAACATGGGCCAGCTCGTGGCAGTGTCTATCGGGGCTCGG 3444
Qy 3298 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTAGTCTGATGACAGACG 3357
Db 3445 AAGCCACAGTATGACATCTGGGGGAACACACAGTGAATGTCTAGTCTGATGACAGACG 3504
Qy 3358 GGGTCCCGCCAGCAATCCAGGTGACCCAGCAGCTGTACCAAGTCTTACGTGCCAAGGCG 3417
Db 3505 GGGTCCCGCCAGCAATCCAGGTGACCCAGCAGCTGTACCAAGTCTTACGTGCCAAGGCG 3564
Qy 3418 TACCAGCTGAGTGTGAGGGGTGTCAGGTGAAGGCGCAAGGGGAGATGACCACTAC 3477
Db 3565 TACCAGCTGAGTGTGAGGGGTGTCAGGTGAAGGCGCAAGGGGAGATGACCACTAC 3624

Qy 3478 TTCCTCAATGGGCCCCCAGCAGTTAAACAGGGCCCCAGCCACAAAATTCAGCTGAAGGGACC 3537
Db 3625 TTCCTCAATGGGCCCCCAGCAGTTAAACAGGGCCCCAGCCACAAAATTCAGCTGAAGGGACC 3684
Qy 3538 AAGGTGGGCACT 3549
Db 3685 AAGGTGGGCACT 3696
RESULT 3
US-07-793-961A-1
; Sequence 1, Application US/07793961A
; Patent No. 5334521
; GENERAL INFORMATION:
; APPLICANT: Yoshihiro Ishikawa
; TITLE OF INVENTION: Cloning and Character-
; TITLE OF INVENTION: Cloning of a Cardiac Adenylyl Cyclase
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Alan M. Gordon
; STREET: 1937 West Main Street,
; STREET: P.O. Box 60
; CITY: Stamford
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII from DNA
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07793,961A
; FILING DATE: 19911118
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,705
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203 321 2719
; TELEFAX: 203 321 2971
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4046 base pairs listed
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-793-961A-1

Query Match 84.3%; Score 2990.4; DB 1; Length 4046;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 3229; Conservative 0; Mismatches 311; Indels 12; Gaps 4;
Qy 1 ATGTCATGCTTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGAAACAGCCCTGGGGT 60
Db 131 ATGTCGTTAGTGGCTCTCTGCTCCCAAGTGGATGAACGAAACAGCCCTGGGGT 190
Qy 61 GAACCAATGGCAGAGAGGTTTCGGCGGCGCTGCGACTCGGGCAGGTGGCTTCTGCAG 120
Db 191 GAACCAATGGCAGAGAGGTTTCGGCGGCGGACTCGGACAGTGGCTTCTGCAG 247
Qy 121 CCCGCTATATGAGTGTCTCGGGATGCAGAGCACCAGCCCGCCCGCCCGCCCGCC 180
Db 248 CCCGCTATATGAGTGTCTCGGGATGCAGAGCACCAGCCCGCCCGCCCGCCCGCC 307

Db 2462 CCCGCTGACATCACTGCTGCCACCTGCAGCAGCTCAATTACTCTCTGGGCTGGATGCT 2521
Qy 2398 CCCCTGTGTGAGGACCATGCCACCTGCAGCTTTCCTGAGGTGTCATCGGGAACATG 2457
Db 2522 CCGTGTGTGAGGACCGCCACCCACTTGCAGCTTCCCTGAGTACTCTGTTGGGNACATG 2581
Qy 2458 CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCTGCTGCACATCAGCAGCATCGGGAAGTTGCC 2517
Db 2582 CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCTGCTGCACATCAGTAGCATCGGGAAGTTGCC 2641
Qy 2518 ATGATCTTTGCTTGGGGCTCATATTTTGGTGTGCTTCTGCTGGGTCCCCAGCCGCC 2577
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Qy 2578 ATCTTTGACAACATGACCTACTGCTTGGCGTCCATGCTTGGCTTCTTCCAATGAGACC 2637
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Db 2822 ATTCTGCTGGTGTGTTGGCCTGGCCTGTATCTGCACGCCCGCAGCAGGTGGAATCAACTGCA 2881
Qy 2758 CGCCTAAACTTCCCTCTGAAAACACAGGCAACAGGGGAAAGAGAGATGAGGAGCTA 2817
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Qy 2818 CAGGCATACACCGGAGGCTGCTGCATTAACATCTCTGCCAAGGAGGTGGCCGCCCACTTC 2877
Db 2942 CAGGCCTACACCGAAGGCTGCTGCATTAACATCTCTGCCAAGGAGGTGGCTGCCCACTTC 3001
Qy 2878 CTGCGCCGGAGCCCGCAATCATCACTACTACTAGTCTGTGAGTGTGTGCTGCT 2937
Db 3002 CTGCGCCGGAGCCCGCAAGCAGTCTACTACCAGTCTGTGAGTGTGTGCGCTC 3061
Qy 2938 ATGTTTGCTCCATTGCCAACTTCTCTGAGTCTATGTGGAGCTGGAGCAAAACATGAG 2997
Db 3062 ATGTTTGCTCCATTGCCAACTTCTCTGAGTCTATGTGGAGCTGGAGCAAAACATGAG 3121
Qy 2998 GGTGCCGAGTGCCTGCGGCTGCTCAACGAGATCACTGCTGATTTGATGAGATTAATCAGC 3057
Db 3122 GGTGTCGAGTGCCTGCGGCTGCTCAACAAATCATCGCCGACTTTGATGAGATCATCAGC 3181
Qy 3058 GAGGAGCGGTTCCGGCAGCTGAAAGATCAAGACGATTTGTAGCACCTACATGCTGCC 3117
Db 3182 GAGGAGCGGTTCCGGCAGCTGGAGAAAATCAAGACGATCGGTAGCACGATACATGCTCGG 3241
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Db 3242 TCGGGGCTGAACGCCAGCACCTACGATCAGCGCGGCGGCTCCACATCACTGCCCTGGCC 3301
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Db 3302 GACTATGCCATCGCGCTCATGAGCAGATGAACACATCAACGAGCACTCTCTTCAACAAC 3361
Qy 3238 TTCCAGATGAAGATTGGGCTGAACATGGGCCAGTCTGGCAGGTGTATCGGGGCTCGG 3297
Db 3362 TTCCAGATGAAGATTGGGCTGAACATGGGCCAGTGTGGCAGGGGCTCATTTGGGGCTCGG 3421
Qy 3298 AAGCCACAGTATGACATCTGGGGAAACACAGTGAATGTCTCTAGTCTGATGGACAGCAGC 3357
Db 3422 AAGCCACAGTATGACATCTGGGGNACACAGTGAATGTCTCTAGCCGTATGGACAGCAGC 3481
Qy 3358 GGGTTCGCCCGCAATCCAGTGTACCCAGCTGTATACCAGTTTCTAGCTGCCAAGGCG 3417
Db 3482 GGGGTTCTGACCGAATCCAGTGTACCCAGCTGTGTACCAGTTTCTAGCTGCCAAGCGG 3541
Qy 3418 TACCAGCTGGAGTGTGCGAGGGTGTCTAAGGTGAAGGGCAAGGGGAGATGACCACTAC 3477
Db 3542 TACCAGCTGGAGTGTGCGAGGGTGTCTAAGGTGAAGGGCAAGGGGAGATGACCACTAC 3601

Qy 3478 TTCCTCAATGGGGCCCCCAGCAGTTAAACAGGGCCCCAGCCACAAATTCAGCTGAAGGGACC 3537
Db 3602 TTCCTCAATGGGGCCCCCAGCAGTTAGCAGAGCCAGCTACAAAGTTCAAGTCTGTCAGGACC 3661
Qy 3538 AAGTGGGCACT 3549
Db 3662 AAGTGGGCATT 3673

RESULT 4

US-08-240-357-1
; Sequence 1, Application US/08240357
; Patent No. 5578481
; GENERAL INFORMATION:
; APPLICANT: Ishikawa, Yoshihiro
; TITLE OF INVENTION: Cloning and Characterization of a
; TITLE OF INVENTION: Cardiac Adenylyl Cyclase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240.357
; FILING DATE: 10-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,705-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4046 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 131..3625
US-08-240-357-1

Query Match 84.3%; Score 2990.4; DB 1; Length 4046;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 3229; Conservative 0; Mismatches 311; Indels 12; Gaps 4;

Qy 1. ATGTCATGTTAGTGGGCTCTCTGGTCCCTAAAGTGGATGAACAGGAAACAGCCTGGGGT 60
Db 131 ATGTCGTGTTAGTGGGCTCTCTGGTCCCTAAAGTGGATGAACAGGAAACAGCCTGGGGT 190
Qy 61 GAACCAATGGCACAAGCGTTTCGGCGCGCGCTGCGCACTCGGGCAGGTGGCTTCGCAGC 120
Db 191 GAACCAATGGCACAAGCGT---CCACGCCCGGAGCTCGGACAGTGGCTTCTGCAGC 247
Qy 121 CCCCCTATATGAGTGGCTCCCGGATGCAGACCCACCCACCCCTCGGGGCCCC 180
Db 248 CCCCCTATATGAGTGGCTCCCGGATGCAGACCCACCCCTCGGGCTCCC 307
Qy 181 CCTCGGTGCCCTGCGAGATGACGCTTCATCCGGAGGGGCGGCCAGGCAAGGCAAG 240
Db 308 CCTCGGTGCCCTGCGAGATGAGGCTTCATCCGGAGAGGCGGCCCGGCAAGGCAAG 367

Db 2522 CCCTGTGTGAGGGCAGCCGCCACCTTGCAGCTTCCCTGAGTACTCTGTTGGGAACATG 2581
Qy 2458 CTGCTGAGCTCTTGGCCAGCTCTGTCTTCTGTCACATCAGCAGCATCGGGAAGTTGGCC 2517
Db 2582 CTGCTGAGCTCTTGGCCAGCTCTGTCTTCTGTCACATCAGTAGCATCGGGAAGTTGGCC 2641
Qy 2518 ATGATCTTTGCTTTGGGGCTCATCTATTGTTGGTGTCTGCTTCTGCTGGTCCGCCAGCCGCC 2577
Db 2642 ATGATCTTTGCTTTGGGGCTCATCTATTGTTGGTGTCTGCTTCTGCTGGGCCCCCAGCAGC 2701
Qy 2578 ATCTTTGACAACATATGACCTACTGCTTGGGTCCTCATGCTGCTTCTTCAATGAGAC 2637
Db 2702 ATCTTTGACAACATATGACCTACTGCTTGGTGTCTTCAATGAGAC 2761
Qy 2638 TTTGATGGCTGGGACTGTCCAGCTCAGGAGGGTGGCCCTCAAAATATATGACCCCTGTG 2697
Db 2762 TTTGATGGCTGGGACTGCCAGCTGCGGGGAGGGTGGCAGCTGAATATACACCCCTGTG 2821
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Db 2822 ATTCTGTGTTGTTGGCTGGCGCTGTATCTGCACGCCAGCAGTGGAACTCAACTGCA 2881
Qy 2758 CGCCTAAACTTCTCTGGAACACTACAGCACAACAGGGGAAAGAGGAGATGAGGAGCTA 2817
Db 2882 CGTCTGGACTTCTCTGGAACACTGAGGCAACAGGGGAGAGGAGAGATGAGGAGCTC 2941
Qy 2818 CAGGCATACAACCGAGGCTGCTCATACATCTCTGCCCAAGGAGCTGGCGGCCACATTC 2877
Db 2942 CAGGCCTACAACCGAGGCTGCTCAVAACATCTTGCCTAAGGAGCTGGCTGCCACATTC 3001
Qy 2878 CTGGCCCGGAGCGCGCAATGATGAACCTACTACTAGTCTGCTGAGTGTGTGCTGTT 2937
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Qy 2938 ATGTTTGGCTCCATTTGCCAATCTCTCTGAGTCTATGTGGAGCTGGAGGCAAAACATGAG 2997
Db 3062 ATGTTTGGCTCCATTTGCCAATCTCTCTGAGTCTATGTGGAGCTGGAGGCAAAACATGAG 3121
Qy 2998 GGTCCGAGTGCCTGGCGCTGCTCAACGAGATCATCGCTGACTTTTGATGAGATTATCAGC 3057
Db 3122 GGTGTCGAGTGCCTGGCGCTGCTCAACGAAATCATTCGCGGACTTTGATGAGATCATCAGC 3181
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Db 3182 GAGGAGCGGTTCCGCGAGCTGGAAGAAATCAAGAGCTATGTTAGTACCTACATGCTGCC 3241
Qy 3118 TCAGGGCTGAACGCGAGCACTAGATCAGGTGGGCGCTCCACATCACTGCTGCTGCT 3177
Db 3242 TCAGGGCTGAACGCGAGCACTAGATCAGGCGGCGCTCCACATCACTGCTGCTGCTGCT 3301
Qy 3178 GACTACGCTATGCGGCTCATGAGCAGATGAAGCAGATCAATGAGCAGCTTCTTCAACAT 3237
Db 3302 GACTATGCGATGCGGCTCATGAGCAGATGAACACATCAACAGCAGCTTCTTCAACAC 3361
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Db 3422 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTTCTAGCCGTATGACACAGCAG 3481
Qy 3358 GGGTTCCTGACCGAATCAGGTGACCGACGACCTGTACCGAGTCTAGCTGCCAAGGC 3417
Db 3482 GGGTTCCTGACCGAATCAGGTGACCGACGACCTGTACCGAGTCTAGCTGCCAAGGC 3541
Qy 3418 TACAGCTGGAGTGTGAGGGGTGTCAAGTGAAGGCAAGGGGAGATGACACCTAC 3477
Db 3542 TACAGCTGGAGTGTGAGGGGTGTCAAGTGAAGGCAAGGGGAGATGACACCTAC 3601
Qy 3478 TTTCTCAATATGGGGGCCCGCAGCAGTTAAACAGGGGCCAGCCACAAATTCAGCTGAAGGAGC 3537
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Db 3602 TTCCTCAATGGGGGCCGCCAGTTAGCAGAGCCAGCTTACAAGTTTCAAGTCTGTCAGGACC 3661
Qy 3538 AAGGTGGCACT 3549
Db 3662 AAGGTGGCACT 3673
RESULT 5
US-08-726-214-11
; Sequence 11, Application US/08726214
; Patent No. 6107076
; GENERAL INFORMATION:
; APPLICANT: Tang, Wei-Jen
; APPLICANT: Gilman, Alfred G.
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08726,214
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005,498
; FILING DATE: 04-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSD:450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4131 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-726-214-11

Query Match 77.5%; Score 2751.2; DB 3; Length 4131;
Best Local Similarity 86.7%; Pred. No. 0;
Matches 3080; Conservative 0; Mismatches 463; Indels; 11; Gaps 4;
Qy 1 ATGTCATGTTTGTAGTGGCTCCTGCTCCCTAAAGTGGATGAACGGAACACAGCTGGGT 60
Db 56 ATGTCATGTTTGTAGTGGCTCCTGCTCCCAAGTGGATGAACGGAACACAGCTGGGC 115
Qy 61 GAACCAATGGCAGAGCGTTTCGGCGGCGCTTGGCACTTCGGCAGGTGGCTTCTGCACG 120
Db 116 GAACCAATGGCAGAGCG---CCACGCCAGCGACCCGAGCCGCTGGCTTCTGCAGC 172
Qy 121 CCCCGCTATATGAGTGGCTCCTCGGGATGAGAGCCACCCAGCCCTCGGGGCC 180
Db 173 CCCCGCTATATGAGTGGCTCCTCAAGATGTGGAGCCACCCAGCCCTCGCTCGAGCTCGC 232
Qy 181 CCTCGGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGGGCGCCAGGCAAGGCAAG 240
Db 233 ACTCGGTGCCCTGGCAGGATGAAGCTTTCATCAGAGGGCTGGCCCGGGAAGGGGTGTG 292
Qy 241 GAGCTGGGGCTGCGGGCAGTGGCCCTTGGGCTTTCGAGGATACCGAGGTGACACACAGCG 300
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Db 293 GAGCTGGGGCTCGGTCAGTGGCTTGGGTTTGTGATGACACTGAGGTG---ACCACACCG 349
QY 301 GGGGGACGGCTGAGTGGCGCCGACGCGTGGCCAGGAGTGGCGCATCTGCTGCGCG 360
Db 350 ATGGGACAGCTGAGTGGCACCGCACACATCGCTCGAAGCGGTCCGTCTGCTGCGCAC 409
QY 361 CGTTTGGTGCAGGTGTTCCAGTGAAGCAGTTCGGTTTCGGCCAAAGCTGGAGCGCCTGAC 420
Db 410 CGGCTAGCGCAGGTGTTCCAGTCTAAGCAGTTCGCCGTCCGCCAAGCTGGAGCGTCTGAC 469
QY 421 CAGGGTACTTTTCCAGATGAACACAGCAGCCTGACGCTGCTGTTGGGGTCTGCTGGT 480
Db 470 CAGGGTACTTTTCCAGATGAACACAGCAGCCTGACGCTGCTGTTGGGGTCTGTTGTG 529
QY 481 CTGCTACAGCGGTGCTGCTGGCTTTCCAAAGCCGACCCGCCCTCAGCCTGCGCTAT 540
Db 530 CTCCTCATGCTGACTGTTGACCTTCCACGCCGCGCTGCCCTGCTCAGCCTGCTTAT 589
QY 541 GTGGCACTGTTGGCTGTGCGCGCGCCCTGTGTGTGGGGTCAATGTTGGTGTGTAAACCG 600
Db 590 GTGGCCCTGCTGACCTGTGCTCGCTCGCTTTTGTGGTACTCATGTTAGTGTAAACCGA 649
QY 601 CATAGCTTCGCCAGGACTCCATGTGGTGGTGAAGTAACGTGTGCTGGGCATCTCGCG 660
Db 650 CATAGCTTCGCCAGGACTCCATGTGGTGAAGTAACGTGTGCTGGGCATCTCGACGA 709
QY 661 GCAGTCAGGTGCGGGGCGCTTTCCAGCAGCAGACCCGCCGACCCCTCTCGGGGCTCTGG 720
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QY 721 TGCCCTGTGTTCTTGTATACATCGCATACACGCTCTCCCATCFCGCGCTGCGGGCTGCC 780
Db 770 TGCCCGGTGTTCTCGTCTACATCACCTACACACTTCTCCCATTCATGTCGAGCGGCC 829
QY 781 GTCTCAGCGCCTGGGCTCTCACCTTGCAATTTGATCTTGGCTGGCACTTAACCGT 840
Db 830 GTGCTCAGTGGCTTGGTCTTTCCACCTCGCATTTGATTTGGCTTGGCATCTCAACAAT 889
QY 841 GGTGATGCCCTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTCTGTCACCAAC 900
Db 890 GGTGACCCCTTCCTTTGGAAGCAGCTCGGTGCTTAACGTGGTCTCTGTCACCAAT 949
QY 901 GTCAATAGCATGCGACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 960
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QY 961 ACCGCGAGTTACATCCAGCGCGCTCCACTGCAGCATGAGATCGGACGAGGACGG 1020
Db 1010 ACCGCTGGTTACATCCAGCGCGGCTGCATTTGCAGCATGAGATCGACAGGAGAACTG 1069
QY 1021 CTGCTGCTGCTGATTTGCCCGCCAGCAGCTTGCCATGGAGATGAAGAAGACATCAACACA 1080
Db 1070 CTGCTGCTGCTGTTGGCCCGCAGCATGTTGCCATGGAATGAAGAAGATATCAACACA 1129
QY 1081 AAAAAAGAGAC---ATGTTTCCAAAGATCTACATACAGAAGCATGACAATGTCAAGATC 1137
Db 1130 AAAAAAGAGACATGATGTTTCCAAAGATTTACATCCAGAAGCATGACAATGTCAAGATC 1189
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QY 1258 CTGAGGATCAAGATCTTTGGGGACTGTTTACTACTGTGTGTCAGGCTGCCGAGGCCCGG 1317
Db 1310 CTGAGGATCAAGATCTTAGGAGACTGTTTACTACTGTGTGTCGGGGCTGCGGAGGCCCGG 1369
QY 1318 GCGACCATGCCACTCTCTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG 1377
Db 1370 GCAGACATGCCACTCTCTGTGGAGATGGGGGTAGACATGATCGAGGCCATCTCGCTG 1429

QY 1378 GTACGTGAGGTGACAGGTGTAATGTGAACATGCGCTGGGCATCCACAGCGGCGCGTG 1437
Db 1430 GTGCGTGAAGTAAACGGGTGTAATGTGAACATGCGCGTGGGCATCCACAGCGGCGTGT 1489
QY 1438 CACTGCGGCTGCTTGGCTTTCGCGAAATGCGATTCGATGTGTTGGTCCAATGATGTGACC 1497
Db 1490 CACTGCGGCTGCTTGGCTTTCGCGAAATGCGAGTTGATGCTGTGTTCAACAGTGTGACC 1549
QY 1498 CTGCGCAACACATGGAAGCAGGAGCCGGCTGGCGCATCCACATCACTCTCGGCAACA 1557
Db 1550 CTGCGCAACACATGGAAGCGGGGGCGCGCGCATCCACATCACTCTCGGCGCAC 1609
QY 1558 CTGCAGTACCTGAACCGGGACTACGAAGTGGAGCAGCGCGTGTGTCAGCAGCGAACGCG 1617
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QY 1618 TACTCAAGGAGCAGCATTGAGACTTTCCTCATCTCTGGGCGCCAGCCAGAACGGA 1677
Db 1670 TACTCAAGGAGCAGTGCATTGAGACTTTCCTCATCTAGGAGCCAGCCAGAACGGA 1729
QY 1678 GAGGAGAAAGCATGCTGGCCAAAGCTGCAGCGGACTCGGGCAACTCCATGGAAGGCTG 1737
Db 1730 GAGGAGAAAGCATGCTGGTCAAGCTGCAGCGGACGCGGGCCAACTCCATGGAAGGACTG 1789
QY 1738 ATGCGCGCATGGGTTCCTGATCTGCTTCTCCCGGACCAAGGACTCCAAGGCTTCGCG 1797
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QY 1798 CAGATGGCATATGATGATTCAGACAAAGAACCGGGGCGCCAAAGATGCCCTGAACCT 1857
Db 1850 CAGATGGCATATGATGATCTAGCAAAAGAACCGGGGTGCCCAAGATGCTGAACCT 1909
QY 1858 GAGGATCAGGTGATGATTCCTGAGCGGTGCCATCCATGCCGACGATGATGACGCTG 1917
Db 1910 GAGGATCAGGTGACGAGTTCCTGGCGCGAGCCATCATGCCGAGCATCGACGACTG 1969
QY 1918 CGAAGGACCATGTGCGCGGTTTTTCTCACCTTCCAGAGAGAGGATTTTGAGAAGAAG 1977
Db 1970 CGTAAGGACCATGTGCGCGGTTCTCTGCTCACCTTCCAGAGGAGGATCTCGAGAAGAAG 2029
QY 1978 TACTCCCGAAGTGGATCCCGCTTCGGAGCCTACGTTGCCTGCGCTGTGTTGCTTTC 2037
Db 2030 TATTCAGGAAGTAGACCTTCGTTTCGGAGCCTACGTCGCTGTGCGCTTTCGCTTTC 2089
QY 2038 TGCTTCATCTGCTTCATCCAGCTTCTAATTTCCACACTCCACCCCTGATGCTGGGAT 2097
Db 2090 TGCTTCATCTGTTTCATCCAGTTCCTCGTATTTCCACACTCCGCGCTGATCTCGGAT 2149
QY 2098 TATGCCAGCATCTTCTGCTGCTGCTAATCACCGTGTGATCTGTGCTGTACTCTCTGT 2157
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QY 2158 GGTTCCTGTTCCCTAAGGCCCTGCAACGCTGTGTCCGCGAGCATGTCGCTCAGCGGCA 2217
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QY 2218 CATAGCACCGAGTGGCATCTTTTCCGCTCCTGCTGTGTTTACTTCTGCTGCCATGCCAAC 2277
Db 2270 CACAGCAGGCTGTGGAGTCTTCTCGGTTCCTGCTGTTGTTCTGCTGCTGCTGCTGCTGCT 2329
QY 2278 ATGTTCACTGTAACACACACCCCATACGAGCTGTGTCAGCCCGGATGCTGAATTTAA 2337
Db 2330 ATGTTCACTGTCAGTACACCCCATCAGGACCTGTGCGCGCGGATGCTGAACTTAA 2389
QY 2338 CCGTCTGACATCACTGCTGCCCTGCCAGCTGCAAGCTCAATTTACTCTCTGGGCTGGATGCT 2397
Db 2390 CCGTCCGATGTCAGCGCTGCCACTACGACAGCTCAATTTACTCTCTGGGACTGGAAGCT 2449
QY 2398 CCCTGCTGTCAGGCGCACATGCCACTGAGCTTTTCTGAGGTGTCATCGGGAACATG 2457
Db 2450 CCCTGCTGTCAGGCGCACCCGACCCCTGAGCTTCTCTGAGTACTTTGTCGGGAGTGTG 2509

QY 2458 CTGCTGAGTCTCTTGGGCCAGAGCTGTGCTTCTCTGCACATCAGCAGCATCGGGAAGTTGGCC 2517
Db 2510 CTGCTGAGTCTCTTGGGCCAGCTCGCTTCTCTGCACATCAGCAGCATTTGGCAAGCTAGTT 2569
QY 2518 ATGATCTTTCTCTTGGGGCTCATCTATTGTTGCTGCTTCTGCTGGGTCCCGCCAGCCGCC 2577
Db 2570 ATGACCTTTGCTTGGGGTCTACTTCTGCTTCTGCTTCTGCTGGGTCCCGCCAGCCGCC 2629
QY 2578 ATCTTTGACAACTATGACCTACTGCTTGGGGTCCATGGCTTGGCTTCTTCCAAATGAGACC 2637
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Db 2690 TTCGATGGGTGGACTGCCAGCGGTAGGGAGGTGCGCTCAAAATATATGACCCCTGTG 2749
QY 2698 ATTCTGCTGCTTGGCTGGCGCTGTATCTGATCTCAGCAGGTGGAATCAGCTGCC 2757
Db 2750 ATTCTGCTGCTTGGCGCTGGCACTGTATCTACACGCAACAGGTGGAATCTACCGCC 2809
QY 2758 CGCCTAAACTTCTCTGAAACTACAGGCAACAGGGGAAAGAGAGATGGAGGAGCTA 2817
Db 2810 CGCCTGACTTCTCTGGAAGTCTGAGGCAACAGGGGAGAGAGATGGAGGAGTTG 2869
QY 2818 CAGGATACAAACCGGAGGCTGCTGATATCTGCTGAGGAGGTGGCGGCCACTTC 2877
Db 2870 CAGGCTTACAAACCGGCGCTGCTGATATCTGCTGAGGAGGTGGCGGCCACTTC 2929
QY 2878 CTGGCCCGGAGCGCCCAATGATGAACTCTACTATCAGTCGCTGAGTGTGGCTGTT 2937
Db 2930 CTGGCCCGGAGCGCCCAAGAGCTGTACTTACCAATCTCTCGAGTGGCTGGCTGTC 2989
QY 2938 ATGTTTGCCTCCATGTCGAACTTCTGAGTCTTATGAGGTGGAGGCAACAAATGAG 2997
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QY 2998 GGTGCGGAGTGCCTGGCGCTGCTCAACGAGATCATGCTGACTTGTATGATGATATCAGC 3057
Db 3050 GGCCTGAGTGCCTGGCGCTGCTCAATGAGATCATGCTGCGGACTTGTATGATGATCATCAGT 3109
QY 3058 GAGGAGCGGTTCGGCGAGCTGGAAGATCAAGAGATTTGGTAGCACCCTACATGGCTGCC 3117
Db 3110 GAGGAGAGGTTCGGCGAGCTGGAAGATCAAGACCATCGGTAGCACCCTACATGGCGGCC 3169
QY 3118 TCAGGCTGAAACGAGCAGCTACGATCAGGTGGCGCTGCCACATCAGTGCCTGGCT 3177
Db 3170 TCCGGGCTAAATGCCAGCCTATGACAGGTGCGCGCTGCGACATCAGCGCCCTGGCA 3229
QY 3178 GACTACGCCATGCGGCTCATGGAGCAGATGAAGCAGATCAATGAGCAGCTCTTCAACAAT 3237
Db 3230 GACTACGCCATGCGGCTTATGGAGCAATGAACACATCAACAGCAACACTCTTTCAACAAC 3289
QY 3238 TTCCAGATGAAGATTGGGCTGAACATGGCCAGTCTGCGAGGTGCATCGGGGCTCGG 3297
Db 3290 TTCCAGATGAAGATTGGGCTGAACATGGGCTCGGTTGAGCAGGTGTCTTGGGGCCCGG 3349
QY 3298 AAGCCAGATGATGATCTGGGGAACACAGTGAATGTCTTCTAGTCTGATGGAGCAGCAG 3357
Db 3350 AAGCCAGATGATGATCTGGGGAACACAGTGAATGTCTTCCACCGGTATGGAGCAGCACA 3409
QY 3358 GGGTCCCGCAGCGAATCCAGGTGACCGAGCAGCTGTACAGGTTTCTAGCTGCGCAAGGGC 3417
Db 3410 GGAGTTCTCTGACCGAATACAGGTGACCGAGTCTCTTACAGGTTCTAGCTGCGCAAGGGC 3469
QY 3418 TACCAGTGGAGTGTCCAGGGGTGGTCAAGGTGAAGGCAAGGGGAGATGACCACCTAC 3477
Db 3470 TACCAGTGGAGTGTCCAGGGGTGGTCAAGGTGAAGGGAAGGGGAGATGACCACCTAC 3529
QY 3478 TTCTCAATGGGGCCCGCAGCAGTTAACAGGGCCCA--GCCACAAATTTAGCTGAAGGGA 3535
Db 3530 TTCTCAATGGGGCCCGCAGCAGTTAGCAGAGCCAGAGTGGGAATTTCAACCAAGGGA 3589
QY 3536 CCAAGTGGGCACT 3549

Db 3590 CCAAGTGGGCACT 3603
RESULT 6
US-09-008-097-3
: Sequence 3, Application US/09008097
: Patent No. 6306830
: GENERAL INFORMATION:
: APPLICANT: Hammond, H. Kirk
: APPLICANT: Insel, Paul A.
: APPLICANT: Ping, Peipel
: APPLICANT: Post, Steven R.
: APPLICANT: Gao, Melhua
: TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
: TITLE OF INVENTION: HEART FAILURE
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 PAGE MILL ROAD
: CITY: PALO ALTO
: STATE: CA
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/008,097
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Dylan, Tyler M
: REGISTRATION NUMBER: 37,612
: REFERENCE/DOCKET NUMBER: 22000-20567.21
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-813-5600
: TELEFAX: 650-494-0792
: TELEX: 706141
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1812 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Coding Sequence
: LOCATION: 1..1812
: OTHER INFORMATION:
US-09-008-097-3

Query Match 51.0%; Score 1808.4; DB 4; Length 1812;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 636 TAACTGCTGCTGGGCACTCTCTGGGGCCCTCTGGTGCCTGTGTTCTTTGTATACATCGCATACAGCT 755
Db 3 TAACTGCTGCTGGGCACTCTCTGGGGCCCTCTGGTGCCTGTGTTCTTTGTATACATCGCATACAGCT 62
QY 696 GCGCAGCCCCCTCTGGGGCCCTCTGGTGCCTGTGTTCTTTGTATACATCGCATACAGCT 755
Db 63 GCGCAGCCCCCTCTGGGGCCCTCTGGTGCCTGTGTTCTTTGTATACATCGCATACAGCT 122
QY 756 CCTCCCCATCGCATCGGGGCTGCGCTCCTCAGCGGCTGGGCCCTCTCCACCTTCGATTT 815
Db 123 CCTCCCCATCGCATCGGGGCTGCGCTCCTCAGCGGCTGGGCCCTCTCCACCTTCGATTT 182
QY 816 GATCTTGGCCCTGGCAACTTAACCCGTGGTGTGATGCCTTCTCTGGAAGCAGCTCGGTGCCAA 875

Db 183 GATCTTGGCTGGCACTTAACCGTGGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAA 242
QY TGTGCTGCTCTTCTCTGCAACCAAGCTCATTAGCATCTGCACACATATCCAGCAGAGGT 935
Db 243 TGTGCTGCTCTTCTCTGCAACCAAGCTCATTAGCATCTGCACACATATCCAGCAGAGGT 302
QY GTCTCAGCGCCAGCGCTTTTCAGGAGAGCCCGCAGTTACATCCAGCGCCGGCTCCACCTGCA 995
Db 303 GTCTCAGCGCCAGCGCTTTTCAGGAGAGCCCGCAGTTACATCCAGCGCCGGCTCCACCTGCA 362
QY GCATGAGAAATCGCAGCAGAGCGGTGCTGCTGCTGGTATTTGCCCGCAGCAGGTTCGCAT 1055
Db 363 GCATGAGAAATCGCAGCAGAGCGGTGCTGCTGCTGGTATTTGCCCGCAGCAGGTTCGCAT 422
QY GGAGATGAAGAAGACATCAACCAAAAAAGAGACATGTTCCACAAGATCTACATACA 1115
Db 423 GGAGATGAAGAAGACATCAACCAAAAAAGAGACATGTTCCACAAGATCTACATACA 482
QY 1116 GAAGCATGACAATGTCAGCATCTCTGTTGTCAGACATTTAGGGCTTCCAGCGCTGGCATC 1175
Db 483 GAAGCATGACAATGTCAGCATCTCTGTTGTCAGACATTTAGGGCTTCCAGCGCTGGCATC 542
QY 1176 CCAGTGCACCTGCCAGAGCTGTCATGACCTGAATGAGCTCTTTCGCCGGTTTGACAA 1235
Db 543 CCAGTGCACCTGCCAGAGCTGTCATGACCTGAATGAGCTCTTTCGCCGGTTTGACAA 602
QY 1236 GCTGGCTGCGGAGAATCACCTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGT 1295
Db 603 GCTGGCTGCGGAGANTCACCTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGT 662
QY 1296 GTCAGGGCTGCCGAGGCGCGCGGACCATGCCCCACTGCTGTGTGGAGATGGGGTAGA 1355
Db 663 GTCAGGGCTGCCGAGGCGCGCGGACCATGCCCCACTGCTGTGTGGAGATGGGGTAGA 722
QY 1356 CATGATTGAGGCCATCTCGCTGTGTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGT 1415
Db 723 CATGATTGAGGCCATCTCGCTGTGTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGT 782
QY 1416 GGGCATCCACAGCGGCGCTGCACCTCGCGCTCCTTGGCTTGGGAATGGCAGTTTCGA 1475
Db 783 GGGCATCCACAGCGGCGCTGCACCTCGCGCTCCTTGGCTTGGGAATGGCAGTTTCGA 842
QY 1476 TGTGTGTCATGATGTGACCTTGGCCCAACCACTGGAAGCAGGAGCGGCTGGCCG 1535
Db 843 TGTGTGTCATGATGTGACCTTGGCCCAACCACTGGAAGCAGGAGCGGCTGGCCG 902
QY 1536 CATCCACATCACTCGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGAGCCAGG 1595
Db 903 CATCCACATCACTCGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGAGCCAGG 962
QY 1596 CCCTGTTGGCAAGCGCAACCGTACCTCAAGGAGCAGCACATTTGAGACTTTTCCTCATCCT 1655
Db 963 CCCTGTTGGCAAGCGCAACCGTACCTCAAGGAGCAGCACATTTGAGACTTTTCCTCATCCT 1022
QY 1656 GGGCGCCAGCCAAACGGAAGAGAGAAAGCATGCTGGCCCAAGCTGCAGCGGACTCG 1715
Db 1023 GGGCGCCAGCCAAACGGAAGAGAGAAAGCATGCTGGCCCAAGCTGCAGCGGACTCG 1082
QY 1716 GGGCAACTCCATGGAAGGGCTGATGCCGATGSGTTCTCTGATCGTGCCTTCCCGGAC 1775
Db 1083 GGGCAACTCCATGGAAGGGCTGATGCCGATGSGTTCTCTGATCGTGCCTTCCCGGAC 1142
QY 1776 CAAGGACTCCAAAGCGCTTCCGCCAGATGGGCATTTGATTTCCAGCAAAAGACAACCGGG 1835
Db 1143 CAAGGACTCCAAAGCGCTTCCGCCAGATGGGCATTTGATTTCCAGCAAAAGACAACCGGG 1202
QY 1836 CACCCAGATGCCCTGAACCGCTGAGGATGAGGTGGATGAGTTCCTGAGCGGTGCCATCGA 1895
Db 1203 CACCCAGATGCCCTGAACCGCTGAGGATGAGGTGGATGAGTTCCTGAGCGGTGCCATCGA 1262
QY 1896 TGCCCGCAGCATTGATGATGAGTGGGAGGACCATGTCGCGGCTTTTGTCTACCTTCCA 1955

Db 1263 TGCCCCCAGCATTTGATCAGCTGGGGAAGACCATTGTGGCGGGTTTTTTGCTACCTTCCA 1322
QY 1956 GAGAGAGCATTTTTCAGAAGAAGTACTCCCGAAGGTGGATCCCGCTTCGGAGCCTAGCT 2015
Db 1323 GAGAGAGCATTTTTCAGAAGAAGTACTCCCGAAGGTGGATCCCGCTTCGGAGCCTAGCT 1382
QY 2016 TGCTGTGCCCTGTGTGCTTCTCTGCTTCATCTGCTTCATCCTCAGCTTCTAAATTTTCCACA 2075
Db 1383 TGCTGTGCCCTGTGTGCTTCTCTGCTTCATCTGCTTCATCCTCAGCTTCTAAATTTTCCACA 1442
QY 2076 CTCACCCCTGATGCTGGGATTTATGCCAGCATCTTCTGCTGCTAATCACCCTGCT 2135
Db 1443 CTCACCCCTGATGCTGGGATTTATGCCAGCATCTTCTGCTGCTAATCACCCTGCT 1502
QY 2136 GATCTGTGCTGTGTACTTCTCTGCTTCTGCTTCCCTAAGGCCCTGCAACGCTCTGTCCCG 2195
Db 1503 GATCTGTGCTGTGTACTTCTCTGCTTCTGCTTCCCTAAGGCCCTGCAACGCTCTGTCCCG 1562
QY 2196 CAGCATTTGCTCGCTCAGGGCAGCATAGCAGCGGAGTTGGCATCTTTTCCGCTGCTGTGT 2255
Db 1563 CAGCATTTGCTCGCTCAGGGCAGCATAGCAGCGGAGTTGGCATCTTTTCCGCTGCTGTGT 1622
QY 2256 GTTTACTTCTGCCATTTGCCAACAATGTTACCTGTTAACCCACACCCCATACGGAGCTGTC 2315
Db 1623 GTTTACTTCTGCCATTTGCCAACAATGTTACCTGTTAACCCACACCCCATACGGAGCTGTC 1682
QY 2316 AGCCCGGATGCTGAATTTAACACCTGCTGACATCAGCTGCGCTGCCACCTGCAGCAGCTCAA 2375
Db 1683 AGCCCGGATGCTGAATTTAACACCTGCTGACATCAGCTGCGCTGCCACCTGCAGCAGCTCAA 1742
QY 2376 TTACTTCTCTGGGCTGGATGCTCCCTGTGTGAGGGCAGCATGCCACCTGTCAGCTTTC 2435
Db 1743 TTACTTCTCTGGGCTGGATGCTCCCTGTGTGAGGGCAGCATGCCACCTGTCAGCTTTC 1802
QY 2436 TGAGGTGCTCC 2445
Db 1803 TGAGGTGCTC 1812

RESULT 7
US-09-473-716-1
; Sequence 1, Application US/09473716
; Patent No. 6436672
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James
; APPLICANT: Cor Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYL
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5027-01-US
; CURRENT APPLICATION NUMBER: US/09/473,716
; CURRENT FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: PCT/US98/13540
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,901
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,362
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4523
; TYPE: DNA
; ORGANISM: human type V adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (139)..(3921)
US-09-473-716-1

Query Match 48.0%; Score 1703.4; DB 4; Length 4523;
Best Local Similarity 71.3%; Pred. No. 0;
Matches 2356; Conservative 0; Mismatches 911; Indels 36; Gaps 7;
QY 214 CGGAGGGGGGGCCCGCCAGGCAAGGCAAGGAGCTGGGGCTGCGGGCAGTGGGCCCTGGGGCTTC 273

QY	2413	ACCATGCCACCTGCAGCTTTCTCTGAGGTGTCCTATCGGGAAACATGCTGCTGAGTCTCTTG	2472
Db	2836	CCCTGGCCCAACTGCAACTTTCGCCGAGTACTTCACCTACAGCGTGCCTGCTCAGCCTCGTG	2895
QY	2473	GCCAGCTCTCTTCCCTGACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGTGCTTG	2532
Db	2896	GCCTGCTCGGTCTCTGCAGATCAGCTGCATCGGGAAGCTGTGTCTCATGCTGGCCATC	2955
QY	2533	GGGCTCATCTATTGTTGGTGTGCTTCTGCTGGGTCCCCAGCCGCCATCTTTTGACAACTAT	2592
Db	2956	GAGCTCATCTA---CGTGCTCATCGTGAGGTGCCAGGTGCACGCTCTTCGCAACAGCC	3012
QY	2593	GACCTACTGTTGGCGTCCATGGCTTGGCTTCTTCCATGAGACCTTTTGATGGGCTGGAC	2652
Db	3013	GACCTGCTGTGTACCGCCCAACGCCATAGACTTCTTCA---ACAACGGGAGCCTCCACGTG	3069
QY	2653	TGTCCAGCTGCAGGGAGGTGGCCCTCAAAATATATGACCCCTGTGATTTCGTGGTGTGTT	2712
Db	3070	CCTGAGCATGCAACAAAGTGGCATTTGAAGTGTGTGACGCCCATCATCATCTCAGTCTTT	3129
QY	2713	GCCTGGCGTGTATCTGCTCATGCTCAGCAGGTGGAAATCGACTGCCGCCCTAAACTTCCCT	2772
Db	3130	GTCTGGCCCTGTACCTGTCACGCCAGCAGGTGGAGTCCACTGCCCCGCTCGACTTCCCT	3189
QY	2773	TGGAATAACAGCACAAGGGAAAAGAGNGATGGAGGAGCTTACAGGCATACAACCGG	2832
Db	3190	TGGAATAACAGCACAAGGGAAAAGAGAGATGGAGGAGCTTACAGGCATACAACCGG	3249
QY	2833	AGGCTGCTGCATAAACAATTGCCCCAAGACGCTGGCGGCCCACTTCTTGGCCCGGAGCGC	2892
Db	3250	CGCTGCTGCACAACATCTGCCCCAAGACGCTGGCCGCTCACTTCTGCCCCGAGCGG	3309
QY	2893	CGCAATGATGAACCTTACTATCAGTGTGTGAGTGTGTGGCTGTATTGTTGGCTCCATT	2952
Db	3310	CGCAATGATGAGCTCTACTATCAGTCTGTGAGTGTGTGGCGGTGATGTTGCGCTCCATC	3369
QY	2953	GCCAACTCTCTGAGTTCATCTGAGCTGGAGGCAACAATGAGGCTGCCGAGTGCCTG	3012
Db	3370	GCCAACTCTCGAGTTCATCTGAGCTGGAGGCAACAAGAGGTGTGAGTGGCTG	3429
QY	3013	CGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGCAGGAGCGGTTCGGG	3072
Db	3430	CGGCTACTCAATGAGATCATCGCTGACTTTGATGAGATCATCAGCAGGATCGTTCGGG	3489
QY	3073	CAGCTGGAAAAGATCAAGACGATTGGTAGACCTATATGGTGCTCAGGGGTGAAGCC	3132
Db	3490	CAGCTGGAAAAGATCAAGACCATCGGCAGCACCTACATGGTGTCTCCGGCTCAACGAC	3549
QY	3133	AGCACCTACGATCAGTGGGCGCTCCACATCATCTGCCCTGGCTGACTACGCCATCGCG	3192
Db	3550	TCTACCTACACAGGTGGGCAAGACCCACATCAAGGCACCTTGGCCGACTTTGCCATGAAG	3609
QY	3193	CTCATGGAGCAGATGAAGCACATCAATGAGCACCTCTTCAACAATTTCCAGATGAAGATT	3252
Db	3610	CTGATGGACCAGATGAAGTACATCAATCAGCACCTCTTCAACAACATCTCCAGATGAAGATC	3669
QY	3253	GGGCTGAACATGGGCCCCAGTGTGGCAGGTGTCTCGGGGCTCGGAAGCCACAGTATGAC	3312
Db	3670	GGGCTCAACATCGGCCCGGTGGTGGCGGGGTGATAGGGGACGAAAGCTCTAGTACGAC	3729
QY	3313	ATCTGGGGCAACACAGTGAATGTCTTAGTGTGATGGACAGCAGGGGGTCCCGCACCGA	3372
Db	3730	ATCTGGGGCAATATCCGTGACCTGGCCAGCCCATGAGACAGCACCGGTGTACCCGACCGC	3789
QY	3373	ATCCAGGTGACCACGGACCTGTACCAGGTTCTTAGCTGCCAAGGGCTACCAAGCTGGAGTGT	3432
Db	3790	ATCCAGGTCAACACAGACATGTACCAGGTGTGCTGCTGCCAACAGTACCAGCTGGAGTGC	3849
QY	3433	CGAGGGGTGGTCAAGGTGAAGGGCAAGGGGAGAGATGACCACCTACTTCTTCATATGGGGC	3492
Db	3850	CGGGGCGTGGTCAAGGTCAAGGGCAAGGGGAGAGATGATGACCTACTTCTTCATATGGAGG	3909

QY 3493 CCC 3495
!!!
Db 3910 CCC 3912

RESULT 8
US-08-726-214-9
; Sequence 9, Application US/08726214
; Patent No. 6107076
; GENERAL INFORMATION:
; APPLICANT: Tang, Wei-Jen
; APPLICANT: Gilmann, Alfred G.
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM: .
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,214
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005,498
; FILING DATE: 04-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: OTSD:450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3924 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-726-214-9

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QY	645	CTTGGCATCTCTGGCGGCACTCCAGGTCTGGGGGCGCTTTCCACAGCAAGCCGGCGCAGCCC	704
DB	428	CATTGAGATGGTGTGGCGGTCCAGGTAGTGGGCGCTGTGTCTGCCACAGCCAGCCAGCGC	487
QY	705	CTCTGGGGCCCTCTGGTGGCCCTGTCTCTTTGTATACATGCGATACAGCTCTCTCCCCAT	764
DB	488	CTCCGAGGGCATCTGGTGGACCGGTCTTCTCATCTATACCATCTACACCCCTGTGCTCTGT	547
QY	765	CCGATCTGGGGCTTGGCGTCTCTCAGCGGGCTTGGGCTCTCCACCTTGCATTGTATTTGGC	824
DB	548	CGCATGATGGGTCTGGGTCTCAGCGGGTGTCTTCTGTGCGCTCTCCACTTGGCCATCTC	607
QY	825	CTGGCAACTTACCGTGTGATGCCCTCTCTGTGAAGCAGCTCGGTGCGCAATGTGCTGCT	884
DB	608	TCTGCAACCAACGCCAGCCAGCTTTCTGTGTAAACAGCTTCTCTCCAACGTCTCTCAT	667
QY	885	GTTCCTCTGCACCAAGCTCATTTAGCATCTGCACACACTATCCACGAGAGTGTCTCAGCG	944
DB	668	CTTCTCTTGACCAACATCGTGGGTGTGTGCACCTACTTACCACCGCAGGTCTCCACAG	727
QY	945	CCAGGCGTTTTCAGGAGACCCGCAAGTTACATCCAGGCCGGCTCCACCTGTGAGCATGASAA	1004
DB	728	ACAAGCCTCCAGGAGACCCGGAGTGCATCCAAGCTCGGCTCCACTCAGACGGGAGAA	787
QY	1005	TCGGCAGAGGAGCGGCTCTCTCTCTCGGTATGTGCCCCAGACAGTGTGCCATGTGAGATGAA	1064
DB	788	CCAGCAAGGAGCGTCT	847
QY	1065	AGAAGACATCACACAAAAAAGAGA--CATGTTCCACAAGATCTACATACAGAGCA	1121
DB	848	AGCAGACATCAACGCCAAACAGAGGATATGATGTTCCACAAGATTTACATCCAGAACA	907
QY	1122	TGACAATGTCAAGCATCCTCTTTTCAGACATTTAGGGCTTCCACGAGCTTGGCATCCCCAGT	1181
DB	908	TGACAATGTGAGCATCTCTTTTCTTGACATCGAAGCTTCTACTAGCTGGCATCCCACTG	967
QY	1182	CACCTGGCAGGAGCTGGTCAATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGC	1241
DB	968	TACTGCCCAAGAACTGGTCAATGACCCCTCAACGAGCTCTTCTGCCCGGCTTTGACAAGTTTGC	1027
QY	1242	TGCGGAGAACTACTGCTGAGGATCAAGATCTTGGGGGACTGTTACTACTCTGTGTCTCAGG	1301
DB	1028	TGCGGAGAACTACTGCTTACGGATTAAGATCCTCGGGGATTTGTTACTACTGTGTCTCGGG	1087
QY	1302	GCTGCGGAGGCGCGGCGCACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGAT	1361
DB	1088	GCTGCTGAAGCCAGAGCTGACCAACGCCACTGCTGCGCTAGAGATGGGAATGGACATGAT	1147
QY	1362	TGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATGTGCGCTGGGCAT	1421
DB	1148	CGAGGCCATCTCTCTGGTCCGGGAGGTACAGGGGTGAACGTGAACATGCGTGTGGCAAT	1207
QY	1422	CCACAGGGGCGGTGCATCTGGGCGTCTTGGCTTTCGGGAAATGGCAATTCGATGTGTG	1481
DB	1208	TCACAGCGGGAGAGTACATCTGGGTGTCTTGGGCTCAGAAGTGGCAATTCGACGTGTG	1267
QY	1482	GTCCAATGTGACCTTGGCAACCAATGATGAAGCAAGAGCGGGCTGGCCGCATCCA	1541
DB	1268	GTCTACGATGTCACTGTGCCAACCAATGGAAGCTGGCGCAAGGCAAGCCGCATCCA	1327
QY	1542	CATCACTCGGGCAACACTCAGTACTGAACGGGACTACGAAGTGGAGCCAGCCGCTGG	1601
DB	1328	CATCAACAGGCCACACTCACTACCTGAACGGGACTATCAGGTGGAGCCAGGCTGTGG	1387
QY	1602	TGGCAGCGCAACCGGTACTCAAGGACGACACATTCAGACTTTTCTCTCATCTCTGGGCGC	1661
DB	1388	TGGTGAAGCCAAATGCCCTACCTCAAGGAGCACAGCATCGAGACCTTCTCTCATCTCTCGCTG	1447
QY	1662	CAGCCAGAACGGAAGAGAGAAAGGATGCTGCCAAGCTGCAGCGGACTCGCGGCCAA	1721
DB	1448	TACCCAGAGCGGAAGAGAGAGGCCATGATCCCAAGATGAACGCCAGAGAACCA	1507
QY	1722	CTCCATGGAAGGCTGATGCCCGATGGGTCTCTCTGATCGTGCCTTCTCTCC-----	1770

[illegible]

Db 2576 GGCCACAGAAGAGGAGAGATGGAGGAGCTGCAGGCGCTACAACGGCGCTTGCTGCA 2635
QY 2844 TAACATTCTGCCAAGAGACGTGGCGGCCACTTCTTGGCCGGGAGCGCGCAATGATGA 2903
Db 2636 CAACATTCTGCCAAGAGACGTGGCTGCCACTTCTTGGCCGGGAGCGCGCAATGATGA 2695
QY 2904 ACTCTACTATCATCTGTGTGAGTGTGGCTGTATATGTTTGGCTTCCATTGCCAATCTTC 2963
Db 2696 ACTGTACTACCAATCTCGGAGTGCCTGGTGTGATGTTTGGCTTCCATCCCACTTCTC 2755
QY 2964 TGAGTTCTATGTGAGCTGCAGGCAACATGAGGTGCGGAGTGCCTGGGCTGCTCAA 3023
Db 2756 CGAATCTAGCTGGAGCTAGAGCCCAACATGAGGCGTGTGAATGCTACGGTGTCTCAA 2815
QY 3024 CGAGATCATCGCTGACTTTGATGAGATTATCAGCGAGGAGCGTTCGGGAGCTGGAATA 3083
Db 2816 TGAGATCATCGCAGACTTTGATGAGATCATCATGAGGATCGGTTCAAGCAGCTGGAATA 2875
QY 3084 GATCAAGACATTTGGTAGCACCTACATGGCTGCTCAGGGCTGAAGCCAGCACCTTACGA 3143
Db 2876 GATCAAGACCATAGTAGCACCTTACATGGCTGCTCAGGGCTCAAGCAGCTTCCACCTATGA 2935
QY 3144 TCAGGTGGCGCGCTCCACATCACTCCCTGGCTGACTAGCCCATGGGCTCATGGAGCA 3203
Db 2936 CAAGGAGGCAAGACCCACATCAAGGCTCTTGCAGACTTGGCCATGAAGCTGATGACCA 2995
QY 3204 GATGAAGCACATCAATGAGCAGCTTCAACAATTTCCAGATGAAGATTGGGCTGAACAT 3263
Db 2996 AATGAAGTACATCAATGAGCAGCTTCTTCAACAATTTCCAGATGAAGATTGGGCTTAACT 3055
QY 3264 GGGCCAGTGTGGCAGGTGTCTATCGGGGCTCGGAAGCCACAGTATGACATCTGGGGGAA 3323
Db 3056 TGGACCTGTAGTGGCTGGGCTCATTTGGGCTCGCAAGCCCTCAGTATGACATCTGGGGCAA 3115
QY 3324 CACAGTGAATGTCTAGTGTGTATGACAGCAGCGGGTCCCGACCGAATCAGGTGAC 3383
Db 3116 TACAGTAATATTTGGCCAGCGGTATGACAGCAGCTGGGGTGGCTTGGCCGATCCAGGTAC 3175
QY 3384 CACGGACCTGTACAGGTTCTAGCTGCCAAGGCTACCAAGCTGGAGTGTGAGGGGTGGT 3443
Db 3176 TACAGATATGTACCAAGTGTGGCCGCCCAACACATACCAGCTGAGTGGCGGGTGTGGT 3235
QY 3444 CAAGGTGAAGGCAAGGGGAGATGACCACCTACTTCTTCAATGGGGGCC 3494
Db 3236 CAAGGTGAAGGCAAGGGTGAATGATGACCTACTTCTTCAATGGAGGGCC 3286

RESULT 9

US-08-726-214-1
; Sequence 1, Application US/08726214
; Patent No. 6107076
; GENERAL INFORMATION:
; APPLICANT: Tang, Wei-Jen
; APPLICANT: Gilman, Alfred G.
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYL CYCLASE
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,214
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005,498
; FILING DATE: 04-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSD:450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3978 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-726-214-1

Query Match 16.8%; Score 595; DB 3; Length 3978;
Best Local Similarity 51.9%; Pred. No. 9.3e-138;
Matches 1750; Conservative 0; Mismatches 1485; Indels 134; Gaps 13;
QY 153 GCCACCCAGCCCGCCGCGGCGCCCTCGGTGCCCTGCGAGGATACGCCCTTCAT 212
Db 25 GCGCCCGCGCGCTCGCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 84
QY 213 CCGGAGGGCGCGCCAGGCAAGGCAAGGAGCTGGGGCTCGCGGCGAGTGGCGCTT 272
Db 85 CCCTCATGGCGCTGGGATGGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGGA 144
QY 273 CGAGGATACCGAGGTGACAAACAGACAGCGCGCGGAGCGGTGAGGTGGCGCCCGCGCGGT 332
Db 145 GCGCGCGCGCGCGAGTCTGGGGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 204
QY 333 GCCCAGAG-----TGGCGCATCTCTGCTGCGCGCGCTTGGTGCAGGTGTTCCAGTCAAG 387
Db 205 CTGCGGCGTGGCGATGAGGAGTTTCGCGTCCCGAGCTGGAGCGCTGTTTCGCGGCTAC 264
QY 388 CAGTTCCGTTCCGCCAAGCTGGAGCGCTGTACACAGCGGTACTTTTCCAGATGAACCAAG 447
Db 265 ACCCTGGGCTGGAGCAGCGCGCGCGCTGAAGCGCTGCGCGCTGCTACAGCTTGGCG 324
QY 448 AGCAGCTGACGCTGCTGTTGGCGGTGCTGCTGCTACAGCGGTGCTGCTGGCTTTC 507
Db 325 GCGCGCTGCGCGTGGCGCGAGCTGCTGGCGCGCGCGCGCGCGCGCGCGCGCTGGTAA 384
QY 508 CAAGCGCACCGCGCGCGCTCAGCTGCTATGTTGCGACTGTTGGCTGTGCGCGCGCG 567
Db 385 GGCTCGACCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 444
QY 568 CTGTTCTGGGGCTCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 618
Db 445 TCGCTCAGGTGCGCCAGCTGCGAGAGGTGCGCGAGCTGCGCGCTGCTTTCAGCTCAAC 504
QY 619 TCCATGTTGGTGTGAGTAACTGTTGGGCGATCCTGCGCGCGAGTGCAGGTGCGGGGG 678
Db 505 TCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 563
QY 679 GCTTTCGACAGACCGCGCGCGCTCCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 738
Db 564 -----GGCAGCGGTGCGCGCGAGCGCGGATCAGGAGTCTGCGAGCTTCTTTTGGTCAAC 618
QY 739 TACATCGCATACAGCTCCTCCCGCATCGCGGCTGCGCGCTGCTGCTGCTGCTGCTGCTG 798
Db 619 TTCGTTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 678
QY 799 CTCTCCACCTTGCAAT---TGATCTTGGCTGGCAACTTAACCGTGGTGGTATGCTTCCCT 855
Db 679 GTGGCGCGCTGCGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 738
QY 856 TCGAAGCAGCTCGTGGCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 915
Db 739 TGGAGAACGCTGGGTGCCAACGCTCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 798

QY	916	ACACACTATCCAGCAGAGAGTGTTCTCAGCGCCAGGCGCTTTTCAGGAGACCCCGAGTTACATC	975
Db	799	GTGAGGATCCTGCTGAGCGGCCCAGAGAAAGGCGCTTCTGTCAGGCGCCGGAATCGCATT	858
QY	976	CAGGCCGGCTCCACCTCAGCATGAGAAATCGGCAGCAGGAGGGCTGCTGTCGCGTA	1035
Db	859	GAGGACCGCTGAGGCTGAGAGTGAGAAATGAGAAAGCAGGCGGCTGCTCATGAGCGCTC	918
QY	1036	TTGCCCCAGCAGCTTCCCATGAGATGAAGAAGACATCAACACAAAAAAGAGACATG	1095
Db	919	CTGCCCTCGGAATGTTGCCATGGAGATGAAGGAGACTTCCTGRAGCCCTCGAGAGATT	978
QY	1096	TTCCACAAGATCTACATACAGAAAGCATGACAATGTACAGCATCTCTGTTTGAGACACATTGAG	1155
Db	979	TTCCACAAGATTACATCCAGCGGATGACAACGTGAGCATCTCTTTTGAGACACATCGTG	1038
QY	1156	GGCTTCCACAGCCTGGCATCCCAAGTGCACTCGCAGGAGCTGGTCAATGACCCCTGAATGAG	1215
Db	1039	GGCTTCCAGGCTTGGCGTCAGAGTCACAGCCCGCCAGAGCTGGTGAATCTTCATATGAG	1098
QY	1216	CTCTTTGCCGGTGTGACAAGCTGGCTCGGAGAAATCACTGCCTTGAGGATCAAGATCTTTG	1275
Db	1099	CTCTCGGGAAGTTTGACGAGCTGGCCACAGAAACCACTGCCGCCGATCAAGATCCTG	1158
QY	1276	GGGGACTGTTACTACTGTGTGTACAGGCTGCCGAGGCGCGGGCCGACCATGCCCACTGC	1335
Db	1159	GGAGATTGCTACTGTGCGTGTCTGGGCTCACTCAGGCCAAGAGTGAACGCGCCACTGC	1218
QY	1336	TGTTGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGT	1395
Db	1219	TGTTGAGATGGGCTGGACATGATCAGACCATCACTCCGTGGCTGAGGCCACTGAG	1278
QY	1396	GTGAATGTGAACATGCGGCTGGGCATCCACAGCGGGCGGTGCACTGCGGCGTCTTGGC	1455
Db	1279	GTGGACTTGAACATGCGTGTGGGCTGCACACCGGAGGTCCTCTGCGGGGTCTCTGGGC	1338
QY	1456	TTGCGAAATGSCAGTTCGATGTGTGGTCCCAATGATGTGACCTGGCCCAACCACTGGAA	1515
Db	1339	CTGCTAAGTGGCAGTATGATGTGTGGTCCCAACGAGTGAACCTGGCCCAACGTCATGGAG	1398
QY	1516	GCAGGAAGCGGGCTGGCGCATCCACATCACTCGGGCAACACTGCACTGACCTGAACCGG	1575
Db	1399	GCTGCGCGCTTCCTGTGGAAAGTTCCACATCAAAAGACCACCTCGGCTGCTGAATGGT	1458
QY	1576	GACTACGAAGTGGAGCGAGCGGTGGTGGGAAGCGCAACGGTACCTCAAGGAGCAGCAC	1635
Db	1459	GACTATGAGTGGAGCGGGACACGACACGAGAGAACTGTTTCTTGAAAACTCATAA	1518
QY	1636	ATTGACACTTTCCTCATCTCGGCGCCAGCCAGAAAGCGAAAGAGGAGAAAGCATGCTG	1695
Db	1519	ATTGACACCTTTTATTGTGCCCTC-----GCATGGCGAAAGATTATTCAGGGCTG	1572
QY	1696	GCCAAAGCTGCAGCGACTGCGGCCAACTCCATGGAAGGCTGTATGCCCGATGGGTTCCT	1755
Db	1573	ATTCTCTCAGACATAAAACCGGCCAAGAGGTGAAGTTCAAAGACCGTGTCTACCTGCTG	1632
QY	1756	GATCGTGCCTCTTCGCGACCAAGACATCCAAAGGCTTCCGCCAGATGGGCATTGATGAT	1815
Db	1633	GTGACGCTCATGCACTGCGGGAAGATGTTCAAGGCCGAGATCCCTTTCTCCAACGTCATG	1692
QY	1816	TCCAGCAAAAGCAACCGGGGCAACCAAGATCCCTGAAACCTGAGGATGAGGTGGATGAG	1875
Db	1693	ACCTGTGAGGATGA-----CGCAAGGGGAGGCACTGAGAACAGCCTCGGAAAA	1742
QY	1876	TTCTGTAGCGGTGCCATCATGCCGACAGCATTTGATAGCTGCGGGAAGGACCATGTGCGC	1935
Db	1743	ACTCAGAAACCGCTGCTCTTCTCTACA-----	1770
QY	1936	CGGTTTTTCTCACTTCCAGAGAGAGGNTTTTGAGAAGAACTACTCCCGGAAGGTGGAT	1995
Db	1771	AACGTTGTCCAAACACCCCGGCAACAGTGTCAACAGGTACATCGCGCGCTCTCTGGAA	1830

QY	1936	CCCCCTCTGGAGCC	TACGTTGCCGTGGCCCTTGGTCTTCTGCTTTCATCTCTGCTTCATC	2055
DB	1831	GGCCCCAGATGG	--AGCTGAGATGGAGACCTGAACCTTCTTTCACCCCTGAAGTACAAG	1887
QY	2056	CAGCTTCTAAATTT	TCCACACATCCACCCCTGATGCTTTGGATTATGCCAGCATCTTCCCTG	2115
DB	1888	CAAGCTGAGCGAGAG	GGAAAGTACCACCAAGCTTCAGGACGAGTATTTTCACCAAGCGCGTG	1947
QY	2116	CTGCTGCTAAAT	CACCGTGTGATCTGTCTGTGTACTCTCTGTGGTTCTCTGTTTCCCTAAG	2175
DB	1948	GTTCTGGCTCTAT	TCTGCGCCCTTATTCGGCCTGTCTACCTTCTAATAATCCACAG	2007
QY	2176	GGCCCTCAACGTC	TGTCGCCGACGATTTGCCGTACAGGGCACATAGCACCGCATGTGGC	2235
DB	2008	AGTGTGGCTGTCT	GTCTGTCTGTGTGTCTGCATCTGCTTCTCGTGGCGCTGTGTCTGT	2067
QY	2236	ATCTTTTCCGTC	CTGCTGTGTGTACTTCTGCATTTGCCAATGTTCCAACTGTTCACTCTAACCAC	2295
DB	2068	TACCTACACAT	CACCGGGT-----CCAGTGTTTTCAGGGTGGCTGACCATCC	2116
QY	2296	ACCCCCATACGAG	GTGTGCAGCCGGATGCTGAATTTAACACCTGCTGACATCACTGCC	2355
DB	2117	AGATCCGACCGT	CTTGTGTCATCTCATGCTGTAACTTACTCTGTGTGGCCCAAGGC-	2175
QY	2356	TGCCACCTGACAG	CTCAATTTACTCTCTGGGCGCTGGATGCTCCCGCTGTGTAGGGCAAC	2415
DB	2176	-----TGCTGT	GGGCTGCCCTGTGGTCTGGAGCTCCAGTCCCAACGGGTGCC	2227
QY	2416	ATGCCCACTGCAG	CTTCTGAGTGTCCATCGGGAACATGCTGCTGAGTCTCTTTGGCC	2475
DB	2228	TGGTGGTCTCTG	TTCTGGGGCGCGGACCGAGTGTGCTGTG--TCCGCGCCTCGGAGTCT	2286
QY	2476	AGCTCTGTCTCT	CGACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGTCTTTGGGG	2535
DB	2287	GGCGCCCATGCC	TCTGCTGGCGCTCTGTGGCACCCCTCCGCTGGCCATATTTCTTCCGG	2346
QY	2536	CTCATCTATTTGG	TGCTGTCTGGGTGCCCGCCAGCCGCCATCTTTGACAACTATGAC	2595
DB	2347	GTCTCTCTCTG	CCAAAAATGATCTGTCTCGCGCTGCACCACTCTTACATCTCTGTC	2406
QY	2596	CTACTGCTTGGG	TCATGGCTTGGCTTCTTCCAAATGAGACCTTTGATGGGCTGGACTGT	2655
DB	2407	CTGGAGCTCAGCG	-----GGTACAGGAAGGCCATG	2436
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DB	2437	GGGGCGGTGCC	ATCTCAGGGCGCAGCTTCGAGCCCATCATGGCCATCTGCTATTCTCG	2496
QY	2716	CTGGCGCTGTAT	CTGCATGCTCAGCAGGTGGAATCGACTGCCCGCTTAACTTTCTCTGG	2775
DB	2497	TGCACGCTGGCC	CTGCACCCCGCAGGTGGATGTCAAGCTGCGGCTGGACTACCTCTGG	2556
QY	2776	AAACTACAGGCA	ACAGGGGAAAAGAGAGATGGAGGCTACAGGCATACACCCGGAGG	2835
DB	2557	GGCGCCACGGCA	GAGAGCGGGATGACATGGAAAGTGAAGCTGGACAACAAGAGG	2616
QY	2836	CTGCTGCATAA	CAATTTCTGCCAAGGACGTGGCGGCCACTTCTGTGCCCGGAGCGCGC	2895
DB	2617	ATTCTTCAACT	CTCTGCCACCCAGTTGCCACGACTTCTTAATGTCCAACCTCGC	2676
QY	2896	AATGATGAAC	TACTATTCAGTCTGTGTAGTGTGGCTGTATATGTTGGCTTCCATGGC	2955
DB	2677	AAATGGACCTG	TATTACAGTCACTCGCAGGTGGGGTGCATGTTTGCATCCATCCCC	2736
QY	2956	AACTTCTGAG	TTCTATGTGGAGCTGGAGGCAAAAGTAGGGGTGCCGAGTGCCTGCGG	3015
DB	2737	AACTTTCAAT	GACTTCTACATCGAGCTGGATGGCAACAACATGGGGTGGAAATGCTACGC	2796
QY	3016	CTGCTCAACG	AGATCATCGCTGACTTTGATGAGATTATCAGCGAGGAGCGGTTCCCGCAG	3075
DB	2797	CTTCTGAAT	TGAGATCATCGCTGACTTTGATGAGCTCATGGACAAGAGCTTTTACAAGGAC	2856
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QY 3187 ATCGGGCTATGAGCAGATGAAGCAGACATCAATGAGCAGCTTCTCAACAATTTCCAGATG 3246
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RESULT 10
US-09-412-210-2
; Sequence 2, Application US/09412210
; Patent No. 6403358
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE
; FILE REFERENCE: 5800-47
; CURRENT APPLICATION NUMBER: US/09/412,210
; CURRENT FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3518
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 21529 adenylate cyclase
; NAME/KEY: CDS
; LOCATION: (247)...(3480)
US-09-412-210-2

Query Match 14.2%; Score 505.2; DB 4; Length 3518;
Best Local Similarity 50.0%; Pred. No. 1.6e-115;
Matches 1560; Conservative 0; Mismatches 1488; Indels 72; Gaps 9;

QY 435 CCAGATGAACAGAGCAGCGCTGACGTGCTGTGGCGGTGCTGCTGCTACAGCGGT 494
Db 318 CCAGAGTACCCGCTGCTGCTGCTGTGGGATGCTGCTGTGGCGCTCGCGCGCT 377
QY 495 GCT----GCTGGCTTTCCANGCGCACCCGCCGCCCTAG--CCTGCCATATGCGCACT 548
Db 378 GCTCGAGTGGGCTGGGCCAGCGGCGGAGCTGACCTCAGACCCGAGCTTCTCGACCAC 437
QY 549 GTTGGCTGTGCGCGCCCTGTTGCTGGGCTCATGTTGGTGTGTAACCGGCATAGCTT 608
Db 438 TGTGCTGTGCGCGCTGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 497
QY 609 CGGCCAGGACTCCATGTGGTGTGAGTAACGTGGTGTGCTGGGATCCTTGGCGCAGTGCA 668
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QY 729 GTTCTTTGTATACATGCATACACGCTCCCTCCCATCCGATCGGGCTGCCGCTCCAG 788
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QY 789 CGCGCTGGGCGCTTCCACCTTGCATTTGATCTTGGCTGGCAA-----CTTAACC 838
Db 678 GGGCCTCGCGCTCTCACTCTCGCATCTGCTGCTGCTCGGCGCTGATCTTGGGCCACAG 737
QY 839 GTGGTATGCTTCTCTCTG--GAAGACGCTGGTGGCAATGTGCTGTGTTCTCTGTCAC 896
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QY 916 ACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCCTTTTCAGGAGACCCCGACTTACATC 975
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Db 1459 GACTATGAGTGGGCGGACAGCAGCAGGAGGACAGTTCCTGAAATCTATAAC 1518
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QY 1696 GCCAAGCTGAGCGGCTGCGGCGCACTCATGGAAGGCTGATGCGCGCATGGTTCCT 1755
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QY 1936 CGGTTTTGTCTACCTTCCAGAGAGAGGATTTTGAAGAAGTACTCCCGGAAGGTGGAT 1995
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QY 2116 CTGCTGCTAATACCGTGTGATCTGCTGTGTACTTCTGCTGCTTCTGTTTCCCTAAG 2175
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Db 1818 CCGTACCCCGGGGACTAGATGATGAGTGGACACCGGGGATGCCAAGTTCCTCCAGGT 1877
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Db 2655 CCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2714

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Qy 3246 GAAGATGGCTGAGATGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3305
Db 3195 GCGAGTGGGTTGAACCATGAGCCCTGAGTGGAGTTATGGGCCCCAGAGCCGCA 3254
Qy 3306 GTATGACATCTGGGGGAAACACAGTGAATGCTCTAGTCTGATGGACAGCAGGGGCTCC 3365
Db 3255 ATATGACATTTGGGCAACACAGTGAACGCTGGCCAGCCGCTGAGAGTACAGAGTCT 3314
Qy 3366 CGACCGAATCAGTGGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3425
Db 3315 TGGAAAATCAAGTGAAGTGAAGCAGATGGGCTTACAGTCCCTGGGCTACACCTG 3374
Qy 3426 GGAGTGTGAGGGGTGGTCAAGGCAAGGCAAGGGGAGATGACCACTTCTTCTCAA 3485
Db 3375 CTACAGCGGGGTGCTCATCAAGGTGAAGGCAAGGGAGCTCTGCTGCTGCTGCTGCTGCT 3434

RESULT 11

US-08-726-214-15

; Sequence 15, Application US/08726214

; Patent No. 6107076

; GENERAL INFORMATION:

; APPLICANT: Tang, Wei-Jen

; APPLICANT: Gilman, Alfred G.

; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE

; TITLE OF INVENTION: AND USES THEREFOR

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P. O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: United States of America

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:450
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 4601 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-726-214-15

Query Match 13.1%; Score 463.6; DB 3; Length 4601;
Best Local Similarity 51.5%; Pred. No. 3.8e-105;
Matches 1439; Conservative 0; Mismatches 1194; Indels 159; Gaps 10;

QY 712 GGCCTCTGGTGGCTGTGTTTATATCGCATACACGCTCCTCCCATCCGCATG 771
DB 1575 GGCATAGGCTAGTGTGTTTATACATCTTCGCCACCTACAGCATGCTCCGCTGCTCTC 1634
QY 772 CGGGCTGCCGCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATCTGGCCCTGGCAA 831
DB 1635 ACCTGGGCTAGTGTGGCGGCTGGGACATCTGCTGCAAGTCACATTTCAAGTGCTC 1694
QY 832 CTTAAACCGTGTGATGCTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTCTCTC 891
DB 1695 ATACCCAGACTAGCGTCTTTCCATCACCAGTCTCTGGCCAGGTGGTGTCTTCATG 1754
QY 892 TGCACCAAGCTATTAGCATATGCACTATCCAGCAGAGGTCTCTCAGCGCCAGGCGC 951
DB 1755 TGCAATGAATACAGCAGGCTCTTATCATAGTTACCTTTTCAGACCGCGCCAGCGGCGC 1814
QY 952 TTTTCAGGAGACCGCAGTATACATCCAGCGCGCTCAGCTGCGACGATGAGAACTCGGAG 1011
DB 1815 TTCCTGGAGACCGGAGGTGTGGAGCGCAGGCTCCGCTGGAGACAGAGAAACAAAGA 1874
QY 1012 CAGGAGCGGCTGCTGCTCGGTATTTGCCAGCAGCTTTGCCATGAGATGAAGAAGAC 1071
DB 1875 CAGGAGCGGCTGTGCTCTCTGCTGCCAGGTTTGGCTCTAGAAATGATCAATGAC 1934
QY 1072 ATCAACACAAAAGAAG-----ACATGTTCCACAGATCTACATACAGAAG 1119
DB 1935 ATGACCAATGTGGAGGAGCAGCAGCTGCGAGCATCAGTTCCACCGCATCTACATCTCGC 1994
QY 1120 CATGCAATGTGACATCTCTTTTCAGACATTTGAGGCTTTCACAGCGTGGCATCCCGAG 1179
DB 1995 TACGAGAACGTCAGTATCTTTTTCAGATGTCAAGAGTTTACCAACCTCTCTACGACC 2054
QY 1180 TGCACCTGGCAGGAGCTGGTGTGATGACCTGATGAGCTCTTTGCCGCTTTGACAAGCTG 1239
DB 2055 TTGCTGCTCAGGAGCTGTGAGATGCTCAACAGGCTCTTTGCGAGATTTGATCGGCTG 2114
QY 1240 GCTCGGAGAACTACTGCTGAGGATCAAGATCTTTGGGGACTGTTACTACTGTGTGCA 1299
DB 2115 GCCCATGAGCATCTCTCTTCGCAATTAATCTCTGGGGACTCTACTACTGTGTGCA 2174
QY 1300 GGGCTCGGAGGCGCGGCGGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATG 1359
DB 2175 GGACTGCTCAGCGCGCGGCGGAGGACCATGCTCATTTGCTGTGTGAAATGGGCGCTCAGCATG 2234
QY 1360 ATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGATGTGACATGCGCGTGGCG 1419
DB 2235 ATCAAACTATCAGGTTTGTGAGGTCAGGACCAAGCATGATGTTGACATGCGAAATGGA 2294

QY 1420 ATCCACACGCGGCGGCTGACACTGCGGCGTCTTTGGCTTGGGAAATGCCATTTGATGTG 1479
DB 2295 ATCCATTCAGGCTCTGCTGTGTGTGCTGTGGCTGAGAAAATGCGACTTTGATGTG 2354
QY 1480 TGTCCAATGATGTGACCTTGGCCACACCATGGAAGCAGGAGCGGCTGGCCGCGATC 1539
DB 2355 TGGCTTTGGGATGTGACATCGCAAAACAACTTGAATCTGGAGGAATCCCTGGGAGAATT 2414
QY 1540 CACATCACTCGGGCAACACTGTCAGTACCTGAACGGGACTACGAAGTGGAGCCAGCGCGT 1599
DB 2415 CACATTTCCAAAGCCACACTGGATTGCCCTCAGTGTGACTATATGTGGAAGAGGCGCAC 2474
QY 1600 GGTGGCAAGCGCAACCGGTACCTCAAGGAGCAGACATTTAGAGACTTTCTCTATCCTGGGC 1659
DB 2475 GGTAAAGAGAGGAATGAATCTTTGAGGAGCATAATATAGAGACCTATTGATTAGCAG 2534
QY 1660 GCCAGCCAG-----AACGGGAAGAGGAGAAAGCATGCTGGGCCA 1699
DB 2535 CCGAGGAGAGTTTGTCTATCTTGCCTGAAGATATAGTTAAGGAGTGGTGAAGTCTGCTG 2594
QY 1700 AGCTGACGCGGACTCGGGCCAACTCCATGGAAGGCTGATGCCGCGATGGTTCTCTGATC 1759
DB 2595 GACAGGAGAAACAGTGGGCAACGTTTCACAGAGGATCTCGGAGCCAGACTGCCATTC 2654
QY 1760 GTGCTTCTCCCGGACCAAGGACTCCAAAGCCTTCGCCAGATGGGCATTTGATGATTC-- 1817
DB 2655 GACACATCGTGGGCAACAGAAATCTCTGGCTGCCCTAACAGAAATTCATAAATCTG 2714
QY 1818 --CAGCAAGAACAAACCGGGCACCCCAAGATGCCCTCAACCCCTGAGGATGAGTGGATGAG 1875
DB 2715 CTTCCAAACCATCTCGCACAACTTTGCATGTCCAGTCTGGGCGCTGAGGAATTAACAAG 2774
QY 1876 TTCCTGAGCGGTGCCATGATGCCGCAAGTGTGATCAGCTCGGAAGACCATTTGCGGC 1935
DB 2775 AGAATAGAGCATACCATCGACTTGGCGAGTGGCGATAAGTTGAGAAGAGAGCATATCAAG 2834
QY 1936 CGGTTTTGCTCACCCTCCAGAGAGAGGATTTTGAAGAAGTACTCCCGGAGGTGGAT 1995
DB 2835 CCATCTCAGCTGATGTTTAAAGACTCCAGCCTGGAGCACAAGTATTTCTCAATGGGGAT 2894
QY 1996 CCCCCTTCGGAGCCTAGCTTGCCTGTGCCCTGTGGTCTCTCTGCTCATCTGCTTCATC 2055
DB 2895 GAAGTATTCAAGTCAAACTTGTCTGTGCAATTTATGTTCTCTCTTTATCTACTCGGAT 2954
QY 2056 CAGCTTCTAAATTTCCACACTCCACCCTGATGCTGGGATTTATGCCAGCATCTTCCTG 2115
DB 2955 CAAAGTTTGTCT---CCCTCTCGAGGCTGATGCTATGACCATCAGTCTCTCCATCTG 3011
QY 2116 CTGCTGCTAAATCACCCTGCTGATCTGTGCTGTGACTCCTGTGGTCTCTGTTCCCTAAG 2175
DB 3012 ATCATGTGCACTCCGCCCTGTT-----CCTCA 3039
QY 2176 GCCCTGCAACCTGTCTCCGCGAGCATTTGTCGCTCAGGGGACATAGCACCGCAGTTGGC 2235
DB 3040 TCACACGGGAGAGACTATAAGTGTCTGCTCTCATTTCTCGGAAAACCTGTGTTG-- 3097
QY 2236 ATCTTTTCCGCTGCTGTGTTTACTTCTGCCATTTGCCAACTGTTCCACCTGTAAACAC 2295
DB 3098 -----GATTAACGAGACCTATTGGCCCGCAAGCATCATCTTTGCTTCC 3143
QY 2296 ACCCCCATACGGAGCTGTGACGCGCGGATGCTGAATTTAACACCTGCTGACATCAGTGGC 2355
DB 3144 ATCTTGATTAATTTCTCGGGAGCGCTATAAATATCTGTGTGTGATTTTGACAAGTCG 3203
QY 2356 TGGCACCTGACAGAGCTCAATTAATCTCTGCGCTGAGTGTCTCCCTGCTGAGGGGAC 2415
DB 3204 ATACCTTTGAAGAACCTGACTTTCAAT-----TCTCAGCTGTGT-----TT 3245
QY 2416 ATGCCCACTTGCAGCTTTCTCTGAGTGTCTCATCGGGAACATGCTGTGAGTCTCTGGCC 2475
DB 3246 ACAGATATCTGCTCTACCCAGAGTACTTTGTCTTCTACTGGGTGTTGGCCATGCTGACG 3305
QY 2476 AGCTCTGCTCTCTGTCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTTGTCTGGGG 2535

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; APPLICANT: Iyengar, Srinivas Ravi
; TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND ADENYLYL
; FILE REFERENCE: 29770
; CURRENT APPLICATION NUMBER: US/08/307,896C
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 4008
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-08-307-896-5

Query Match      12.9%; Score 459; DB 3: Length 4008;
Best Local Similarity 50.8%; Pred. No. 4.9e-104;
Matches 1370; Conservative 0; Mismatches 1240; Indels 87; Gaps 8;

Db 3306 TGTCAGATATTTCTCGGCTTAACCTGTCTCTGAAGCTGGCTGTCTGCTCAATTATGATC 3365
QY 2536 CTGATCTATTGTGTGCTGCTTCTGTGCTGGTCCCGAGCCGCAATCTTTGACAACTATGAC 2595
Db 3366 GCATCTT-----AC 3374
QY 2596 CTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACCTTTGATGGGCTGGACTGT 2655
Db 3375 GCCTGCTGACAGAGACCATCTATGAGGCTCTTCTTGAGTTATGACAACCTGAACAC 3434
QY 2656 CAGCTGACAGGAGGTGGCCCTCAATATATGACCCCTGTGTGATCTGTCTGGTGTGGTGG 2715
Db 3435 AGTGGAGAAGATTTCTGGGACCAAGGAGCATCTGCTACTGATGGCCATGTTCCCTT 3494
QY 2716 CTGGCGCTGTATCTGATGCTCAGCAGGTGGAATGCACTGCCGCTTAACTTTCCTCTGG 2775
Db 3495 CTTGCTGTATTACCATGACAGCAGCTGGAGTACACAGCCGCCCTAGATTTCTCTGTGG 3554
QY 2776 AAACACAGCAACAGGGGAAAGAGAGATGGAGAGCTACAGGCATACAACCCGAGG 2835
Db 3555 CGAGTACAGGCCAAAGAGAGATCAACGAGATGAAGGACTTGAGGAAACACAAATGAGAAC 3614
QY 2836 CTGCTGCATAAATCTGCCCAAGAGAGCTGGCGGCCCACTTCTTGGCCCGGAGCGCCG 2895
Db 3615 ATGCTTTCGAATATCTTACCCGCGCCACGTGGCCCGCCACTTCTTGGAGAAGACAGAGAC 3674
QY 2896 AATGATGAACCTACTATCATGCTGTGTGAGTGTGGCTGTATGTTTGCTCCATGCC 2955
Db 3675 AATGAGAGCTGTATTCTCAATCCTATGATGCCGTTGGGGTAATGTTTGCTCCATTCCT 3734
QY 2956 AACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAAAGTAAGGCTGCCGAGTCCCTGGG 3015
Db 3735 GGATTTGCAGACTTTTACTCTCAGACAGAAATGAACAAACCAGGAGTGAATGCTCGCG 3794
QY 3016 CTGCTCAACGAGATCATGCTGATCTGTATGAGATTATCAGCAGAGAGCGGTTCCGCGCAG 3075
Db 3795 TTGCTGAATGAGATCATGCTGATCTGTATGAGTTTACTTGGAGAGGACCGCTTTCAGGAC 3854
QY 3076 CTGGAAAGATCAAGACGATTTGTGTAGCACCATACATGGCTGCTCAGGCTGGAACGCCAGC 3135
Db 3855 ATAGAGAGATTAAAGACATTGCTAGTACATACATGGCTGCTCAGGACTGTCCACAGAG 3914
QY 3136 ACCTACGA----TCAGTGGCGCGCTCCACATCACTGCCCTGGCTGACTACGCCATGCGG 3192
Db 3915 AAACAGCAATGTGAAGATAAATGGGACATTTGTGTGCCCTGGCTGACTTCTCTCTGCC 3974
QY 3193 CTCATGGAGCAGATGAAGCACATCAATGAGCAGCTCCTTCAACAATTTCCAGATCAAGATT 3252
Db 3975 CTGACTGAAGAGCATACAAGAGATCAACAGCATTCGTTCAACAATTTTGAATCCCGTATT 4034
QY 3253 GGGCTGAACATGGCGCCAGTGGTGGCAGGTGTCTATCGGGCTCGGAAGCCACAGTATGAC 3312
Db 4035 GGCATCAGCATCGCTCAGTGGTAGAGGTCTAATTTGGCGCTAAGAACCACAGATGAC 4094
QY 3313 ATCTGGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCAGCGGGTCCCGACCGA 3372
Db 4095 ATTTGGGCTAAAATGTGAACTTTGGAAAGCCGAATGGACAGCAGAGTGAAGTGGCGCG 4154
QY 3373 ATCCAGGTGACACAGGACCTGTACAGGTTCTAGCTGCCAAGGCTACCAAGCTGGAGTGT 3432
Db 4155 ATCCAAGTCTCAGGAGACCTATCTCATCTTGAAGGATCAGGCGCTTGGCTTCGACTAC 4214
QY 3433 CGAGGGTGTCAAGGTGAAGGCAAGGGGA 3464
Db 4215 CGGGAGAGATATATGTGAAGGGCATCAGCGA 4246
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RESULT 12

US-08-307-896-5

; Sequence 5, Application US/08307896C

; Patent No. 6034071

; GENERAL INFORMATION:

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; APPLICANT: Iyengar, Srinivas Ravi
; TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND ADENYLYL
; FILE REFERENCE: 29770
; CURRENT APPLICATION NUMBER: US/08/307,896C
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 4008
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-08-307-896-5

Query Match      12.9%; Score 459; DB 3: Length 4008;
Best Local Similarity 50.8%; Pred. No. 4.9e-104;
Matches 1370; Conservative 0; Mismatches 1240; Indels 87; Gaps 8;

QY 852 CCTCTGGAAGCAGCTCGGTGCCAATGTGTGCTGTCTGCAACCAACGCTCATATGAT 911
Db 624 CCTGTTCTGGCAGATACTGGCCAATGTGATCATTTTCTTGTGGAACTTGGCGGAGC 683
QY 912 CTCACACACTATCCAGCAGAGGTGTCTAGCGCCAGGCGCTTTCAGGAGACCCGAGTTA 971
Db 684 CTACCAACAAGCAGCTCATGGAGCTTGCTTTCAGCAAAACCTATCGGACACAGTGAATTG 743
QY 972 CATCCAGGCGCGCTCCACCTGCAGCATGAGAAATCGGCAGCAGGAGCGCTGTGCTGTC 1031
Db 744 CATCAAGTCCCGGATCAAGCTGGAAATTTGAAAACGCGCAGCAGGAGCGCTCTGCTCTC 803
QY 1032 GGTATTGCCCGCCAGCAGTTCCTCATGGAGATGAAAGAAAGACATCA----- 1075
Db 804 CTTGCTGCCAGCTCACATCGCATCGCATGAGATGAAAGCTGAAATCATTCAGAGGCTGCAGGG 863
QY 1076 -----ACACAAAAAAGAGACATGTTCCACAAGATCTACATACAGAAGCA 1121
Db 864 CCCCAAAGCAGGACAGATGGAAAACACAAACAACTCCACAATCTGTGTCAAAACGACA 923
QY 1122 TGCAATGTGAGCATCCTGTTTCAGACATTTAGGCGCTTCACCAGCCTGGCATCCCGAGT 1181
Db 924 CACCAAGCTGAGCATATTATACGCTGACATTTGTGGCTTCACCGCGCTTCGAAGCGATTG 983
QY 1182 CACTGGCAGGAGTGGTCAATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACANGCTGG 1241
Db 984 CTCCTCTGGCGAACTGGTCCACATGCTGTAATGAACCTTTTGGGAAGTTTGTATCAAAATAGC 1043
QY 1242 TCGCGAGAATCACTGCTGAGGATCAAGATCTTGGGGGACTGTTTACTACTGTGTGTCAGG 1301
Db 1044 AAGGAGAATGAATGATGAGAATTTAAATTTTAGGAGACTGCTATTACTGTGTTCCTGG 1103
QY 1302 GCTGCCGAGGCGCGCGCCAGCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGAT 1361
Db 1104 GCTCCTATATCACTCCCTAACCATGCCAAGACTGTGTGAAATGGATTTGGATATGTG 1163
QY 1362 TGAGGCCATCTCGTGGTGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCAT 1421
Db 1164 CGAAGCCATAAAGAAAGTGAAGGATGCTACCGGAGTTGATATCAACATGCGTGTAGGAGT 1223
QY 1422 CCACAGGCGCGCTGACCTGCGCGCTCTTGGCTTCGGGAAATGGCAGTTCGATGTGTG 1481
Db 1224 GCATTCGGGAGAGCTTCTGTGTGTGATTTGGTCTCCAGAAGTGGCAGTATGATGTGTG 1283
QY 1482 GTCCAATGATGTGACCTCGCCCAACACATGGAAGCAGAGAGCGCGCTGGCCGATCCA 1541
Db 1284 GTCTCATGATGTTACTCTGGCAAAACACATGGAAGCTGGAGGAGTCCCTGGCGGTGTCA 1343
QY 1542 CATCACTCGGGCAACACTGCACTACCTGAACGGGACTACGAAGTGGAGCCAGCCCTGG 1601
Db 1344 CATTTCTTCAGTCACCTCTGGAGCAGTTGAATGGGCTTTATAAAGTGGAGGAAGAGATGG 1403
QY 1602 TGGCAAGCGCAGCGGTACCTCAAGGAGCAGACATTTGACACTTCTCTCATCTCTGGCGCG 1661
Db 1404 TGAGATAAGAGACCCCATATTTAAAGCAGCAGCTTGGTGAAGAACCTACTTTTGTAAAT----- 1457
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RESULT 15
US-08-726-214-5
Sequence 5, Application US/08726214
Patent No. 6107076
GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4533 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

Query Match 12.4%; Score 441.6; DB 3; Length 4533;
Best Local Similarity 50.1%; Pred. No. 1.1e-99;
Matches 1359; Conservative 0; Mismatches 1284; Indels 67; Gaps 8;

Qy 853 CTCGTGAGGAGCTCGGTGCCAATGTGCTGCTCTCTCCACCAAGCTATTAGCATC 912
Db 1030 CTGCTGAGGAGATCCTGGCTAACGCTCTTCTACCTGTGCGGCATCATCTGGGCATC 1089
Qy 913 TGCACACACTATCCAGCAGAGGTGCTCAGCGCCAGGCTTTTCAGAGACCCCGAGTTAC 972
Db 1090 ATGTCCTACTATCGGAGACCGGTAAAGCACCAGAGGCTTCTGAGGCGCCGCGCAGTCG 1149
Qy 973 ATCCAGGCGCGCTCCACCTCAGCATGAGATCGGACGAGGAGCGGCTGCTGCTGTCG 1032
Db 1150 CTGGAGGTGAAGATGAATCTGGAGGAGCAGAGCCAGCAGGAGAAACCTTATGCTTCC 1209
Qy 1033 GTATTGCCCCAGCAGCTTGCATGCGCATGAGATGAAGAAGACATCAACACA----- 1080
Db 1210 ATCTCGCCAAAGCATGTGGCTGACGAGATGTTGAAGAGACATGAAGAAGATGAGAGTCAG 1269
Qy 1081 AAAAAGAGACATCTCCACAGATCTACATACAGAGCATGACAATGTGAGCATCTG 1140
Db 1270 AAGGACGACGACGATCAACACCATGTACATGTACCGCCATGAGAAATGTACGATCTG 1329
Qy 1141 TTTGACAGACATTTGAGGGTTTCAACAGCTGGCATCCCAAGTGGCACTCGCAGGAGCTGTC 1200
Db 1330 TTTGACAGATTTGAGGGCTTTTACCAGAGCTGCTCTGCTTGCAGTGCAGGAGCTCGTG 1389

Qy 1201 ATGACCCCTGAATGAGCTCTTTGCCCGTTTGACAAGCTGCTCGGAGAAATCACTGCCTG 1260
Db 1390 AAGTACTCAACGAGCTCTTTGCCCGTTTGACAAGCTGCGGCCAAATACACAGCTG 1449
Qy 1261 AGGATCAAGATCTTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCGGAGGCCCGGGCC 1320
Db 1450 AGGATCAAGATCTTAGCGACTGTTACTACTGCTGCGGCTGCGCTGACTACCGGGAG 1509
Qy 1321 GACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGATTTAGGCCATCTCGCTGGTA 1380
Db 1510 GACCACCGCTGTCTCCATCTGATGGGCTTGCCATGTGTAGAGGCCATCTGCTAGCTG 1569
Qy 1381 CBTGAGGTGACAGGTGTGAATGTGAACATCGGTGGGATCCACAGCGGCGCTGCTAC 1440
Db 1570 CGGAGAAAGACCAAGACCGGAGTGGACATCGGTGGGGGTGCACAGCAGCATGTGCTA 1629
Qy 1441 TGGCGCTCTTGGCTTGGGAAATGSCAGTTGATGTGTGTGTCCTCAATGATGTACCCCTG 1500
Db 1630 GGTGGCTCTTGGCCAGAGCGCTGGCAGTATGATGTATGTTACCGATGTCACTGTG 1689
Qy 1501 GCCAACCATGGAAGCAGGAGCGGGCTGGCGGCATCCACATCACTCGGGCNAACACTG 1560
Db 1690 GCAAAACAAGATGGAGGTGGCGCATCCAGGGCGCTGCACATTTCCCAAGACACCATG 1749
Qy 1561 CAGTACCTGAACGGGACTACGAAGTGGAGCGAGCGGCTGTGTCGAAGCGCAACGCGTAC 1620
Db 1750 GACTGCTGAAGGGAGTTGCGATGTGCACTTGGTGTGATGGTGCAGTCTCGCTGCACTAC 1809
Qy 1621 CTCAGGAGCAGCACATTTGAGACTTTCTCATCTGTGGCGGCCAGCCAGAAAGAGAG 1680
Db 1810 CTAGATGAGAAGGCATCGAAACCTTACCTCATCTATTCCTCCAAAGC-CAGAGGTGAAGAA 1868
Qy 1581 GAGAAAGCATGCTGGCCCAAGCTCAGCGGACTCGGGCCAACTCCATGGAAGGCTGTATG 1740
Db 1869 GACAGCTCAAAATGGCTCAACGGCTCGGGCTCCCAACAGGAGCACCGGCATCCAGACC 1928
Qy 1741 CCGGATGGGTTCCCTGATGCTGCTCTTCCCGGACCAAGGACTCCAAAGGCTTCCGCCAG 1800
Db 1929 CAGTCCCTTCCCTTATGAGACCAAGGAGCCCAATGGGAGTCCCATGCGCAGCGGCTC 1988
Qy 1801 ATGGGCAATTGATGATTCAGCAAGAACACCGGGGGACCCAGATGCGCTGAACCCCTGAG 1860
Db 1989 CACATCAGAGAGGCTGAAGAACAGAGGCGCCAGGCTGACAACCCCTCGTTCCTCCAAACC 2048
Qy 1861 GATGAGTGGATGAGT-TCCGTGAGCGGTGCCATCGATCGCCCGCAGCATTTGATGAGTGC 1919
Db 2049 CCGCGGAGGCTGCGCTTCCAGGACCTGGCAGACCGGTGTGTGGACGCTCTGAGGATGA 2108
Qy 1920 GAAGGACCATGTGCGCGGTTTGTCTCACCTTCCAGAGAGAGGATTTTGAGAAGAAATA 1979
Db 2109 GCAGAACTGAACAGCTTCTTAACGAGGCGCTGCTGGAGCGGAGTCCGCCAGGCTGCT 2168
Qy 1980 CTCGCGGAGGTGATCCCGCTTCCGAGCCTAGCTTGCCTGTGCCCTGTGGTGTGCTGCTG 2039
Db 2169 AAAGAAGAGAAACACATTCCTCTAACGATGAGGTTCATGAGCCCGAGAGATGGAACACG 2228
Qy 2040 CTTGATCTGCTTCCAGCTTCTAATTTTCCACACTCCACCTCGATGCTTGGGATTTA 2099
Db 2229 CTACTCGGTGAGAGAGGAGAGAGAGTGGGGCTGCGCTTCAGCTGTTCTGCTGTGCTGCT 2288
Qy 2100 TGCCAGCATCTTCTGCTGCTGCTAATCACCGTGTGATGCTGTGCTGTACTCTCTGCTG 2159
Db 2289 TTTGACGACGCGCATGTGGAGATCTTATCGACCCCTGGTGTGATGACAAACTACGTGAC 2348
Qy 2160 TTCTCTGTTCCCTAAGGCCCTGCAACGCTGTGTCCGCGAGCATTTGCCGCTCACGGGCA 2219
Db 2349 CTTCTGTTGGAGAGGTTCTGCTCTTGTATCTGATCCTGACCATCTGTTGATGCTGCTCATCT 2408
Qy 2220 TAGCACCCAGTGTGCATCTTTTCGTCCTGCTGCTGTTTACTTCTGCTGCTGCTGCTGCT 2279
Db 2409 CCCCAGGCGATTTTCTAAGAAAGCTCGTGGCCTTCTCATCTTGGATTGACCGGACCCGCTG 2468

||||| 61 GAAGCAATGGCAGAGCGTTCCGCGCGCGTGGCACTCGGGAGGTGGCTTCGCACG 120
QY 121 CCCGGCTATATAGCTGCCCTCCGGATGACAGACCACCGCCACCCCTCGGGGGCCC 180
Db 121 CCCGGCTATATAGCTGCCCTCCGGATGACAGACCACCGCCACCCCTCGGGGGCCC 180
QY 181 CCTGGTGCCCTCGGCAGGATGAGCCCTTCATCCGAGGGCGGCCACGAGGCAAG 240
Db 181 CCTGGTGCCCTCGGCAGGATGAGCCCTTCATCCGAGGGCGGCCACGAGGCAAG 240
QY 241 GAGCTGGGGCTCGGGGAGTGGCCCTCGGGCTTCGAGGATACCGAGGTGACAACACAGCG 300
Db 241 GAGCTGGGGCTCGGGGAGTGGCCCTCGGGCTTCGAGGATACCGAGGTGACAACACAGCG 300
QY 301 GGGGGGAGCGCTGAGGTGGGCGGCGAGCGGTGCCAGGAGTGGCGCATCTGCTGCGCG 360
Db 301 GGGGGGAGCGCTGAGGTGGGCGGCGAGCGGTGCCAGGAGTGGCGCATCTGCTGCGCG 360
QY 361 CGTTTGGTGCAGGTGTTCCAGTCCGAGTTCAGTTCGGTTCGGCCAAAGCTGAGCGCCTGTAC 420
Db 361 CGTTTGGTGCAGGTGTTCCAGTTCGAGTTCGAGTTCGGTTCGGCCAAAGCTGAGCGCCTGTAC 420
QY 421 CAGCGGTACTTTTCCAGATGACAGAGCGCTGACGCTGCTGCTGGTGGCGGTGCTGGTG 480
Db 421 CAGCGGTACTTTTCCAGATGACAGAGCGCTGACGCTGCTGCTGGTGGCGGTGCTGGTG 480
QY 481 CTGCTCAGCGGTGCTGCTGGCTTTCCAAAGCGCACCCCGCCCTCAGCCCTGCCATAT 540
Db 481 CTGCTCAGCGGTGCTGCTGGCTTTCCAAAGCGCACCCCGCCCTCAGCCCTGCCATAT 540
QY 541 GTGCGACTGTTGGCGCTGTGCGCGCGCGCTGTTCCAGCGGCTCATGTTGTTGTTAAACGG 600
Db 541 GTGCGACTGTTGGCGCTGTGCGCGCGCGCTGTTCCAGCGGCTCATGTTGTTGTTAAACGG 600
QY 601 CATAGCTTCGCGCAGGACTCCATGCTGGTGGTGAATGAGTGGCTGGCGATCCTGGCG 660
Db 601 CATAGCTTCGCGCAGGACTCCATGCTGGTGGTGAATGAGTGGCTGGCGATCCTGGCG 660
QY 661 GCAGTGCAGGTTCGGGGCGCTTTCCAGCAGACCCCGCGCAGCCCTCTGGGGGCTCTGG 720
Db 661 GCAGTGCAGGTTCGGGGCGCTTTCCAGCAGACCCCGCGCAGCCCTCTGGGGGCTCTGG 720
QY 721 TGCCCTGTGTTTGTATACATCGCATACACGCTCTCCCATCCGATCGCGGCTGCC 780
Db 721 TGCCCTGTGTTTGTATACATCGCATACACGCTCTCCCATCCGATCGCGGCTGCC 780
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Db 781 GTCCCTAGCGGCTGGGCTCTCCACCTTGCAATTTGATTTGGCTGGCACTTAACCGT 840
QY 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTGTTCCCTCGCACCAAC 900
Db 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTGTTCCCTCGCACCAAC 900
QY 901 GTCATTAGCTCTGCACACACTATCCAGCAGAGGTGCTCAGCGCCAGGCGTTTCAGGAG 960
Db 901 GTCATTAGCTCTGCACACACTATCCAGCAGAGGTGCTCAGCGCCAGGCGTTTCAGGAG 960
QY 961 ACCCGAGTTACATCCAGGCGCGCTCCACCTGCAGCATGAGAATCGCAGCAGGCGG 1020
Db 961 ACCCGAGTTACATCCAGGCGCGCTCCACCTGCAGCATGAGAATCGCAGCAGGCGG 1020
QY 1021 CTGCTGTGTCGGTATTGCCCGCAGCAGGTTGCCATGGAGATGAAGAAGACATCAACACA 1080
Db 1021 CTGCTGTGTCGGTATTGCCCGCAGCAGGTTGCCATGGAGATGAAGAAGACATCAACACA 1080
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Db 1081 AAAAAAAGACATGTTCCCAAGATCTACATACAGAAGCATGACAATGTACGATCCTG 1140
QY 1141 TTTGCAGACATTGAGGCTTCCACGAGCTGGCATCCAGTGCACGTGCGAGGAGCTGGTC 1200
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Db 1141 TTTGCAGACATTGAGGCTTCCACAGCTTGGCATCCAGTGCACGTGCGCAGGAGCTGGTC 1200
QY 1201 ATGACCTGATAGCTGCTTTTGGCCGTTTGAAGAAGTGGCTGCGGAGAAATCACTGCTG 1260
Db 1201 ATGACCTGATAGCTGCTTTTGGCCGTTTGAAGAAGTGGCTGCGGAGAAATCACTGCTG 1260
QY 1261 AGGATCAAGATCTTTGGGGACTGTTACTGTGTGTACAGGCTGCCGAGGCGCGGGCC 1320
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Db 1381 CGTGAGTGCAGGTGTGAATGCAACATGCGCTGGGCATCCACAGCGGCGCGTGCAC 1440
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Db 1441 TGGGGCTCCTTGGCTTGGCGAATGCGAGTTGATGTGTGGTCCAATGATGTACCTG 1500
QY 1501 GCCAACCACATGGAAGCAGGAAGCCGGCTGGCGCATCCACATCACTCGGGCAACACTG 1560
Db 1501 GCCAACCACATGGAAGCAGGAAGCCGGCTGGCGCATCCACATCACTCGGGCAACACTG 1560
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QY 1681 GAGAAAGCATGCTGGCCAAAGCTGCAGCGACTCGGGCCAACTCCATGGAAGGCTCATG 1740
Db 1681 GAGAAAGCATGCTGGCCAAAGCTGCAGCGACTCGGGCCAACTCCATGGAAGGCTCATG 1740
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QY 1801 ATGGGCATTGATGATTCAGCAAGACAAACGGGGCACCCCAAGATGCCCTGAACCCCTGAG 1860
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QY 1861 GATGAGTGGATGATGATTCCTGAGCCGTGCCATCGATCCCGCAGCATTTGATAGCTGCGG 1920
Db 1861 GATGAGTGGATGATGATTCCTGAGCCGTGCCATCGATCCCGCAGCATTTGATAGCTGCGG 1920
QY 1921 AAGSACCATGTGCGCCGGTTCCTGATCGTCCCTTCCCGGACCAAGGACTCCAAAGGCTTCCGCGCAG 1980
Db 1921 AAGSACCATGTGCGCCGGTTCCTGATCGTCCCTTCCCGGACCAAGGACTCCAAAGGCTTCCGCGCAG 1980
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QY 2041 TTCACTGCTTCATCCAGCTTCTAAATTTCCACACTCCACCTGATGCTTGGGATTTAT 2100
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QY 2101 GCCAGCATCTTCCTGCTGCTGCTAATCACCCTGCTGATGCTGTGTGTACTCTCTGCTGGT 2160
Db 2101 GCCAGCATCTTCCTGCTGCTGCTAATCACCCTGCTGATGCTGTGTGTACTCTCTGCTGGT 2160
QY 2161 TCCTGTTCCCTAAGGCCCTGCACGCTGTCCCGCAGCATTTGTCGCTCACGGGCACAT 2220
Db 2161 TCCTGTTCCCTAAGGCCCTGCACGCTGTCCCGCAGCATTTGTCGCTCACGGGCACAT 2220
QY 2221 AGCACCAGTTGGCATCTTTTCCGCTGCTGCTGTTTACTTCTGCAATTTGCCAAGCATG 2280
Db 2221 AGCACCAGTTGGCATCTTTTCCGCTGCTGCTGTTTACTTCTGCAATTTGCCAAGCATG 2280
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Qy 301 GCGGGAGCGCTGAGGTGGCGCCGACGCGTGCCAGGAGTGGCGGATCCTGCTGCGC 360
Db 301 GCGGGAGCGCTGAGGTGGCGCCGACGCGTGCCAGGAGTGGCGGATCCTGCTGCGC 360
Qy 361 CGTTTGTGAGGTGTTCCAGTGAAGCAGTTCGGTTCGGCCAAAGCTGGAGGCGCTGAC 420
Db 361 CGTGTGAGGTGTTCCAGTGAAGCAGTTCGGTTCGGCCAAAGCTGGAGGCGCTGAC 420
Qy 421 CAGGGGTACTTTTCCAGATGAACAGAGAGCGCTGAGCTGCTGGTGGCGGTGCTGGTG 480
Db 421 CAGGGGTACTTTTCCAGATGAACAGAGAGCGCTGAGCTGCTGGTGGCGGTGCTGGTG 480
Qy 481 CTGCTCAGCGGTGCTGCTGGCTTTCCAAAGCCGACCCCGCCGCTCAGCCCTGAC 540
Db 481 CTGCTCAGCGGTGCTGCTGGCTTTCCAAAGCCGACCCCGCCGCTCAGCCCTGAC 540
Qy 541 GTGCGACTGTTGGCTGTGCGCGCGCCCTGTTGCTGGGGCTCATGGTGGTGTAAACGG 600
Db 541 GTGCGACTGTTGGCTGTGCGCGCGCCCTGTTGCTGGGGCTCATGGTGGTGTAAACGG 600
Qy 601 CATAGCTTCGCGCAGGACTCCATGTGGTGGTGAAGTAACTGCTGGGCTGCTGGCG 660
Db 601 CATAGCTTCGCGCAGGACTCCATGTGGTGGTGAAGTAACTGCTGGGCTGCTGGCG 660
Qy 661 GCAGTGCAGGTTCGGGGCGCTTTCGACAGACCCGCGAGCCCTCTGCGGGGCTCTGG 720
Db 661 GCAGTGCAGGTTCGGGGCGCTTTCGACAGACCCGCGAGCCCTCTGCGGGGCTCTGG 720
Qy 721 TGCCCTGTGTTGTATACATCGCATACAGCTCTCTCCCATCCGATCCGGGCTGCC 780
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Qy 781 GTCTCAGCGGCTGGGCTCTCCACCTTGCAATTTGATTTGGCTGGCAACTTAAACCGT 840
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Db 1081 AAAAAAGAGACATGATTTTCCACAAGATCTACATACAGAGCATGACAATGTTCAGCATC 1140
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Db 1141 CTGTTTGCAGACATTTAGGGGCTTACCAGCCTGGCATCCCACTGCTGCTGCTGCTGCTG 1200
Qy 1198 GTCATGACCCCTGAATAGACTCTTTGCCCGGTTTGACAGCTGGCTGGGAGAAATCACTGC 1257
Db 1201 GTCATGACCCCTGAATAGACTCTTTGCCCGGTTTGACAGCTGGCTGGGAGAAATCACTGC 1260
Qy 1258 CTGAGGATCAAGATCTTTGGGGACTGTTTACTGCTGCTGCTGCTGCTGCTGCTGCTG 1317
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Qy 1318 GCCGACCATGCCACTGCTGTGTGAGATGGGGGTAGACATGATTTAGGGCCATCTCGCTG 1377
Db 1321 GCCGACCATGCCACTGCTGTGTGAGATGGGGGTAGACATGATTTAGGGCCATCTCGCTG 1380

Qy 1378 GTACGTGAGGTGACAGGTGTGAATGTGAACATGGCGGTGGCATCCACAGCGGCGCGTG 1437
Db 1381 GTACGTGAGGTGACAGGTGTGAATGTGAACATGGCGGTGGCATCCACAGCGGCGCGTG 1440
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Qy 1858 GAGGATGAGGTGATGATTTCTGAGCGGCTGCCATCGATGCCCGCAGCATTTGATCAGCTG 1917
Db 1861 GAGGATGAGGTGATGATTTCTGAGCGGCTGCCATCGATGCCCGCAGCATTTGATCAGCTG 1920
Qy 1918 CGGAGAGACCATGTGCGCGGTTTTTCTCATCCTTCCAGAGAGAGGATTTTGAGAAGAAG 1977
Db 1921 CGGAGAGACCATGTGCGCGGTTTTTCTCATCCTTCCAGAGAGAGGATTTTGAGAAGAAG 1980
Qy 1978 TACTCCCGGAAGTGGATCCCGCTTCGAGGCTTACGTTGCTGTGCCCTGTTGGTCTTC 2037
Db 1981 TACTCCCGGAAGTGGATCCCGCTTCGAGGCTTACGTTGCTGTGCCCTGTTGGTCTTC 2040
Qy 2038 TGCTTTCATCTGCTTTCATCCAGCTTCTAATTTTCCACACTCCACCCTGATGCTTGGGATTC 2097
Db 2041 TGCTTTCATCTGCTTTCATCCAGCTTCTAATTTTCCACACTCCACCCTGATGCTTGGGATTC 2100
Qy 2098 TATCCAGCATCTTCTGCTGCTCTAATCAACGCTGCTGATCTGCTGTGCTGCTGCTGCTG 2157
Db 2101 TATCCAGCATCTTCTGCTGCTCTAATCAACGCTGCTGATCTGCTGTGCTGCTGCTGCTG 2160
Qy 2158 GGTTCCTGTTTCCCTAAGGCGCTGCAACGCTGTGCCGAGCATTTGCCGCTCAGGGCA 2217
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Db 2221 CATAGCAGCGAGTTGGCATCTTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
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Db 2521 ATGATCTTTGTTGGGGCTCATCTATTGTTGGTGTCTTCTGCTGGTCCCGCCAGCGCC 2580
QY 2578 ATCTTTGACAACTATGACCTACTGCTTTGGGTCCTCATGGTCTTCTTCCAATGAGACC 2637
Db 2581 ATCTTTGACAACTATGACCTACTGCTTTGGGTCCTCATGGTCTTCTTCCAATGAGACC 2640
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Db 2701 ATTCTGCTGTGTTGGGCTGGGCTGTATCTGCTATCTCAGCAGGTGGAGTGCAGCTGCC 2760
QY 2758 CGGCTAAACTTCTCTGGAACCTACAGGCAACAGGGGAAAAAGAGGAGATGGAGAGCTA 2817
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QY 3058 GAGGAGCGGTTCCGGCAGCTGGAAGAGATCAAGACGATTTGGTAGCCTACATGGCTGCC 3117
Db 3061 GAGGAGCGGTTCCGGCAGCTGGAAGAGATCAAGACGATTTGGTAGCCTACATGGCTGCC 3120
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Db 3121 TCAGGGCTGAACGCCAGCAGCTAGGATCAGGTGGGCGCTGCCACATCATCTGCCCTGGCT 3180
QY 3178 GACTACGCCATGGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCTTCAACAAT 3237
Db 3181 GACTACGCCATGGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCTTCAACAAT 3240
QY 3238 TTCAGATGAAGATTGGGCTGAACATGGGCCAGTCTGTCGAGGTGTCATCGGGGCTCGG 3297
Db 3241 TTCAGATGAAGATTGGGCTGAACATGGGCCAGTCTGTCGAGGTGTCATCGGGGCTCGG 3300
QY 3298 AAGCCACAGTATGACATCTCGGGGAACACAGTGAATCTCTAGTCTGATGGACAGCAG 3357
Db 3301 AAGCCACAGTATGACATCTCGGGGAACACAGTGAATCTCTAGTCTGATGGACAGCAG 3360
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Db 3361 GGGTCCCGGACCAATCCAGGTGACCAAGGACCTGTACCAGGTCTTAGCTGCCAAGGGC 3420
QY 3418 TACCAGCTGGAGTCTGAGGGGTGGTCAAGTGAAGGCAAGGGGGAGATGACCAACCTAC 3477
Db 3421 TACCAGCTGGAGTCTGAGGGGTGGTCAAGTGAAGGCAAGGGGGAGATGACCAACCTAC 3480
QY 3478 TTCTCTAATGGGGCCCCAGCAGTTAAGAGGCCCGCCAGCCACAAATTCAGCTGAAGGAGCC 3537
Db 3481 TTCTCTAATGGGGCCCCAGCAGTTAAGAGGCCCGCCAGCCACAAATTCAGCTGAAGGAGCC 3540
QY 3538 AAGTGGGCACT 3549
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Db 3541 AAGGTGGGCACT 3552
RESULT 3
US-10-201-000-1
; Sequence 1, Application US/10201000
; Publication No. US20020187540A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/10/201,000
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US/05/474,076
; PRIOR FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-10-201-000-1
Query Match 98.0%; Score 3478.4; DB 9; Length 4942;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 3513; Conservative 0; Mismatches 36; Indels 3; Gaps 1;
QY 1 ATGTCATGCTTTAGTGGCCCTCTGTCCTCTAAAGTGGATGAACGAAACAGCCTGGGGT 60
Db 145 ATGTCATGCTTTAGTGGCCCTCTGTCCTCTAAAGTGGATGAACGAAACAGCCTGGGGT 204
QY 61 GAACGCAATGGGCAGAGCGTTGCGGCGCGGTGGCACTCGGGCAGGTGCTTCTGCACG 120
Db 205 GAACGCAATGGGCAGAGCGTTGCGGCGCGGTGGCACTCGGGCAGGTGCTTCTGCACG 264
QY 121 CCGGCTATATGAGCTCCCTCGGGATGCAGACCCAGCCGCCCTCGGGGCCCC 180
Db 265 CCGGCTATATGAGCTCCCTCGGGATGCAGACCCAGCCGCCCTCGGGGCCCC 324
QY 181 CCTCGGTGCCCTTGGCAGGATGACGCCCTTCATCCGAGGGGCGGCCAGGCAAG 240
Db 325 CCTCGGTGCCCTTGGCAGGATGACGCCCTTCATCCGAGGGGCGGCCAGGCAAG 384
QY 241 GAGCTGGGCTCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACAGCG 300
Db 385 GAGCTGGGCTCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACAGCG 444
QY 301 GGGGGAGCGCTGAGTGGCGCCCGCAGCGCTGCCAGGAGTGGCGCTCTGCTGGCGC 360
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QY 361 CGTTTGTGTCAGGTGTTCCAGTCCAGTCCGTCGCGCAAGCTGGAGCGCTGTAC 420
Db 505 CGTCTGTGTCAGGTGTTCCAGTCCAGTCCAGTCCGTCGCGCAAGCTGGAGCAGCTGTAC 564
QY 421 CAGCGGTACTTTTCCAGATGAACAGAGCAGCCTGACGCTGCTGCTGGGCTGCTGGT 480
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QY 481 CTGCTACAGGGTGTCTGGCTTTTCCAGCGCAGCCCGCCCTCAGCCTGCCTAT 540
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Qy	541	GTGCACTGTTGGCCTGTGCCGCGGCCCTTGTTCTGTGGGGCTCATGGTGGTGTGTAAACCGG	600
Db	685	GTGCACTGTTGGCCTGTGCCGCGGCCCTGTGTTCTGTGGGGCTCATGGTGGTGTGTAAACCGG	744
Qy	601	CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAAGTACGTTGGTCTCTGGGCATCCTGGCG	660
Db	745	CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAAGTACGTTGGTCTCTGGGCATCCTGGCG	804
Qy	661	CGAGTGCAGTTCGGGGGCGTTTTCGCAGCAGACCGCGCGCAGCCCTCTGCGGGGCTCTGG	720
Db	805	CGAGTGCAGTTCGGGGGCGCTCTCGCAGCAGACCGCGCGCAGCCCTCTGCGGGGCTCTGG	864
Qy	721	TGCCCTGTGTTCTTTGTATACATTCGCAATACAGCTCTCTCCCATCCGCATGCGGGCTGCC	780
Db	865	TGCCCTGTGTTCTTTGTCTACATTCGCTACAGGCTCTCCCATCCGCATGCGGGCTGCC	924
Qy	781	GTCCTCAGCGGCTGGGCGCTCCACTTTGCATTTGATCTTGGCTTGGCACTTAAACCGT	840
Db	925	GTCCTCAGCGGCTGGGCGCTCCACTTTGCATTTGATCTTGGCTTGGCACTTAAACCGT	984
Qy	841	GGTGATGCCCTTCTCTGGAAGAGCTCGGTGGCAATGTGCTGCTTCTCTGCACCAAC	900
Db	985	GGTGATGCCCTTCTCTGGAAGAGCTCGGTGGCAATGTGCTGCTTCTCTGCACCAAC	1044
Qy	901	GTCATTTAGCATCTGCACACACTATTCAGCAGAGTGTCTCAGCGCCAGGCCCTTTCAGGAG	960
Db	1045	GTCATTTGGCATCTGCACACACTATTCAGCAGAGTGTCTCAGCGCCAGGCCCTTTCAGGAG	1104
Qy	961	ACCCGCGAGTTTACATCCAGGCGCGGCTCCACCTGCAGCATGAGAATCGCAGCAGAGCGG	1020
Db	1105	ACCCGCGGTTACATCCAGGCGCGGCTCCACCTGCAGCATGAGAATCGCAGCAGAGCGG	1164
Qy	1021	CTGCTGCTGTCGGTATTGCCGCCAGCAGCTTGCCATGGAGATGAAAGAAGACATCAACACA	1080
Db	1165	CTGCTGCTGTCGGTATTGCCGCCAGCAGCTTGCCATGGAGATGAAAGAAGACATCAACACA	1224
Qy	1081	AAAAAAGAAGAC--ATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGATC	1137
Db	1225	AAAAAAGAAGACATGATGTTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGATC	1284
Qy	1138	CTGTTTTCAGACATTTGAGGCGCTTCACAGCGCTGGCATCCCACTGCACATCGCCAGAGCTG	1197
Db	1285	CTGTTTTCAGACATTTGAGGCGCTTCACAGCGCTGGCATCCCACTGCACATCGCCAGAGCTG	1344
Qy	1198	GTCATGACCTGAATGAGCTCTTTGCCCGGTTTGACAGCTGGGCTCGGAGAACTACTGTC	1257
Db	1345	GTCATGACCTGAATGAGCTCTTTGCCCGGTTTGACAGCTGGGCTCGGAGAACTACTGTC	1404
Qy	1258	CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTCTCAGGGCTCGCGGAGGCCCGG	1317
Db	1405	CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTCTCAGGGCTCGCGGAGGCCCGG	1464
Qy	1318	GCCGACCATCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG	1377
Db	1465	GCCGACCATCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG	1524
Qy	1378	GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGATCCACAGCGGGCGGTG	1437
Db	1525	GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGATCCACAGCGGGCGGTG	1584
Qy	1438	CACGTGGCGGCTCTGGCTTGGGGAATGSGCAGTTTCGATGTCGTCCCAATGATGTGACC	1497
Db	1585	CACGTGGCGGCTCTGGCTTGGGGAATGSGCAGTTTCGATGTCGTCCCAATGATGTGACC	1644
Qy	1498	CTGGCCAACCACTGGAAGCAGGAAGCGCGGCTGGCCGCTCCACATCACATCGCGGCAACA	1557
Db	1645	CTGGCCAACCACTGGAAGCAGGAAGCGCGGCTGGCCGCTCCACATCACATCGCGGCAACA	1704
Qy	1558	CTCAGTATACCTGAACGGGAGCTACGAAGTGTGAGCAGCGCGGTGTGGCAAGCGCAACGG	1617
Db	1705	CTCAGTATACCTGAACGGGAGCTACGAAGTGTGAGCAGCGCGGTGTGGCAAGCGCAACGG	1764

QY	1618	TAC	TCAAGGAGCAGCACATTTGAGACTTTCCTCATCTCTGGGCGCCAGCAGAAACGGAAA	1617
Db	1765	TAC	TCAAGGAGCAGCACATTTGAGACTTTCCTCATCTCTGGGCGCCAGCAGAAACGGAAA	1824
QY	1678	GAG	GAGAAAGCATGCTGCGCAACGTGCAAGCGGACTCGSGCCAACTCCATGAGAGGGCTG	1737
Db	1825	GAG	GAGAAAGGCATGCTGCGCAACGTGCAAGCGGACTCGSGCCAACTCCATGAGAGGGCTG	1884
QY	1738	ATG	CGCGCATGGGTTCCTGATCTGCTTCTCCGACCAAGGACTTCCAAGGCCCTTCGCG	1797
Db	1895	ATG	CGCGCATGGGTTCCTGATCTGCTTCTCCGACCAAGGACTTCCAAGGCCCTTCGCG	1944
QY	1798	CAG	ATGGGCATTTGATGATCCAGCAAGACAACCGGGGACCCCAAGATGCCTCGAACCCCT	1857
Db	1945	CAG	ATGGGCATTTGATGATCCAGCAAGACAACCGGGGACCCCAAGATGCCTCGAACCCCT	2004
QY	1858	GAG	GATGAGGTGATGATTCCTTGAGCCGTGCCATCGATGCCCGCAGCATTTGATCAGCTG	1917
Db	2005	GAG	GATGAGGTGATGATTCCTTGAGCCGTGCCATCGATGCCCGCAGCATTTGATCAGCTG	2064
QY	1918	CGA	AGGACCATGTGCGCCGGTTTTTGCTCACCTTCCAGAGAGAGATTTTGAAGAAG	1977
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QY	2038	TGCT	TTCATCTGCATCCAGCTTCTAAATTTTCCACACACTCCACCCCTGATCGTTGGGAT	2097
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QY	2098	TAT	GCAGCATCTTCCCTGCTGCTTAATCACCGTCTGATCTGTGCTGTGACTCTCTGT	2157
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QY	2218	CAT	AGCACCGCAGTTGGCATCTTTTCCGTCTGCTGTGTGTACTTCTTGCCATTGGCCAAC	2277
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QY	2518	ATG	ATCTTTGCTTTGGGGCTCATCTATTTGGTGTGCTTCTGCTGGGTCCCCCAGCCGCC	2577
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QY	2578	ATC	TTTGACAACTATGACCTTACTGCTTTGGGTCATGCGTGGCTTCTTCCAATGAGACC	2637
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QY	2638	TTT	CATGGCTGGACTGTCCAGCTGCAGGAGGGTGGCCCTCAATATATGACCCCTGTG	2697
Db	2785	TTT	CATGGCTGGACTGTCCAGCTGCAGGAGGGTGGCCCTCAATATATGACCCCTGTG	2844
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RESULT 5

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; Sequence 3, Application us/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-240-3

Query Match          51.0%; Score 1808.4; DB 10; Length 1812;
Best Local Similarity 99.9%; Pred.No. 0;
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 7

US-09-989-442-23
; Sequence 23, Application US/09989442
; Publication No. US20030013649A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P208
; CURRENT APPLICATION NUMBER: US/09/989,442
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
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; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/235,836
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/230,438
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
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; PRIOR FILING DATE: 2000-09-14
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; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,401

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; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
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; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065
; PRIOR FILING DATE: 2000-09-14

Query Match 16.5%; Score 586; DB 9; Length 837;
Best Local Similarity 85.3%; Pred. No. 2.3e-135;
Matches 652; Conservative 1; Mismatches 111; Indels 0; Gaps 0;

Qy 2732 ATGCTCAGCAGGTGGAATCGACTGCCCGCCTAAACTTCTCTGGAAACTACAGGCAACAG 2791
Db 1 ACGCCACAGAGTGGAGTCCACTGCCCGCCTCGACTTCTCTGGAGACTCGAGGCCACAG 60

Qy 2792 GGGAAAAGAGGAGATGGAGGAGCTACAGCATACAAACCGAGGCTGCTGCATAACATTC 2851
Db 61 AGGAGATAGAGGAGATGGAGGAGCTGCAGGCCCTACAACCGGCGCTGCTGCACAACATCC 120

Qy 2852 TGCCCAAGGACGTGGCGGCCACATTCCTGGCCGGGAGCGCCGAATGATGAATCTACT 2911
Db 121 TGCCCAAGGACGTGGCGGCTCACTTCTGGCCCGAGCGCGCAATGATGAGTCTACT 180

Qy 2912 ATCAGTCTGTGAGTGTGTGGCTGTATGTTGCTCCTCATTCGCCAACTCTCTGAGTTCT 2971
Db 181 ATCAGTCTGTGAGTGTGTGGGCTCATGTTGCGCTCCATCGCCAACTCTCTCCGAGTTCT 240

Qy 2972 ATGTGGAGCTGGAGGCAACAAATGAGGGTGCAGAGTGCCTGCGGCTGCTCAACGAGATCA 3031
Db 241 ACSTTGAGCTGGAGGCCAACAAACGAGGCTGTCGAGTGCCTGCGGCTACTCAATGAGATCA 300

Qy 3032 TCGCTGACTTTGATGAGATTATCAGCGAGGAGCGTTCGGCAGCTGAAAAGATCAAGA 3091
Db 301 TCGCTGACTTTGATGAGATCATCAGCGAGGATCGGTTCCGCGCAGCTGGAGAAGATCAAGA 360

Qy 3092 CGATTGCTAGCACCTACATGCTGCCTCAGCGCTGAACGCCAGCACCTACCATCAGGTGG 3151
Db 361 CCATCGCAGCACCTACATGCTGCCTCCGCGCTCAACGACTCTACCTACGACAGGTGG 420

Qy 3152 GCGCTCCACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3211
Db 421 GCAAGACCCACATCAAGGCACTGGCGGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 480

Qy 3212 ACATCAATGAGCACTCTTCAACAATTTCCAGATGAGATGAGATGAGATGAGATGAGATGAG 3271
Db 481 ACATCAATGAGCACTCTTCAACAATTTCCAGATGAGATGAGATGAGATGAGATGAGATGAG 540

Qy 3272 TCGTGGCAGGTGTCTATCGGGGCTCGGAAGCCACAGTATGACATCTGGGGGAAACAGTGA 3331
Db 541 TGGTGGCGGGGTGATAGGGGCAACGAAGCCTCAGTACGACATCTGGGGCAATACCGTGA 600

Qy 3332 ATGTCTCTAGTCTGATGAGACAGCGGGGGTCCCGGAGCCGAATCCAGGTGACCGAGACC 3391
Db 601 ACGTGGCCAGCCGCATGGACAGCACCGGCTGTACCCGACCGCATCCAGGTCCACCAGACA 660

Qy 3392 TGTACCAAGTTCTAGCTGCCAAGGGCTACAGCTGGAGTGGAGGTGGTTCAGAGGTGA 3451
Db 661 TGTACCAAGTTCTAGCTGCCAAGGGCTACAGCTGGAGTGGAGGTGGTTCAGAGGTGA 720

Qy 3452 AGGCAAGGGGAGATGACCACTTCTTCTCAATGGGGGCCCC 3495
Db 721 AGGCAAGGGGAGATGACCACTTCTTCTCAATGGAGGGCCC 764

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; PRIOR APPLICATION NUMBER: 60/236,327
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; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
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; PRIOR FILING DATE: 2000-09-29
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; PRIOR FILING DATE: 2000-09-05
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; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
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; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
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; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
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; PRIOR APPLICATION NUMBER: 60/230,438
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; PRIOR FILING DATE: 2000-06-30
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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065
; PRIOR FILING DATE: 2000-09-14

Query Match 14.9% Score 529 6; DB 9; Length 915;
Best Local Similarity 85.2% Pred. No. 2.2e-121;
Matches 600; Conservative 2; Mismatches 101; Indels 1; Gaps 1;

QY 2792 GGAAAGAGGAGATGAGGAGCTACAGGCATACACCGAGGAGCTGCTCATAAATTC 2851
Db 12 GRAGWAAAGAGGAGATGGAGGAGTGCA-CCCTACACCGCGGCTGCTGCACAACATCC 70
QY 2852 TGCCCAAGGACGTGGCGCCCACTTCTTGCGCCGGGAGCGCCCAATGATGAATCTACT 2911
Db 71 TGCCCAAGGACGTGGCGCGCTCACTTCTTGCGCCGGGAGCGCGCAATGATGAGCTCTACT 130
QY 2912 ATCAGTCTGTGAGTGTGGCTGTTATGTTTGCTCCATTTGCCAATCTCTGAGTTCT 2971
Db 131 ATCAGTCTGTGAGTGTGGCGGTATGTTTGCGCTCCATTCGCCAATCTCTCGAGTTCT 190
QY 2972 ATGTGAGCTGGAGGCAAAACAATGAGGTCGCCAGTGCCTTGCGGCTGCTCAACAGATCA 3031
Db 191 ACCTTGAGCTGGAGGCAAAACAAGAGGTGTGAGTGCCTGCGGCTACTCAATGAGATCA 250
QY 3032 TCCTGTACTTTGATGATATATCAGCAGGAGGCGGTTCGCGCAGCTGGAAGAATCAAGA 3091
Db 251 TCCTGTACTTTGATGATATATCAGCAGGAGATCGGTTCCGGCAGCTGGAGAAGATCAAGA 310
QY 3092 CGATTGGTAGCACCTACATGGCTGCCTCAGGGGTGAACCGCAGCACCTACGATCAGGTGG 3151
Db 311 CCATCGGCACACCTACATGGCTGCCTCGCGCCTCAACGACTCTACCTACGACAAGGTGG 370
QY 3152 GCCGCTCCACATCACTGGCCCTGGCTGACTACGCCATCGCGCTCATGAGGACAGATGAAC 3211
Db 371 GCAAGACCCACATCAAGGCACTGGCCGACTTTGCCATGAAGCTGATGAGCAGATGAAGT 430
QY 3212 ACATCAATGAGCACTCCTTCAACAATTTCCAGATGAAGATTGGCTGAACATGGGCCAG 3271
Db 431 ACATCAATGAGCACTCCTTCAACAATTTCCAGATGAAGATCGGGCTCAACATCGGCCCG 490
QY 3272 TCCTGCGAGTGTATCGGGGCTCGGAAGCCACAGTATGACATCTGGGGGAACACAGTGA 3331
Db 491 TGGTGGCGGGGTGATAGGGGACGAAAGCCTCAGTACGACATCTGGGGCAATACCGTGA 550
QY 3332 ATGCTCTACTGTATGACAGCAGCGGGTCCCGACCGCAATCCAGGTACACCGGACC 3391
Db 551 ACCTGGCCAGCCGATGGACAGCAGCGGTGTACCCGACCGCATCCAGGTACACACAGACA 610
QY 3392 TGTACCAGGTTCTAGCTGCCAAGGGCTTACCAGCTGGAGTGTGAGGGGTGGTCAAGTGA 3451
Db 611 TGTACCAGGTTCTAGCTGCCAAGGGCTTACCAGCTGGAGTGTGAGGTGCGGGGCGTCAAGTGA 670
QY 3452 AGGCAAGGGGGAGTACACCATCTTCTCTCAATGGGGGCCCC 3495
Db 671 AGGCAAGGGCGAGATGATGACCTACTTCTCTCAATGGAGGGCCCC 714

RESULT 10

US-10-121-911-2
; Sequence 2, Application US/10121911
; Patent No. US20020164632A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE
; FILE REFERENCE: 5800-47
; CURRENT APPLICATION NUMBER: US/10/121,911
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US/09/412,210
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3518
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 21529 adenylate cyclase
; NAME/KEY: CDS
; LOCATION: (247)...(3480)

US-10-121-911-2
Query Match 14.2%; Score 505.2; DB 9; Length 3518;
Best Local Similarity 50.0%; Pred. No. 4.5e-115;
Matches 1560; Conservative 0; Mismatches 1488; Indels 72; Gaps 9;
QY 435 CCAGATGAACACAGAGCAGCCTGACGCTGTGGTGGGGTGTGCTGTGCTACAGCGGT 494
Db 318 CCAGCAGTACCCGCTGCTGTGCTGTGCTGGGATCGTGTGCTGCGCGCGCT 377
QY 495 GCT----GCTGGCTTTCCAAAGCCGACCCCGCGCCCTCAG--CCTGCCCTATGTGGCACT 548
Db 378 GCTCGCAGTGGCTGGCCACGCGGAGAGCTGACCTCAGACCCGAGAGCTTCCTTGACCAC 437
QY 549 GTTGGCCTGTGCGCGCGCCCTGTTCGTGGGCTCATGGTGGTGTGTAACCGGCATAGCTT 608
Db 438 TGTGCTGTGCGCGCTGGCGGCTTCTCGTGTGCTGGGCTCGCTCCCGGGAGCAGCG 497
QY 609 CCGCCAGGACTCCATGTGGGTGTGAGTAACGTGGTGTGCTGGGATCCTGCGGCACTGCA 668
Db 498 ACTGCAGCGCTGGACGCGTCCCTGTCCGCTTGGTATGGTGTGCGCTGTAGCGCTAGG 557
QY 669 GGTGGGGGCGCTTTCGACAGCAGCGCGCAGCCCTCTCGGGGCTCTGTGTCCTGTG 728
Db 558 CCAGCGCTTCTGTTCACCGGGGCGTGTGAGCGCTTGGGACCAAGGTGTCTATTTCCT 617
QY 729 GTTCTTTGTATACATGACATACACGCTCCTCCCATCCGCATCGGGCTCGGCTGCTCTAG 788
Db 618 CTTGCTCATCTTCAGGCGGTATGCCATGCTGCGCTTGGGATCGGGACGCGCCGCTCGC 677
QY 789 CGGCTTGGGCTCTCCACCTTGCATTTTGATCTTGGGCTGSCAA-----CTTAACC 838
Db 678 GGGCCTCGCCCTCTCTCTCGCATCTCTGCTGCTGGTCTGCTGGGCTGTATCTTGGGGCACAGCC 737
QY 839 GTGGTGTATGCTTCTCTGTG--GAAGCAGCTCGGTGCGCAATGTGCTGTCTCTCTGCTAC 896
Db 738 GGAATCAGCGCTTGCATGCTGCGGAGTTGGCAGCAACGCACTGCTGTCTCTGTGCGG 797
QY 897 CAACGTCTATTAGCATGTGCACACACTATCCAGGAGGTGTCTCAGGCGCCAGGCTTTCA 956
Db 798 GAACGTTGGCAGGAGTGTACCAAGCGCTGATGGAGCGCGCTCGCGGCCACGTTCCG 857
QY 957 GGAGACCCGCGCTTACATCCAGCGCGGCTCCACCTGACGATGAGATGAAGAAGACATCAA 1016
Db 858 GGAGGCACTCAGCTCCCTGCACTCAGCGCGGCTGGACACCGAGAGAACGACCAAGA 917
QY 1017 GCGGCTGCTGCTGTGCGTATTTGCCAGCACGTTGCCATGGAGATGAAGAAGACATCAA 1076
Db 918 ACACCTTCTCTTGTCCATCTCTCTGCTACCTGGCCCGAGAGATGAAGCAGAGATCAT 977
QY 1077 CACAA-----AAAAAGAGACATGTTCCACAGAT 1106
Db 978 GGCACGGCTGCAGGACGACAGCGGCTCAGCGCAGAGAGCATTAAACAATTTCCACAGCCT 1037
QY 1107 CTACATACAGAAGCATGACAAATCTCAGCATCTTGTGGCAGACATTCAGGCTTCACCAG 1166
Db 1038 CTATGCAAGAGGACACAGGAGTTCAGCGTGTGATGCTGACATGTGGGCTTCAGCG 1097
QY 1167 CTTGGCATCCAGTGTGCTGCGCAGGAGCTGGTGTGCTGACCTGAATGAGCTCTTTGGCCG 1226
Db 1098 GCTGGCCAGCGAGTGTTCCTTAAAGAGCTGGTGTCTCATCTCAATGAGCTCTTTGGCAA 1157
QY 1227 GTTTGACAAGCTGGCTGCGGAGAAATCACTCCCTGAGAGATCAAGATCTTTGGGAGCTGTTA 1286
Db 1158 GTTCGACCAAGATTGCCAAGAGCATGAATGCATGCGGATCAAGATCTTGGGGGACTGTTA 1217
QY 1287 CTACTGTGTGAGGCTGCGGAGGCGCGGACCATGCCCCACTGCTGTGTGGAGAT 1346
Db 1218 CTACTGTGTCTGTGGCTGCGCACTCTCACTGCCAGACCATGSCCATCAACTGCGCTGCGCAT 1277
QY 1347 GGGGTGAGACATGATTGAGGCCCATCTCGCTGTGTGCTGAGGTGACAGGTGTGAATGTGAA 1406
Db 1278 GGGCTGGACATGTGCGGGGCCATCAGGAACCTGCGGGGAGCCACTGCGCTGGACATCAA 1337

Qy	2484	CTTCTG	CACATCAG	CAGCATCG	GAGAGTTG	CCCATGATCTT	TGTTGGGCTCATCTA	2544
Db	2415	CTGCTG	CACGCTGG	GGCTTCTCT	CTCTGCTCC	CTTTCTGC	CACATGAGCTTCG	2474
Qy	2544	TTTGGT	GCTGCTTCT	GCTGGGTC	CCCCAGC	CGCCATCTTT	GACAACATATGACCT	2603
Db	2475	GC	TGCTGCTCT	GCTTGCTGG	CGCATCTT	CTCTTCT	CTGCACTTCCCATGC	2534
Qy	2604	TGGG	GTCCATGG	CTTGGCTTCT	TCCAAATG	AGACCTTTGAT	GGGCTGAGCTTCC	2663
Db	2535	CTG	CTGCGGAATG	CTCATGCT	CGCCTCTATCT	CTGGGCCCTT	GGACTCCAGGCCCGG	2594
Qy	2664	AGG	AGGGTGGCC	CTCAAA	TATATGAC	CCCTGATTTCT	GCTGTTGGCTGGCGCT	2723
Db	2595	AGT	GTGAAGG	CGCCAACTGAT	GGTGCTATCT	CTTCTTCT	CTTCTTCTTACCCCT	2654
Qy	2724	GTAT	GTGCATGCT	CAGCAGT	GGAATCG	ACTGCCCGCTAA	ACTTCTCTGGAAC	2783
Db	2655	CC	TTGCTTGCT	CGCCAG	AATGAGT	ACTTCTGCGCCT	TGGACTTCTGTGGAAGA	2714
Qy	2784	GGCA	CAGGGGAA	AGAGAGAT	GGAGAGCT	TACAGGCTAT	CAACCGGAGGCTG	2843
Db	2715	GCT	GAGCAGG	AGGAGGAG	CACAGACAG	ATGGAGA	ACCTGACTCGGCT	2774
Qy	2844	TAAC	ATTCTGCC	CAAGGAGCT	GGGCGCC	CACCTTCTG	CGCGGAGCGCC	2903
Db	2775	GAC	GTGCTCCCT	GTGCAC	AGTGGCCCC	CAGTTCA	TGGCCAAACCGGCC	2834
Qy	2904	ACT	TACTAT	CAGTCTG	TGAGTGTG	GTGCTTATG	TTTGCTTCCAT	2963
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Qy	2964	TGAG	TTCTATG	TGAGCTGG	AGCACA	CAATGAGGGT	GCCGAGTCC	3023
Db	2895	GG	AGTTCTACT	CTGAA	TCCAACAT	CAATCAGG	CGCTTAGAGTGTCT	2954
Qy	3024	CG	AGATCAT	CGCTGACT	TTTGATG	AGATTATCAG	CAGGAGCGTTC	3083
Db	2955	TG	AGATAAT	TGCTGATTT	GATGAGCT	GTCTTCCA	AGCCCAAGTTCAGT	3014
Qy	3084	GAT	CAAGAC	GATTTGGT	TAGCACTTAC	ATGCTGCCT	CAGGGTGAAC	3137
Db	3015	GAT	CAAG	CACTCGG	CAGCACCTTAC	ATGCGCCAC	AGGCTTAAATG	3074
Qy	3138	-----	CTAG	CATCAG	TGAGTGGG	CGCTCC	CACATCACTG	3185
Db	3075	GG	ATGCA	CAACAG	GATGTCT	GACCGAGCT	TGCAGCCACCTT	3134
Qy	3186	CAT	CGGCTCAT	TGGCAG	ATGAAG	CACATCAAT	CAGCAGCTCTT	3245
Db	3135	CGT	GGCCCTGG	GTCTA	AGCTGG	AGCTCAT	CAACAGCATTC	3194
Qy	3246	GA	AGATTGG	CTGAAC	ATGGGCC	AGTCGTG	GCAGGTGT	3305
Db	3195	GCG	AGTGGG	TTTGA	CCATGG	ACCCCTAGT	AGCTGGAGTT	3254
Qy	3306	GT	ATGACAT	CTGGG	GAACAC	AGTGAATGTCT	TCTAGTATG	3365

; Sequence 332, Application
; Patent No. US20020081659A1

GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 352
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2520)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2572)
; OTHER INFORMATION: n equals a,t,g, or c

US-09-925-297-352

Query Match 11.2%; Score 395.8; DB 10; Length 2601;
Best Local Similarity 51.1%; Pred. No. 4.5e-88;
Matches 1301; Conservative 1; Mismatches 1143; Indels 100; Gaps 12;

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DB 34 AACAGCCGCAAGCACCGAAGACCTTCTCGAGCGCCGCGAGCTGGAGGTGAAGAT 93
QY 987 CCACCTCGAGCATGAGAAATCGGCAGCAGGAGCGCTGTGTCTGGTATTGCCCCAGCA 1046
DB 94 GAACCTGGAAGCAGAGCAGCCAGCAGGAGAACCTCATGCTTCCATCTGCCCCAAGCA 153
QY 1047 CGTTGCCATGAGATGAAGAAGACATCAACACA-----AAAAAAGACAT 1094
DB 154 CGTGGCTGACGAGATGCTGAAGAAGACATGAAGAAAGCAGAGCCAGAGACCGAGCA 213
QY 1095 GTTCCACAAGATACATACAGAAAGATGACAATGTTCAGCATCTGTTTTCAGACATTTGA 1154
DB 214 GTTCAACACCATGTACATGTACCTGACGAGAGCTGACATCTCTTTGCGGACATCGT 273
QY 1155 GGGCTTACCAGCTGGCATCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1214
DB 274 GGGCTTTACCAGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 333
QY 1215 GCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAAATCACTGCTGAGGATCAAGATCTT 1274
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: Patent No. US20020103147A1
: GENERAL INFORMATION:
: APPLICANT: Hammon, H. K.
: APPLICANT: Insel, P. A.
: APPLICANT: Ping, P.
: APPLICANT: Post, S. R.
: APPLICANT: Gao, M.
: TITLE OF INVENTION: GENE THERAPY FOR CONG
: TITLE OF INVENTION: FAILURE
: FILE REFERENCE: 220002056723
: CURRENT APPLICATION NUMBER: US/09/750,240
: CURRENT FILING DATE: 2001-10-12
: PRIOR APPLICATION NUMBER: US 09/472,667
: PRIOR FILING DATE: 1999-12-27

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; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 314
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(314)
; OTHER INFORMATION: n = A,T,C or G
US-09-750-240-1

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Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0

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RESULT 13
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; Sequence 11, Application US/09915582
; Patent No. US20020120103A1
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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: I7 Human Secreted Proteins
; FILE REFERENCE: PS723P1
; CURRENT APPLICATION NUMBER: US/09/915,582
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
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; NUMBER OF SEQ ID NOS: 97
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; LENGTH: 1180
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; ORGANISM: Homo sapiens

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; Patent No. US20020132753A1
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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
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GenCore version 5.1.3
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5	3478.4	98.0	4942	42	US-10-201-000-1	Sequence 1, Appli
6	3379.2	95.2	3582	29	US-09-750-240-12	Sequence 12, Appl
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Qy 1201 ATGACCTGTAATGAGCTCTTTGCCCCTGTTGACAAGCTGGCTGGGAGAAATCACTGGCTG 1260
Db 1201 ATGACCTGTAATGAGCTCTTTGCCCCTGTTGACAAGCTGGCTGGGAGAAATCACTGGCTG 1260
Qy 1261 AGGATCAAGATCTTGGGGAGCTGTTACTACTGTGTGTCAGGGCTGCCGAGGCCCGGGCC 1320
Db 1261 AGGATCAAGATCTTGGGGAGCTGTTACTACTGTGTGTCAGGGCTGCCGAGGCCCGGGCC 1320
Qy 1321 GACCATGCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGGCATCTCGCTGGTA 1380
Db 1321 GACCATGCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGGCATCTCGCTGGTA 1380
Qy 1381 CGTAGGTGACAGGTGTAATGTGAACATGCGCGTGGGCATCCACAGGGCGCGTGCAC 1440
Db 1381 CGTAGGTGACAGGTGTAATGTGAACATGCGCGTGGGCATCCACAGGGCGCGTGCAC 1440
Qy 1441 TGGCGCTGCTTGGCTTGGCGAAATGCGAGTTCGATGTGTCGCAATGATGTGACCCCTG 1500
Db 1441 TGGCGCTGCTTGGCTTGGCGAAATGCGAGTTCGATGTGTCGCAATGATGTGACCCCTG 1500
Qy 1501 GCCAACACATGGAAGCAGGAGCGGGCTGGCGGCATCCACATCACTCGGGCAACACTG 1560
Db 1501 GCCAACACATGGAAGCAGGAGCGGGCTGGCGGCATCCACATCACTCGGGCAACACTG 1560
Qy 1561 CAGTACCTGAAGGGGACTAGAGTGGAGCCAGCGCTGGTGGCAAGCGCAACGCTGAC 1620
Db 1561 CAGTACCTGAAGGGGACTAGAGTGGAGCCAGCGCTGGTGGCAAGCGCAACGCTGAC 1620
Qy 1621 CTCAGGAGCAGCATTGACATTTCTCATCTCTGGCGGCAGCAGAAACGGAAGAG 1680
Db 1621 CTCAGGAGCAGCATTGACATTTCTCATCTCTGGCGGCAGCAGAAACGGAAGAG 1680
Qy 1681 GAGAAAGCATGTGCGCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTGATG 1740
Db 1681 GAGAAAGCATGTGCGCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTGATG 1740
Qy 1741 CCGGATGGGTTCCTGATGCTGCTTCTCCGGACCAAGGACTCCAAGGCCCTCCGCCAG 1800
Db 1741 CCGGATGGGTTCCTGATGCTGCTTCTCCGGACCAAGGACTCCAAGGCCCTCCGCCAG 1800
Qy 1801 ATGGGCATTGATGATTCAGCAAGACAACCGGGGCACCCCAAGATGCCCTGAACCCCTGAG 1860
Db 1801 ATGGGCATTGATGATTCAGCAAGACAACCGGGGCACCCCAAGATGCCCTGAACCCCTGAG 1860
Qy 1861 GATGAGGTGATGATGCTGAGCGCTGCCATGCGATGCCCGCAGCATGATGATGATGCGG 1920
Db 1861 GATGAGGTGATGATGCTGAGCGCTGCCATGCGATGCCCGCAGCATGATGATGATGCGG 1920
Qy 1921 AAGGACCATGTGCGCGGTTTTGCTCACCTTCCAGAGAGGATTTTGAGAAAGATAC 1980
Db 1921 AAGGACCATGTGCGCGGTTTTGCTCACCTTCCAGAGAGGATTTTGAGAAAGATAC 1980
Qy 1981 TCCCGAAGGTGGATGCCCGCTTCGGAGCCTACGTTGCTGCGCTGTTGGCTTCTGCG 2040
Db 1981 TCCCGAAGGTGGATGCCCGCTTCGGAGCCTACGTTGCTGCGCTGTTGGCTTCTGCG 2040
Qy 2041 TTCATGCTTTCATCCAGCTTCTAATTTTCCACACTCCACCCCTGATGCTTGGATTTAT 2100
Db 2041 TTCATGCTTTCATCCAGCTTCTAATTTTCCACACTCCACCCCTGATGCTTGGATTTAT 2100
Qy 2101 GCCAGCATCTTCCTGCTGCTTAATCACCGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTG 2160
|||||

Db 2101 GCCAGCATCTTCCTGCTGCTTAATCACCGTGTGATCTGTGCTGTGCTGCTGCTGCTG 2160
Qy 2161 TCTCTGTTCCCTAAGGCCTGCAAGCTGTCGCCGACATGTTCCGCTCAGGGCACAT 2220
Db 2161 TCTCTGTTCCCTAAGGCCTGCAAGCTGTCGCCGACATGTTCCGCTCAGGGCACAT 2220
Qy 2221 AGCACCGAGTTGGCATCTTTTCCGCTCCTGCTGTGTTTACTTCTGCTGCTGCTGCTGCTG 2280
Db 2221 AGCACCGAGTTGGCATCTTTTCCGCTCCTGCTGTGTTTACTTCTGCTGCTGCTGCTGCTG 2280
Qy 2281 TTCACCTGTAACACACACCCCATACGGAGCTGTGAGCCCGGATGCTGAATTTAACACCT 2340
Db 2281 TTCACCTGTAACACACACCCCATACGGAGCTGTGAGCCCGGATGCTGAATTTAACACCT 2340
Qy 2341 GCTGACATCACTGCTGCCACCTGCAGCAGCTCAATTAATCTCTGCGGCTGATGCTGCC 2400
Db 2341 GCTGACATCACTGCTGCCACCTGCAGCAGCTCAATTAATCTCTGCGGCTGATGCTGCC 2400
Qy 2401 CTGTGTGAGGACACATGCCACCTGACAGTTTCTGAGGTGTCCATCGGGAACATGCTG 2460
Db 2401 CTGTGTGAGGACACATGCCACCTGACAGTTTCTGAGGTGTCCATCGGGAACATGCTG 2460
Qy 2461 CTGAGTCTCTTGGCAGCTGCTTCTGACATCAGCAGCATCGGGAAGTTGGCCATG 2520
Db 2461 CTGAGTCTCTTGGCAGCTGCTTCTGACATCAGCAGCATCGGGAAGTTGGCCATG 2520
Qy 2521 ATCTTTGTTGGGCTCATCTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
Db 2521 ATCTTTGTTGGGCTCATCTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
Qy 2581 TTTGACAACTATGACCTACTGCTTGGCTCCATGGCTTGGCTTCTTCCAATGAGACCTTT 2640
Db 2581 TTTGACAACTATGACCTACTGCTTGGCTCCATGGCTTGGCTTCTTCCAATGAGACCTTT 2640
Qy 2641 GATGGCTGGACTGTCAGCTGTCAGGAGGCTGGCCCTCAAAATATATGACCCCTGTGAT 2700
Db 2641 GATGGCTGGACTGTCAGCTGTCAGGAGGCTGGCCCTCAAAATATATGACCCCTGTGAT 2700
Qy 2701 CTGCTGTTGTTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
Db 2701 CTGCTGTTGTTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
Qy 2761 CTAACATTCCTCTGAAACTACAGCAACAGGGGAAAAGAGGAGTGGAGGCTACAG 2820
Db 2761 CTAACATTCCTCTGAAACTACAGCAACAGGGGAAAAGAGGAGTGGAGGCTACAG 2820
Qy 2821 GCATACACCGAGGCTGCTGCATAAATCTGCCCCAAGGAGTGGCGGCCCTTCCCTG 2880
Db 2821 GCATACACCGAGGCTGCTGCATAAATCTGCCCCAAGGAGTGGCGGCCCTTCCCTG 2880
Qy 2881 GCCGGGAGCGCCCAATGATGAATCTTACTATCAGTCTGCTGAGTGTGCTGCTGCTGCTGCTG 2940
Db 2881 GCCGGGAGCGCCCAATGATGAATCTTACTATCAGTCTGCTGAGTGTGCTGCTGCTGCTGCTG 2940
Qy 2941 TTTGCTCCATGGCACTTCTGAGTTCTATGAGCTGAGCTGGAGGCAACAAATGAGGT 3000
Db 2941 TTTGCTCCATGGCACTTCTGAGTTCTATGAGTGTGAGTGGAGGCAACAAATGAGGT 3000
Qy 3001 GCCGAGTGCCTGCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGCCAG 3060
Db 3001 GCCGAGTGCCTGCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGCCAG 3060
Qy 3061 GAGCGTTTCCGGCAGCTGGAAGATCAAGAGTGTGCTAGCACCCTACATGCTGCTGCTGCTGCTG 3120
Db 3061 GAGCGTTTCCGGCAGCTGGAAGATCAAGAGTGTGCTAGCACCCTACATGCTGCTGCTGCTGCTG 3120
Qy 3121 GGGCTGAAGCGCAGCACCCTAGATCAGTGGGCGCTGCCACATGCTGCTGCTGCTGCTGCTGCTG 3180
Db 3121 GGGCTGAAGCGCAGCACCCTAGATCAGTGGGCGCTGCCACATGCTGCTGCTGCTGCTGCTGCTG 3180
Qy 3181 TACGCCATGCGGCTCATGGAGCAGATGAAGCAGATCAATGAGCAGCTCTTCAACAATTTTC 3240
Db 3181 TACGCCATGCGGCTCATGGAGCAGATGAAGCAGATCAATGAGCAGCTCTTCAACAATTTTC 3240

QY 3241 CAGATGAAGATTGGGCTGAACATGGGCCAGTGGTGCAGGTGTATCGGGGTCGGAAG 3300
Db 3241 CAGATGAAGATTGGGCTGAACATGGGCCAGTGGTGCAGGTGTATCGGGGTCGGAAG 3300
QY 3301 CCACAGTATGACATCTCGGGGGAACACAGTGAATGTCTCTAGTGTGAGACAGACGGG 3360
Db 3301 CCACAGTATGACATCTCGGGGGAACACAGTGAATGTCTCTAGTGTGAGACAGACGGG 3360
QY 3361 GTCCCCGACCGAATCCAGGTGACACAGGACTGTACAGGTCTTAGCTGCCAAGGGCTAC 3420
Db 3361 GTCCCCGACCGAATCCAGGTGACACAGGACTGTACAGGTCTTAGCTGCCAAGGGCTAC 3420
QY 3421 CAGCTGGAGTGTCCAGGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACACCTACTTC 3480
Db 3421 CAGCTGGAGTGTCCAGGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACACCTACTTC 3480
QY 3481 CTCAATGGGGCCCCCAGCAGTTAAACAGGGCCAGCCACAAATTCAGCTGAAGGGACCAAG 3540
Db 3481 CTCAATGGGGCCCCCAGCAGTTAAACAGGGCCAGCCACAAATTCAGCTGAAGGGACCAAG 3540
QY 3541 GTGGGCACT 3549
Db 3541 GTGGGCACT 3549

RESULT 2
US-09-750-240-5
; Sequence 5, Application US/09750240
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE REFERENCE: 220002036723
; CURRENT APPLICATION NUMBER: US/09750, 240
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-240-5

Query Match 100.0%; Score 3549; DB 29; Length 3549;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTATAGTGCCTCTGGTCCCTAAAGTGGATGAACGGAACAGCCTGGGGT 60
Db 1 ATGTCATGTTTATAGTGCCTCTGGTCCCTAAAGTGGATGAACGGAACAGCCTGGGGT 60
QY 61 GAACGCAATGGGAGACAGCTTCGGGCGCGGTGGCACTCGGCGAGGTGGCTTCTGCACG 120
Db 61 GAACGCAATGGGAGACAGCTTCGGGCGCGGTGGCACTCGGCGAGGTGGCTTCTGCACG 120
QY 121 CCCGCTATATAGTGCCTCTCGGGATGACAGCCAGCCACCCCTGCGGGGCC 180
pb 121 CCCGCTATATAGTGCCTCTCGGGATGACAGCCAGCCACCCCTGCGGGGCC 180

QY 181 CCTCGTGCCTCGGAGGATGAGCCTTCATCCGAGGGCGGCCAGGCAAG 240
Db 181 CCTCGTGCCTCGGAGGATGAGCCTTCATCCGAGGGCGGCCAGGCAAG 240
QY 241 GAGCTGGGGTGGGGAGTGGCCCTCGAGGATACCGAGGTGACAAACACAGCG 300
Db 241 GAGCTGGGGTGGGGAGTGGCCCTCGAGGATACCGAGGTGACAAACACAGCG 300
QY 301 GGGGGAGCGCTGAGGTGGCGCGCGAGCGTGGCCAGGAGTGGCGCATCTCGTGGCGC 360
Db 301 GGGGGAGCGCTGAGGTGGCGCGCGAGCGTGGCCAGGAGTGGCGCATCTCGTGGCGC 360
QY 361 CGTTTGTGTCAGGTGTTCCAGTGCAGACAGTTCGGTTCGGCCAAAGCTGGAGCGCTGTAC 420
Db 361 CGTTTGTGTCAGGTGTTCCAGTGCAGACAGTTCGGTTCGGCCAAAGCTGGAGCGCTGTAC 420
QY 421 CAGGGTACTTTTTCCAGATGAACAGAGAGCGCTGAGCGTGTGGTGGCGTCTGGTG 480
Db 421 CAGGGTACTTTTTCCAGATGAACAGAGAGCGCTGAGCGTGTGGTGGCGTCTGGTG 480
QY 481 CTGCTACAGCGGTGTGCTGGCTTTCCAAAGCCGACCCCGCCCTCAGCCCTGCCAT 540
Db 481 CTGCTACAGCGGTGTGCTGGCTTTCCAAAGCCGACCCCGCCCTCAGCCCTGCCAT 540
QY 541 GTGGCACTGTTGGCCTGTGCGCGCCCTGTTCGTGGGGCTCATGTGTGTGTAAACCGG 600
Db 541 GTGGCACTGTTGGCCTGTGCGCGCCCTGTTCGTGGGGCTCATGTGTGTGTAAACCGG 600
QY 601 CATAGTTCGCCAGGACTCCATGTGGGTGTGAGTAACTGGTGTGGGCATCTGGCG 660
Db 601 CATAGTTCGCCAGGACTCCATGTGGGTGTGAGTAACTGGTGTGGGCATCTGGCG 660
QY 661 GCAGTGCAGGTGCGGGCGCTTTGCGAGAGACCCGCGAGCCCTCTCGGGGCTCTGG 720
Db 661 GCAGTGCAGGTGCGGGCGCTTTGCGAGAGACCCGCGAGCCCTCTCGGGGCTCTGG 720
QY 721 TGCCCTGTGTTTGTATACATCGCATACAGCGTCTCCCATCCCGCATCGGGCTGCC 780
Db 721 TGCCCTGTGTTTGTATACATCGCATACAGCGTCTCCCATCCCGCATCGGGCTGCC 780
QY 781 GTCTCAGCGGCTGGGCGCTCCACCTTCGATTTGATTTGGCTGGCAACTTAAACCGT 840
Db 781 GTCTCAGCGGCTGGGCGCTCCACCTTCGATTTGATTTGGCTGGCAACTTAAACCGT 840
QY 841 GGTGATGCTTCTCTGGAAGAGAGCTCGGTGCCAATGTGTGTCTCTGCGGCTGCC 900
Db 841 GGTGATGCTTCTCTGGAAGAGAGCTCGGTGCCAATGTGTGTCTCTGCGGCTGCC 900
QY 901 GTCAATTAGCATCTGCACACACTATCCAGAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 960
Db 901 GTCAATTAGCATCTGCACACACTATCCAGAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 960
QY 961 ACCCGCAGTTACATCCAGGCGCGCTCCACCTGCAGATGAGATCGGAGAGGAGCGG 1020
Db 961 ACCCGCAGTTACATCCAGGCGCGCTCCACCTGCAGATGAGATCGGAGAGGAGCGG 1020
QY 1021 CTGCTGTGTCGGTATTGCCCCAGCAGCTGGCCATGAGATGAAAGAGACATCAACACA 1080
Db 1021 CTGCTGTGTCGGTATTGCCCCAGCAGCTGGCCATGAGATGAAAGAGACATCAACACA 1080
QY 1081 AAAAAAGACATGTTTCCACAAGATCTACATACAGAGCATGACAAATGTACAGATCCTG 1140
Db 1081 AAAAAAGACATGTTTCCACAAGATCTACATACAGAGCATGACAAATGTACAGATCCTG 1140
QY 1141 TTTTCAGACATTTGAGGCTTACCAGCCTGGCATCCAGTGCACCTGGCAGGAGCTGTC 1200
Db 1141 TTTTCAGACATTTGAGGCTTACCAGCCTGGCATCCAGTGCACCTGGCAGGAGCTGTC 1200
QY 1201 ATCACCCTGAATGAGCTCTTTGCGCGGTTTGAAGCTGGCTGCGGAGATCACTGCTG 1260
Db 1201 ATCACCCTGAATGAGCTCTTTGCGCGGTTTGAAGCTGGCTGCGGAGATCACTGCTG 1260

Db	3421	CAGCTGAGCTGTGAGGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACCACCTACTTTC	3480
Qy	3481	CTCAATGGGGCCCCCAGCAGCTTAACAGGGCCCCAGCCACAAATTCAGCTGAAAGGACCAAG	3540
Db	3481	CTCAATGGGGCCCCCAGCAGCTTAACAGGGCCCCAGCCACAAATTCAGCTGAAAGGACCAAG	3540
Qy	3541	GTGGGCACCT 3549	
Db	3541	GTGGGCACCT 3549	
RESULT 3			
US-09-472-667-10			
: Sequence 10, Application US/09472667			
: GENERAL INFORMATION:			
: APPLICANT: Hammond, H. Kirk			
: APPLICANT: Insel, Paul A.			
: APPLICANT: Ping, Peipel			
: APPLICANT: Post, Steven R.			
: APPLICANT: Gao, Meihua			
: TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART			
: FILE REFERENCE: 220002056722			
: CURRENT APPLICATION NUMBER: US/09/472,667			
: PRIOR FILING DATE: 1999-12-27			
: PRIOR APPLICATION NUMBER: PCT/US99/02702			
: PRIOR FILING DATE: 1999-02-09			
: PRIOR APPLICATION NUMBER: US 09/008,097			
: PRIOR FILING DATE: 1998-01-16			
: PRIOR APPLICATION NUMBER: US 09/021,773			
: PRIOR FILING DATE: 1998-02-11			
: PRIOR APPLICATION NUMBER: US 08/924,757			
: PRIOR FILING DATE: 1997-09-05			
: PRIOR APPLICATION NUMBER: PCT/US97/15610			
: PRIOR FILING DATE: 1997-09-05			
: PRIOR APPLICATION NUMBER: US 08/708,661			
: PRIOR FILING DATE: 1996-09-05			
: PRIOR APPLICATION NUMBER: US 60/048,933			
: PRIOR FILING DATE: 1997-06-16			
: PRIOR APPLICATION NUMBER: 60/058,209			
: PRIOR FILING DATE: 1996-09-05			
: PRIOR APPLICATION NUMBER: PCT/US96/02631			
: PRIOR FILING DATE: 1996-02-27			
: PRIOR APPLICATION NUMBER: US 08/396,207			
: PRIOR FILING DATE: 1995-02-28			
: PRIOR APPLICATION NUMBER: US 08/485,472			
: PRIOR FILING DATE: 1995-06-07			
: NUMBER OF SEQ ID NOS: 11			
: SOFTWARE: FastSeq for Windows Version 4.0			
: SEQ ID NO 10			
: LENGTH: 3552			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
US-09-472-667-10			
Query Match 98.2%; Score 3484.8; DB 18; Length 3552;			
Best Local Similarity 99.0%; Pred. No. 0;			
Matches 3517; Conservative 0; Mismatches 37; Indels 3; Gaps			
Qy	1	ATGTCATGTTTATAGTGCCTCTGTGTCCTTAAGTGGATGAACGGAAAAACAGCCTGGGGT 60	
Db	1	ATGTCATGTTTATAGTGCCTCTGTGTCCTTAAGTGGATGAACGGAAAAACAGCCTGGGGT 60	
Qy	61	GAAGCGAATGGCGAGAGCGTTTCGGCGCCCTGGCACTCGGGCAGGTGGCTTCTGCACG 120	
Db	61	GAAGCGAATGGCGAGAGCGTTTCGGCGCCCTGGCACTCGGGCAGGTGGCTTCTGCACG 120	
Qy	121	CCCCGCTATATGAGCTCCCTCCGGGATGCAGAGCCACCCAGCCCTCGCGGGCCCC 180	
Db	121	CCCCGCTATATGAGCTCCCTCCGGGATGCAGAGCCACCCAGCCCTCGCGGGCCCC 180	
Qy	181	CCTCGGTGCCCTTGGCAGGATGACGCTTTCATCCGAGGGCGGCCAGCAAGGCAAG 240	

QY 1318 GCCGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGGTG 1377
DB 1321 GCCGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGGTG 1380
QY 1378 GTAGCTGAGGTGACAGGTGTGAATGTGAACATGCGGTGGGCATCCACAGGGCGGGT 1437
DB 1381 GTAGCTGAGGTGACAGGTGTGAATGTGAACATGCGGTGGGCATCCACAGGGCGGGT 1440
QY 1438 CACTGCGGCGCTTGGCTTCCGGAATGGCAGTTCCGATGTGTGTCCTCAATGATGTACC 1497
DB 1441 CACTGCGGCGCTTGGCTTCCGGAATGGCAGTTCCGATGTGTGTCCTCAATGATGTACC 1500
QY 1498 CTGGCCAAACACATGGAAGAGAGCGGCTGGCGCATCCACATCACTCTGGGCAACA 1557
DB 1501 CTGGCCAAACACATGGAAGAGAGCGGCTGGCGCATCCACATCACTCTGGGCAACA 1560
QY 1558 CTGAGTACCTGAAGCGGACTACGAAGTGGAGCGAGCCGTGTGGCAAGCGG 1617
DB 1561 CTGAGTACCTGAAGCGGACTACGAAGTGGAGCGAGCCGTGTGGCAAGCGG 1620
QY 1618 TACCTCAAGGAGCAGCATTGAGACTTTCCTCATCTCTGGGCGCAGCCAGAAACGGA 1677
DB 1621 TACCTCAAGGAGCAGCATTGAGACTTTCCTCATCTCTGGGCGCAGCCAGAAACGGA 1680
QY 1678 GAGGAGAAAGGCATGCTGGCCAAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGGTG 1737
DB 1681 GAGGAGAAAGGCATGCTGGCCAAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGGTG 1740
QY 1738 ATGGCGGATGGTTCCTGATGTCGCTTTCCTCGGAGCAAGGACTCCAGGCGCTTCGCG 1797
DB 1741 ATGGCGGCTGGGTTCCTGATGTCGCTTTCCTCGGAGCAAGGACTCCAGGCGCTTCGCG 1800
QY 1798 CAGATGGCATTGATGATTTCAGCAAAAGACAAACCGGGGCAAGGATGCCCTGAACCT 1857
DB 1801 CAGATGGCATTGATGATTTCAGCAAAAGACAAACCGGGGCAAGGATGCCCTGAACCT 1860
QY 1858 GAGGATGAGGTGATGATTTCCTGAGCGGTGCCATGATGCGCCAGCAGCATGATCAGGTG 1917
DB 1861 GAGGATGAGGTGATGATTTCCTGAGCGGTGCCATGATGCGCCAGCAGCATGATCAGGTG 1920
QY 1918 CGGAGGACCATGTGCGCGGCTTTTCTCACCCTCCAGAGAGGATTTTGAGAGAG 1977
DB 1921 CGGAGGACCATGTGCGCGGCTTTTCTCACCCTCCAGAGAGGATTTTGAGAGAG 1980
QY 1978 TACTCCCGGAAGGTGGATCCCGGCTTCGGAGCCTACGTTGCTGTGCGCTGTGGCTTC 2037
DB 1981 TACTCCCGGAAGGTGGATCCCGGCTTCGGAGCCTACGTTGCTGTGCGCTGTGGCTTC 2040
QY 2038 TGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCCTGATGCTGGGAT 2097
DB 2041 TGCTTCATCTGCTTCATCCAGCTTCTCATTCTCCACACTCCACCCTGATGCTGGGATC 2100
QY 2098 TATGCCAGCATCTTCTGCTGCTAATACCGTGTGATGCTGTGCTGTGCTACTCTCTGT 2157
DB 2101 TATGCCAGCATCTTCTGCTGCTAATACCGTGTGATGCTGTGCTGTGCTACTCTCTGT 2160
QY 2158 GGTTCCTGTTCCCTTAAGGCGCTGCAAGCTGTGTCGCCAGCAGCATGTCGCTCAGGSCA 2217
DB 2161 GGTTCCTGTTCCCTTAAGGCGCTGCAAGCTGTGTCGCCAGCAGCATGTCGCTCAGGSCA 2220
QY 2218 CATAGCAGGATGGGATCTTTTCCGCTCTGCTGTGTTTACTTCTGTCATTTGCCAAC 2277
DB 2221 CATAGCAGGATGGGATCTTTTCCGCTCTGCTGTGTTTACTTCTGTCATTTGCCAAC 2280
QY 2278 ATGTTTCACTGTAAACACACCCCATACGGAGCTGTGAGCGCCGATGCTGAATTAACA 2337
DB 2281 ATGTTTCACTGTAAACACACCCCATACGGAGCTGTGAGCGCCGATGCTGAATTAACA 2340
QY 2338 CTTGCTGACATCACTGCTGCACCTGTCAGGAGCTCAATTAATCTCTGCTGGGCTGGATGCT 2397
DB 2341 CTTGCTGACATCACTGCTGCACCTGTCAGGAGCTCAATTAATCTCTGCTGGGCTGGATGCT 2400

QY 2398 CCCCTGTGTGAGGACACATGCCACCTGCACTTTCCTGAGGTGCTCCATCGGGAACATG 2457
DB 2401 CCCCTGTGTGAGGACACATGCCACCTGCACTTTCCTGAGTACTTCAATCGGGAACATG 2460
QY 2458 CTGCTGAGTCTTCTTGGCAGCTGTCTTCTGACATCAAGCAGATCGGGAAGTTGGCC 2517
DB 2461 CTGCTGAGTCTTCTTGGCAGCTGTCTTCTGACATCAAGCAGATCGGGAAGTTGGCC 2520
QY 2518 ATGATCTTTTGTCTTGGGCTCATCTATTGTGTGCTGTCTGCTGGGTGCCCCAGCGCC 2577
DB 2521 ATGATCTTTTGTCTTGGGCTCATCTATTGTGTGCTGTCTGCTGGGTGCCCCAGCGCC 2580
QY 2578 ATCTTTGACAACTATGACCTACTCTTGGCGTCCATGGCTTTGGCTTCTTCCAATGAGACC 2637
DB 2581 ATCTTTGACAACTATGACCTACTCTTGGCGTCCATGGCTTTGGCTTCTTCCAATGAGACC 2640
QY 2638 TTTGATGGGCTGGACTTCCAGCTGCAAGGAGGGTGGCCCTCAAAATATATGACCCCTGTG 2697
DB 2641 TTTGATGGGCTGGACTTCCAGCTGCAAGGAGGGTGGCCCTCAAAATATATGACCCCTGTG 2700
QY 2698 ATTCTGTGTGTGTGTGGCTGGCGCTGTATCTGATGCTCAGCAGGTGGAATTCAGCTGCC 2757
DB 2701 ATTCTGTGTGTGTGTGGCTGGCGCTGTATCTGATGCTCAGCAGGTGGAATTCAGCTGCC 2760
QY 2758 GCGCTAAACTTCTCTGAAACTACAGCAACAGGGGAAAAGAGAGATGGAGAGCTA 2817
DB 2761 GCGCTAGACTTCTCTGAAACTACAGCAACAGGGGAAAAGAGAGATGGAGAGCTA 2820
QY 2818 CAGCATACAAACCGAGGCTGCTGCATAACATTTCTGCCAAGGAGCGTGGCGGCCACTTC 2877
DB 2821 CAGCATACAAACCGAGGCTGCTGCATAACATTTCTGCCAAGGAGCGTGGCGGCCACTTC 2880
QY 2878 CTGGCCCGGAGCGCGCAATGATGAATCTACTATCAGTCGTGTGAGTGTGTGGCTGT 2937
DB 2881 CTGGCCCGGAGCGCGCAATGATGAATCTACTATCAGTCGTGTGAGTGTGTGGCTGT 2940
QY 2938 ATGTTTGCCTCCATTTGCCAACTTCTCTGAGTTCTATGAGCTGGAGGCAACAATGAG 2997
DB 2941 ATGTTTGCCTCCATTTGCCAACTTCTCTGAGTTCTATGAGCTGGAGGCAACAATGAG 3000
QY 2998 GGTCCGAGTCCCTCGGCTCTCAAGCAGATCATCGTGTGCTTTGATGAGATTATCAGC 3057
DB 3001 GGTGTGAGTCCCTCGGCTCTCAAGCAGATCATCGTGTGCTTTGATGAGATTATCAGC 3060
QY 3058 GAGGAGCGGTTTCCGCGAGCTGGAAGATCAAGCAGATTGGTAGCCTACATGCTGCC 3117
DB 3061 GAGGAGCGGTTTCCGCGAGCTGGAAGATCAAGCAGATTGGTAGCCTACATGCTGCC 3120
QY 3118 TCAGGGCTGAAGCGCAGGACCTACGATCAGTGGGCGCTCCACATCACTGCTGCCGT 3177
DB 3121 TCAGGGCTGAAGCGCAGGACCTACGATCAGTGGGCGCTCCACATCACTGCTGCCGT 3180
QY 3178 CACTACGCGCATCGGCTCTCAGCAGATGAAGCAGATCAATGAGCCTCTCTCAACAAT 3237
DB 3181 CACTACGCGCATCGGCTCTCAGCAGATGAAGCAGATCAATGAGCCTCTCTCAACAAT 3240
QY 3238 TTCAGATGAAGATTGGGCTGAACATGGGCCAGCTGCTGGCAGGTGTCTATGGGCTCGG 3297
DB 3241 TTCAGATGAAGATTGGGCTGAACATGGGCCAGCTGCTGGCAGGTGTCTATGGGCTCGG 3300
QY 3298 AAGCCACAGTATGACATCTGGGGAGCAACAGTGAATGCTCTAGTCTGTATGACAGCAG 3357
DB 3301 AAGCCACAGTATGACATCTGGGGAGCAACAGTGAATGCTCTAGTCTGTATGACAGCAG 3360
QY 3358 GGGTCCCGCCGCAATCCAGTGAACAGCCTGTACAGGTTCTAGCTGCTCAAGGCG 3417
DB 3361 GGGTCCCGCCGCAATCCAGTGAACAGCCTGTACAGGTTCTAGCTGCTCAAGGCG 3420
QY 3418 TACCAGCTGGAGTGTGAGGGTGTGCAAGGTGAAGGCAAGGGGAGATGACCACTTAC 3477
DB 3421 TACCAGCTGGAGTGTGAGGGTGTGCAAGGTGAAGGCAAGGGGAGATGACCACTTAC 3480
QY 3478 TTTCTCAATGGGGGCCCCCAGCAGATTAAAGGGCCCGAGCCCAAAATTCAGCTGAAGGGACC 3537

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Db 3481 TTCTCTAATGGGGCCCCAGCAGTTAAACAGGGCCCCAGCCACAAATTCAGTGAAGGACC 3540
Qy 3538 AAGTGGGCACT 3549
Db 3541 AAGTGGGCACT 3552

RESULT 4
US-09-750-240-10
: Sequence 10. Application US/09750240
: GENERAL INFORMATION:
: APPLICANT: Hammon, H. K.
: APPLICANT: Insel, P. A.
: APPLICANT: Ping, P.
: APPLICANT: Post, S. R.
: APPLICANT: Gao, M.
: TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
: TITLE OF INVENTION: FAILURE
: FILE REFERENCE: 220002056723
: CURRENT APPLICATION NUMBER: US/09/750,240
: CURRENT FILING DATE: 2001-10-12
: PRIOR APPLICATION NUMBER: US 09/472,667
: PRIOR FILING DATE: 1999-12-27
: PRIOR APPLICATION NUMBER: US 09/008,097
: PRIOR FILING DATE: 1998-01-16
: PRIOR APPLICATION NUMBER: US 08/924,757
: PRIOR FILING DATE: 1997-09-05
: PRIOR APPLICATION NUMBER: US 60/048,933
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: US 08/708,661
: PRIOR FILING DATE: 1996-09-05
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 10
: LENGTH: 3552
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-750-240-10

Query Match 98.2%; Score 3484.8; DB 29; Length 3552;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 3517; Conservative 0; Mismatches 32; Indels 3; Gaps 1;

Qy 1 ATGTCATGTTTATGGCTCCTGGTCCCTAAAGTGATGAACGAAACAGCCTGGGGT 60
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Db 61 GAAGCCAATGGGCAGAGCGTTCCGGCGCCGCTGGCACTCGGGCAGGTGGCTTCGCAG 120
Qy 121 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGGCGGGCCC 180
Db 121 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGGCGGGCCC 180
Qy 181 CCTCGGTGCCCTTGGCAGGATGAGCCCTTCATCCGGAGGGCGGCCAGGCAAGGCAAG 240
Db 181 CCTCGGTGCCCTTGGCAGGATGAGCCCTTCATCCGGAGGGCGGCCAGGCAAGGCAAG 240
Qy 241 GAGCTGGGGCTGGCGGAGTGGCCCTGGGCTTCGAGATACCGAGGTGACAAACAGACAG 300
Db 241 GAGCTGGGGCTGGCGGAGTGGCCCTGGGCTTCGAGATACCGAGGTGACAAACAGACAG 300
Qy 301 GCGGGAGCGGTGAGGTGGCGCCGAGCGGTGCCAGGAGTGGCGCATCCTGCTGCGCG 360
Db 301 GCGGGAGCGGTGAGGTGGCGCCGAGCGGTGCCAGGAGTGGCGCATCCTGCTGCGCG 360
Qy 361 CGTTTGTGACAGTGTTCACGTGAAGCAGTTCGGTTCGGCCCAAGCTGGAGCGCCCTGAC 420
Db 361 CGTCTGTGACAGTGTTCACGTGAAGCAGTTCGGTTCGGCCCAAGCTGGAGCGCCCTGAC 420
Qy 421 CAGCGGTACTTTTCCAGATGAACCAAGCAGCAGCTGACGCTGCTGGTGGCGGTGCTGGTG 480
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Db 421 CAGCGGTACTTTTCCAGATGAACCAAGCAGCAGCTGACGCTGCTGATGGGGTCTGGTG 480
Qy 481 CTGCTCACAGCGGTGCTGGCTTTCCAAAGCCGCGCCCGCCCTCAGCCTGCGCTAT 540
Db 481 CTGCTCACAGCGGTGCTGGCTTTCCAAAGCCGCGCGCCCGCCCTCAGCCTGCGCTAT 540
Qy 541 GTGCACTGTTGGCCTGTGCCCGCCCTGTTCTGTGGGGCTCATGGTGTGTAACCGG 600
Db 541 GTGCACTGTTGGCCTGTGCCCGCCCTGTTCTGTGGGGCTCATGGTGTGTAACCGG 600
Qy 601 CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAAGTAACTGTGGTGGGATCCTGGCG 660
Db 601 CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAAGTAACTGTGGTGGGATCCTGGCG 660
Qy 661 GCAGTGCAGGTTCGGGGCGCTTTCGGCAGCAGACCCGCGCAGCCCTCTGGGGCTCTGG 720
Db 661 GCAGTGCAGGTTCGGGGCGCTTTCGGCAGCAGACCCGCGCAGCCCTCTGGGGCTCTGG 720
Qy 721 TGCCCTGTGTTTGTATACATCGCATACACGCTCTCCCATCCCATCCGATGCGGGCTGCC 780
Db 721 TGCCCTGTGTTTGTATACATCGCATACACGCTCTCCCATCCCATCCGATGCGGGCTGCC 780
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Db 781 GTCTCAGCGGCTGGGGCTCTCCACCTTGATCTTGATCTTGCGCTGGCAACTTAACCGT 840
Qy 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTCTGTGTTCCCTGTCACCAAC 900
Db 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTCTGTGTTCCCTGTCACCAAC 900
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Db 901 GTCAATTAGCATCTGCACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 960
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Qy 1021 CTGCTGCTGCTGGTATTTGCCCGCCAGCAGCTTCCATGCGAGATGAAGAAGACATCAACAC 1080
Db 1021 CTGCTGCTGCTGGTATTTGCCCGCCAGCAGCTTCCATGCGAGATGAAGAAGACATCAACAC 1080
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Db 1081 AAAAAAGAACGACATGATGTTCCACAGATCTACATACAGAGCATGACATGTCAGCATC 1140
Qy 1138 CTGTTTGCACACATTTGAGGGCTTCACAGCCTGCCAGTCCAGTCCAGTCCGAGGAGCTG 1197
Db 1141 CTGTTTGCACACATTTGAGGGCTTCACAGCCTGCCAGTCCAGTCCAGTCCGAGGAGCTG 1200
Qy 1198 GTCATGACCTGAATGAGCTCTTTGCCCGGTTTACAAAGCTGGCTGGGAGATCACTGC 1257
Db 1201 GTCATGACCTGAATGAGCTCTTTGCCCGGTTTACAAAGCTGGCTGGGAGATCACTGC 1260
Qy 1258 CTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTGTGAGGGCTGCCGAGGCGCGG 1317
Db 1261 CTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTGTGAGGGCTGCCGAGGCGCGG 1320
Qy 1318 GCGGACCATCCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCGCTG 1377
Db 1321 GCGGACCATCCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCGCTG 1380
Qy 1378 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGGTGGGCATGCCACAGCGGCGCGGTG 1437
Db 1381 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGGTGGGCATGCCACAGCGGCGCGGTG 1440
Qy 1438 CACTGGGCGCTCCTTGGCTTGGCGAATGTCAGTTCGATGTGTGGTCCAAATGATGTGACC 1497
Db 1441 CACTGGGCGCTCCTTGGCTTGGCGAATGTCAGTTCGATGTGTGGTCCAAATGATGTGACC 1500
Qy 1498 CTGGCCCAACACATGGAAGCAGGAAACCGGGCTGGCGCATCCACATCACTCCGGCAACA 1557
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Db 1501 CTGGCCAAACCACATGGAGGCGAGGCGCGGCTGGCCGATCCACATCACTCGGGCAACA 1560
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Db 1561 CTGCAGTACCTGAACGGGGACTACGAAGTGGAGCGAGCGCGTGGTGGCGAGCGCAACGCG 1620
Qy 1618 TACCTCAAGGAGCAGCACAATTGAGACTTTCCTCATCTCTGGCGCCAGCAGAAACGGA 1677
Db 1621 TACCTCAAGGAGCAGCACAATTGAGACTTTCCTCATCTCTGGCGCCAGCAGAAACGGA 1680
Qy 1678 GAGGAGAAAGGCATGCTGGCCAAAGCTGCAGGCGACTCGGGCCAACTCCATGGAAGGCGTG 1737
Db 1681 GAGGAGAAAGGCATGCTGGCCAAAGCTGCAGGCGACTCGGGCCAACTCCATGGAAGGCGTG 1740
Qy 1738 ATGCCGCGATGGTTCCTGATGCTGCTTCTCCGGGACCAAGGACTCCAAGGCGCTTCGCG 1797
Db 1741 ATGCCGCGCTGGTTCCTGATGCTGCTTCTCCGGGACCAAGGACTCCAAGGCGCTTCGCG 1800
Qy 1798 CAGATGGGCATTTGATGATTCAGCAAAAGACAACCGGGGACCCCAAGATGCCCTGAACCCCT 1857
Db 1801 CAGATGGGCATTTGATGATTCAGCAAAAGACAACCGGGGACCCCAAGATGCCCTGAACCCCT 1860
Qy 1858 CAGATGAGGTGGATGATGCTCAGCGGTGCCATCGATGCCCGCAGCATTTGATCAGCTG 1917
Db 1861 GAGGATGAGGTGGATGATGCTCAGCGGTGCCATCGATGCCCGCAGCATTTGATCAGCTG 1920
Qy 1918 CGGAAGGACCAATGTGGCGCGGTTTTCCTCACCCTTCCAGAGAGAGGATTTTGAAGAAG 1977
Db 1921 CGGAAGGACCAATGTGGCGCGGTTTTCCTCACCCTTCCAGAGAGAGGATTTTGAAGAAG 1980
Qy 1978 TACTCCCGGAAGGTGGATTCGCGGTTCGGAGCCTTACGTTGGCTGTGGCCCTTTGGTCTTC 2037
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Qy 2038 TGCTTCATCTGCTCATCCAGCTCTCAATTTCCACACTCCACCTCGATGCTTGGGATT 2097
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Qy 2098 TATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTGTGATCTGTGCTGTACTCTCTGT 2157
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Qy 2158 GGTTCCTGTTCCCTAAGGCCCTGCAAGCTGTCTCCCGCAGCATTTGCCGTCAGGGGCA 2217
Db 2161 GGTTCCTGTTCCCTAAGGCCCTGCAAGCTGTCTCCCGCAGCATTTGCCGTCAGGGGCA 2220
Qy 2218 CATAGCACCGAGTTGGCATCTTTTCCGCTGCTGCTTGTGTTTACTTCTGCCATTGCCAAC 2277
Db 2221 CATAGCACCGAGTTGGCATCTTTTCCGCTGCTGCTTGTGTTTACTTCTGCCATTGCCAAC 2280
Qy 2278 ATGTTACCTGTAACCAACACCCCATACGGAGCTGTGAGCGCCCGATGCTGAATTTAACA 2337
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Qy 2398 CCCCTGTGTAGGGCACCATGCCACCTGACGCTTTCCTGAGGTGTCCATCGGGAACATG 2457
Db 2401 CCCCTGTGTAGGGCACCATGCCACCTGACGCTTTCCTGAGGTGTCCATCGGGAACATG 2460
Qy 2458 CTGCTGAGTCTCTTGGCGAGCTGTCTTCTTCCATGACATCAGCAGCATCGGGAAGTTGGCC 2517
Db 2461 CTGCTGAGTCTCTTGGCGAGCTGTCTTCTTCCATGACATCAGCAGCATCGGGAAGTTGGCC 2520
Qy 2518 ATGATCTTTTGTCTGGGCTCATCTATTGTTGTTGCTGCTTCTGCTGGGTCCCCAGCGGCC 2577
Db 2521 ATGATCTTTTGTCTGGGCTCATCTATTGTTGTTGCTGCTTCTGCTGGGTCCCCAGCGGCC 2580
Qy 2578 ATCTTTGACAACTATGACCTACTGCTGGCGTCCATGCTTGGCTTCTTCCAAATGAGACC 2637
Db 2581 ATCTTTGACAACTATGACCTACTGCTGGCGTCCATGCTTGGCTTCTTCCAAATGAGACC 2640

Qy 2638 TTTGATGGGCTGGACTGTCCAGCTGCAGGAGGGTGGCCCTCAAAATATATGACCCCTGTG 2697
Db 2641 TTTGATGGGCTGGACTGTCCAGCTGCAGGAGGGTGGCCCTCAAAATATATGACCCCTGTG 2700
Qy 2698 ATTCTGCTGGTGTGTTGGCTGGCGCTGTATCTGATGCTCAGCAGGTGGAATCGACTGCC 2757
Db 2701 ATTCTGCTGGTGTGTTGGCTGGCGCTGTATCTGATGCTCAGCAGGTGGAATCGACTGCC 2760
Qy 2758 CGCCTAACTTCCCTCTCGAAACTACAGCAACAGGGGAAAAGAGGAGATGAGAGGAGCTA 2817
Db 2761 CGCCTAGACTTCCCTCTCGAAACTACAGCAACAGGGGAAAAGAGGAGATGAGAGGAGCTA 2820
Qy 2818 CAGGCATACAAACCGAGGCTGCTGCATAAACAATTCCTGCCCAAGGACGCTGGCGCCCACTTC 2877
Db 2821 CAGGCATACAAACCGAGGCTGCTGCATAAACAATTCCTGCCCAAGGACGCTGGCGCCCACTTC 2880
Qy 2878 CTGCCCGGAGCGCGCAATGATGAACCTCTACTATCAGTCTGTGAGTGTGGCTGTT 2937
Db 2881 CTGCCCGGAGCGCGCAATGATGAACCTCTACTATCAGTCTGTGAGTGTGGCTGTT 2940
Qy 2938 ATGTTTGGCTCCATTGGCAACTTCTCGAGTTCTATGTGGAGCTGGAGGCAACAATGAG 2997
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Qy 3058 GAGAGCGGTTCCGGCAGCTGGAAAAGATCAAGAGATTGGTAGCACCCTACATGGCTGCC 3117
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Qy 3418 TACCAGCTGGAGTCTCGAGGGGTGGTCAAGGTGAAGGCAAGGGGAGATGACCACTTAC 3477
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Qy 3478 TTCCTCAATGGGGGCCCGCAGCAGTTAACAGGCGCCAGCCACAAATTCAGCTGAAGGGACC 3537
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Qy 3538 AAGGTGGCACT 3549
Db 3541 AAGGTGGCACT 3552

RESULT 5

us-10-201-000-1

; Sequence 1, Application US/10201000
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYL

;
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/10/201,000
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US/09/474,076
; PRIOR FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-10-201-000-1

Query Match 98.08; Score 3478.4; DB 42; Length 4942;
Best Local Similarity 98.94; Pred. No. 0;
Matches 3513; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

QY 1 ATGTCATGGTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGGAACAGCCTGGGGT 60
DB 145 ATGTCATGGTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGGAACAGCCTGGGGT 204

QY 61 GAACCAATGGGAGAGCGTTCCGGCGCGCTGGGACTCGGGAGGTGCTTCGACG 120
DB 205 GAACCAATGGGAGAGCGTTCCGGCGCGCTGGGACTCGGGAGGTGCTTCGACG 264

QY 121 CCCGCTATATAGCTCCGCGGATGACAGAGCCAGCCAGCCAGCCCTGGGGCCCC 180
DB 265 CCCGCTATATAGCTCCGCGGATGACAGAGCCAGCCAGCCAGCCCTGGGGCCCC 324

QY 181 CCTCGGTGCCCTGGCAGGATGACGCTTCATCCGGAGGGCGGCCAGGCAAG 240
DB 325 CCTCGGTGCCCTGGCAGGATGACGCTTCATCCGGAGGGCGGCCAGGCAAG 384

QY 241 GAGTGGGGCTGGGGAGGTGGCCCTGGGCTTCAGAGTACCGAGGTGACAAACAGCG 300
DB 385 GAGTGGGGCTGGGGAGGTGGCCCTGGGCTTCAGAGTACCGAGGTGACAAACAGCG 444

QY 301 GCGGGAGCGCTGAGGTGGCGCGGACGCGGTGCCAGGAGTGGCGATCCTGTGCGC 360
DB 445 GCGGGAGCGCTGAGGTGGCGCGGACGCGGTGCCAGGAGTGGCGATCCTGTGCGC 504

QY 361 CGTTTGTGTCAGGTGTTCCAGTGAAGCAGTTCGTTTCGGCCAGCTGGAGCGCTGTAC 420
DB 505 CGTCTGTGTCAGGTGTTCCAGTGAAGCAGTTCGTTTCGGCCAGCTGGAGCACCTGTAC 564

QY 421 CAGCGGTACTTTTCCAGATGAACCAAGAGAGCTGACGCTGTGTGGGGTGGTGGT 480
DB 565 CAGCGGTACTTTTCCAGATGAACCAAGAGAGCTGACGCTGTGTGGGGTGGTGGT 624

QY 481 CTGCTCAGCGGTGCTGCTGGCTTTCAGCCGACCCCGCCCTCAGCCTGCTAT 540
DB 625 CTGCTCAGCGGTGCTGCTGGCTTTCAGCCGACCCCGCCCTCAGCCTGCTAT 684

QY 541 GTGCACTGTTGGCTGTGGCGCGCCCTGCTGTGGGGCTCATGGTGGTGTGTAACCGG 600
DB 685 GTGCACTGTTGGCTGTGGCGCGCCCTGCTGTGGGGCTCATGGTGGTGTGTAACCGG 744

QY 601 CATAGTCCGCCAGGACTCCATGTGGTGTGAGTAACTGAGTGTGGGATCCTGGCG 660
DB 745 CATAGTCCGCCAGGACTCCATGTGGTGTGAGTAACTGAGTGTGGGATCCTGGCG 804

QY 661 GCAGTGGAGTGGGGCTTTCGACGAGAGCCCGAGCCCTCTGGGGCTCTGG 720

DB 805 GCAGTGCAGGTTCGGGGCGCTCTCGCAGCAGACCCGCGAGCCCCCTCTGGGGCCTCTGG 864
QY 721 TGGCCTGTGTTCTTTGTATATACATCGCATACAGCTCCTCCCATCCCATCCGCGCTGCC 780
DB 865 TGGCCTGTGTTCTTTGTATATACATCGCTCTACAGCTCCTCCCATCCCATCCGCGCTGCC 924
QY 781 GTCCATCAGCGGCTGGGCTCTCCACCTTGATTTGATCTTGGCTGGCACTTAACCGT 840
DB 925 GTCCATCAGCGGCTGGGCTCTCCACCTTGATTTGATCTTGGCTGGCACTTAACCGT 984
QY 841 GGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTGTTCCCTCTGACCAAC 900
DB 985 GGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTGTTCCCTCTGACCAAC 1044
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DB 1045 GTCAATTAGCATCTGCACACACTATCCAGCAGAGGTGCTCAGCGCCAGGCTTTTCAGGAG 1104
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QY 1021 CTGCTGCTGTGGTATTGCCCGCAGCAGCTTGGCCATGGAGATGAAGAAGACATCAACACA 1080
DB 1165 CTGCTGCTGTGGTATTGCCCGCAGCAGCTTGGCCATGGAGATGAAGAAGACATCAACACA 1224
QY 1081 AAAAAAGAAC ---ATGTTCCACAAGATCTACATACAGAAAGCATGACATGTGTCAGCATC 1137
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QY 1138 CTGTTTCAGACATTTAGGGCTTCCACGAGCTGGCATCCAGTGCATCGCGAGGAGCTG 1197
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QY 1198 GTCAATGACCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGAGAAATCACTGC 1257
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DB 1465 GCGGACCATGCCACTCCTGTGTGGAGATGGGGTACACATGTTGAGGCCATCTCCTG 1524
QY 1378 GTACGTGAGGTGACAGGTGTAATGTGAACATGCGCGTGGGCATCCACAGCGGCGCGGTG 1437
DB 1525 GTACGTGAGGTGACAGGTGTAATGTGAACATGCGCGTGGGCATCCACAGCGGCGCGGTG 1584
QY 1438 CACTGCGGCTCCTTGGCTTGGGAAATGGCAGTTCGATGTGGTCCAATGATGTGACC 1497
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DB 1645 CTGCCCCAACCATGGAAGCAGGAAGCGGCTGGCGCATCCACATCACTCCGGGCAACA 1704
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DB 1825 GAGGAGAAAGGCATGCTGGCCAGCTCGGGGACTCGGGCCAACTCCATGGAAGGCTG 1884
QY 1738 ATGCCGCGATGGGTTCCTGTGTCCTTCCCGGACCAAGGACTCCAAGGCCCTCCCG 1797
DB 1885 ATGCCGCGATGGGTTCCTGTGTCCTTCCCGGACCAAGGACTCCAAGGCCCTCCCG 1944

QY 1798 CAGATGGCATGTGATGATTCCAGAAAGACACCGGGGACCCCAAGATGCCCTGAACCCCT 1857
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QY 1858 GAGGATAGGTGGATGAGTCTCTGAGCCGTCGATCGCATCGCCGAGCATGATGATGAGCTG 1917
DB 2005 GAGGATAGGTGGATGAGTCTCTGAGCCGTCGATCGCATCGCCGAGCATGATGATGAGCTG 2064
QY 1918 CGAAGGACCATGTGCGCGGTTTCTCACTTCCAGAGAGAGATTTTGAAGAAG 1977
DB 2065 CGAAGGACCATGTGCGCGGTTTCTCACTTCCAGAGAGAGATTTTGAAGAAG 2124
QY 1978 TACTCCCGAAGGTGGATCCCGCTTCGAGAGCCTACGTTGGCTGTGCCCTGTGCTCTTC 2037
DB 2125 TACTCCCGAAGGTGGATCCCGCTTCGAGAGCCTACGTTGGCTGTGCCCTGTGCTCTTC 2184
QY 2038 TGCCTCATCTGCTCATCCAGCTTCTAATTTTCCACACTCGACCTCATGCTTGGGAT 2097
DB 2185 TGCCTCATCTGCTCATCCAGCTTCTAATTTTCCACACTCGACCTCATGCTTGGGATC 2244
QY 2098 TATGCCAGCATCTTCTGCTGCTAATACCGGTGCTGATCTGTGCTGTGCTTACTCTCTGT 2157
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DB 2305 GGTTCCTCTGTTCCCTAAGGCCCTGCAACGCTGTGCCCGCAGCATGTCCGCTTCACGGGCA 2364
QY 2218 CATAGACCGGATGTGGATCTTTCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2277
DB 2365 CATAGACCGGATGTGGATCTTTTCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2424
QY 2278 ATGTTCACTGTGAACACACACCCCATACGGAGCTGTGAGGCTGTGAGGCTGTGCTGAATTAACA 2337
DB 2425 ATGTTCACTGTGAACACACACCCCATACGGAGCTGTGAGGCTGTGAGGCTGTGCTGAATTAACA 2484
QY 2338 CTTGCTGACATCACTGCTGCCACCTGACGAGCTCAATTAATCTCTGCTGGGCTGGATGCT 2397
DB 2485 CTTGCTGACATCACTGCTGCCACCTGACGAGCTCAATTAATTAATCTCTGCTGGGCTGGATGCT 2544
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DB 2545 CCCCTGCTGAGGACCATGCCACCTGCCAGCTTTCCTGAGGTGCTCATCGGGAACATG 2604
QY 2458 CTGCTGAGTCTTGGCCAGCTCTCTCTCTGTCACATCAGCAGCATCGGGAAGTTGGCC 2517
DB 2605 CTGCTGAGTCTTGGCCAGCTCTCTCTCTGTCACATCAGCAGCATCGGGAAGTTGGCC 2664
QY 2518 ATGATCTTTGCTTGGGCTCATCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2577
DB 2665 ATGATCTTTGCTTGGGCTCATCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2724
QY 2578 ATCTTTGACACTATGACTACTGCTTGGCTGCCATGCTTGGCTTCTTCCAAATGAGACC 2637
DB 2725 ATCTTTGACACTATGACTACTGCTTGGCTGCCATGCTTGGCTTCTTCCAAATGAGACC 2784
QY 2638 TTTGATGGCTGGAGTCTCCAGCTCAGGAGGCTGGCCCTCAATATATGACCCCTGTG 2697
DB 2785 TTTGATGGCTGGAGTCTCCAGCTCAGGAGGCTGGCCCTCAATATATGACCCCTGTG 2844
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QY 2998 GTGTCGAGTGTGCTGCTGCTCAACGAGATCATGCTGACTTTTGATGAGATTTATCAGC 3057
DB 3145 GTGTCGAGTGTGCTGCTGCTCAACGAGATCATGCTGACTTTTGATGAGATTTATCAGC 3204
QY 3058 GAGGAGCGGTTCCGCGAGCTGGAAGATCAAGAGATTGTTAGCACCTTACATGCTGCC 3117
DB 3205 GAGGAGCGGTTCCGCGAGCTGGAAGATCAAGAGATTGTTAGCACCTTACATGCTGCC 3264
QY 3118 TCAGGGCTGAAGCGCAGCACCTACGATCAGTTGGGCGCTCCACATCAGTGCCTCGCT 3177
DB 3265 TCAGGGCTGAAGCGCAGCACCTACGATCAGTTGGGCGCTCCACATCAGTGCCTCGCT 3324
QY 3178 GACTACGCGCATGCGGCTCATGGAGCAGATGAAGCAGATCAATGAGCAGCTTCTTCAACAAT 3237
DB 3325 GACTACGCGCATGCGGCTCATGGAGCAGATGAAGCAGATCAATGAGCAGCTTCTTCAACAAT 3384
QY 3238 TTCCAGATGAAGATTGGGCTGAACATGGGCGCAGTCGTGGCAGGTGTCATCGGGCTCGG 3297
DB 3385 TTCCAGATGAAGATTGGGCTGAACATGGGCGCAGTCGTGGCAGGTGTCATCGGGCTCGG 3444
QY 3298 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGCTCTAGTCTGATGGACAGCAG 3357
DB 3445 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGCTCTAGTCTGATGGACAGCAG 3504
QY 3358 GGGTCCCGGAGCGCAATCCAGGTGACCGAGCTGTACCAGGTTCTAGTCTGCCAAGGCG 3417
DB 3505 GGGTCCCGGAGCGCAATCCAGGTGACCGAGCTGTACCAGGTTCTAGTCTGCCAAGGCG 3564
QY 3418 TACCAGCTGGAGTGTGAGGGGTGCTCAAGGTGAAGGCAAGGGGAGATGACCACTAC 3477
DB 3565 TACCAGCTGGAGTGTGAGGGGTGCTCAAGGTGAAGGCAAGGGGAGATGACCACTAC 3624
QY 3478 TTCTCAATGGGGCGCCGAGGATTAACAGGCGCCAGCCACAATTCAGCTGAAGGAGC 3537
DB 3625 TTCTCAATGGGGCGCCGAGGATTAACAGGCGCCAGCCACAATTCAGCTGAAGGAGC 3684
QY 3538 AAGGTGGCACT 3549
DB 3685 AAGGTGGCACT 3696

RESULT 6

US-09-750-240-12

; Sequence 12, Application US/09750240
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05

NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 12

LENGTH: 3582

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Modified AC-VI

US-09-750-240-12

Query Match 95.2%; Score 3379.2; DB 29; Length 3582;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 3458; Conservative 0; Mismatches 88; Indels 6; Gaps 2;

QY 1 ATGTCATGGTTAGTGGCTCTCGTCCCTAAAGTGTGAACGCAAAACAGCGCTGGGT 60
DB 22 ATGTCATGGTTAGTGGCTCTCGTCCCTAAAGTGTGAACGCAAAACAGCGCTGGGT 81

QY 61 GAACGCAATGGGCAAGAGCGTTCCGGCGCGGTGGCACTCGGGCAGGTGGTCTGCAAG 120
DB 82 GAACGCAATGGGCAAGAGCGTTCCGGCGCGGTGGCACTCGGGCAGGTGGTCTGCAAG 141

QY 121 CCCGCTATATAGCTGCCTCCGGGATGACAGCCACCCAGCCCCACCCCTGCGGGCCCC 180
DB 142 CCCGCTATATAGCTGCCTCCGGGATGACAGCCACCCAGCCCCACCCCTGCGGGCCCC 201

QY 181 CCTCGTGCCCTGGCAGGATGACGCCCTTCATCGGAGGGCGGCCAGGCAAG 240
DB 202 CCTCGTGCCCTGGCAGGATGACGCCCTTCATCGGAGGGCGGCCAGGCAAG 261

QY 241 GAGTCGGGCTGCGGGCAGTGGCCCTGGGCTTCAGAGTACCAGAGTGACAACGACAGCG 300
DB 262 GAGTCGGGCTGCGGGCAGTGGCCCTGGGCTTCAGAGTACCAGAGTGACAACGACAGCG 321

QY 301 GCGGGAGCGCTGAGGTGGCGCGACGCGTCCAGAGGTGGCGATCCTGCTGCGCG 360
DB 322 GCGGGAGCGCTGAGGTGGCGCGCGACGCGTCCAGAGGTGGCGATCCTGCTGCGCG 381

QY 361 CGTTTGGTGCAGGTGTTCCAGTCGAAGCAGTTCGGTTCGGCAAGCTGGAGCGGCTGTAC 420
DB 382 CGTGTGTCAGGTGTTCCAGTCGAAGCAGTTCGGTTCGGCAAGCTGGAGCGGCTGTAC 441

QY 421 CAGCGGTACTTTTCCAGATGAACACAGCAGCCTGACGCTGCTGGTGGCGGTGCTGGTG 480
DB 442 CAGCGGTACTTTTCCAGATGAACACAGCAGCCTGACGCTGCTGGTGGCGGTGCTGGTG 501

QY 481 CTGCTCAGCGGTGCTGCTGGCTTTCCAAAGCCGACCCCGCCCTCAGCCCTGCGCTAT 540
DB 502 CTGCTCAGCGGTGCTGCTGGCTTTCCAGCCGACCCCGCCCTCAGCCCTGCGCTAT 561

QY 541 GTGGCACTGTGGCTGTGGCGCGCCCTGTTCGTGGGGGTCAATGGTGTGTAACCGG 600
DB 562 GTGGCACTGTGGCTGTGGCGCGCCCTGTTCGTGGGGGTCAATGGTGTGTAACCGG 621

QY 601 CATAGCTTCCGCAAGGACTCCATGTGGGTGGTGAATGAAGTGGTGGGATCCTGGCG 660
DB 622 CATAGCTTCCGCAAGGACTCCATGTGGGTGGTGAATGAAGTGGTGGGATCCTGGCG 681

QY 661 GCAGTGCAGGTGCGGGCGGCTTTCGACAGCAGCCGCGCAGCCCTCTGCGGGGCTCTGG 720
DB 682 GCAGTGCAGGTGCGGGCGGCTTTCGACAGCAGCCGCGCAGCCCTCTGCGGGGCTCTGG 741

QY 721 TGCCCTGTGTTTGTATATACATCCATACAGCTTCCTCCCATCCGATCGGGGCTGCC 780
DB 742 TGCCCTGTGTTTGTATATACATCCATACAGCTTCCTCCCATCCGATCGGGGCTGCC 801

QY 781 GTCCTCAGCGGCTTGGGCTCTCCACCTTGATTTGATTTGGCTTGGCTTGAACCGT 840
DB 802 GTCCTCAGCGGCTTGGGCTCTCCACCTTGATTTGATTTGGCTTGGCTTGAACCGT 861

QY 841 GGTGATGCTTCTTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTTCTGTCACCAAC 900
DB 862 GGTGATGCTTCTTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTTCTGTCACCAAC 921

QY 901 GTCAATTAGCATCTGCACACACTATCCAGCAGAGGTGCTCAGCGCCAGGCTTTTCAGGAG 960
DB 922 GTCAATTGGCATCTGCACACACTATCCAGCAGAGGTGCTCAGCGCCAGGCTTTTCAGGAG 981

QY 961 ACCGCGAGTTACATCCAGGCGCGGCTCCACTCGCAGCATGAGAAATCGCAGCAGGACGG 1020
DB 982 ACCGCGGTTTACATCCAGGCGCGGCTCCACTCGCAGCATGAGAAATCGCAGCAGGACGG 1041

QY 1021 CTGCTGCTGTCGGTATTGCCCCAGCAGCTGGCCATGAGATGAAGAGACATCAACACA 1080
DB 1042 CTGCTGCTGTCGGTATTGCCCCAGCAGCTGGCCATGAGATGAAGAGACATCAACACA 1101

QY 1081 AAAAAAGAGAC---ATGTTCCCAAGATCTACATACAGAGCATGACAAATGTCAGCATC 1137
DB 1102 AAAAAAGAGACATGATGTTCCCAAGATCTACATACAGAGCATGACAAATGTCAGCATC 1161

QY 1138 CTGTTTCAGACATTTAGGGCTTCCACAGCCTGGCATCCAGTGCCTGCGCAGGAGCTG 1197
DB 1162 CTGTTTCAGACATTTAGGGCTTCCACAGCCTGGCATCCAGTGCCTGCGCAGGAGCTG 1221

QY 1198 GTCATGACCTGAATGAGCTCTTTGCCCGGTTTACAAAGCTGGCTGGGAGAAATCACTGC 1257
DB 1222 GTCATGACCTGAATGAGCTCTTTGCCCGGTTTACAAAGCTGGCTGGGAGAAATCACTGT 1281

QY 1258 CTGAGGATCAAGATCTTTGGGGGACTGTTACTACTGTTGTGAGGGCTGCCGAGGCCCGG 1317
DB 1282 CTGAGGATCAAGATCTTTAGGAGACTGTTACTACTGCTGTGAGGGCTGCCGAGGCCCGG 1341

QY 1318 GCGGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG 1377
DB 1342 GCGGATCACGCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG 1401

QY 1378 GTACGTGAGGTGACAGGTGTAATGTGAACATGCGCTGGCGCATCCACAGCGGCGGCTG 1437
DB 1402 GTGCGTGAAGTACAGGTGTAACGTGAACATGCGCTGGCGCATCCACAGCGGACGTGTG 1461

QY 1438 CACTGCGGCTGCTTGGCTTTCGGGAAATGCAATGCAATGCTGTTGGTCCATGATGTGACC 1497
DB 1462 CATTGCGGCTGCTTGGCTTTCGGGAAATGCAATGCAATGCTGTTGGTCCAAAGATGTGACC 1521

QY 1498 CTGCGCAACACATGGAAGCAGGAGCGGCTGGCGCATCCACATCACTCCGCGCAACA 1557
DB 1522 CTGCGTAACACATGGAAGCAGGCGGCGGCG---GGCGCGGCATCCACATCACTCCGCGTACA 1578

QY 1558 CTGCACTTACCTGAACGCGGACTAGCAAGTGGAGCGGCGCTGGTGGCAAGCGCAACGCG 1617
DB 1579 CTGCACTTACCTGAACGCGGACTATGAGGTGGAGCGGCGGCTGGTGGCAAGCGCAATGCG 1638

QY 1618 TACCTCAAGGAGCAGCAGATTTGAGACTTTCTCATCTGGGCGCCAGCCAGCAACGGA 1677
DB 1639 TACCTCAAGGAGCAGTGCATTTGAGACTTTCTCATCTGGGCGCCAGCCAAACGGA 1698

QY 1678 GAGGAGAAAGCATGCTGGCCAAAGCTCAGCGGACTCGGCGCAACTCCATGGAAGGCGTG 1737
DB 1699 GAGGAGAAAGCATGCTGGCCAAAGCTTACGCGGACAGCGGCGCAACTCCATGGAAGGACTG 1758

QY 1738 ATGCGCGGATGGGTTCCTGATGCTGCTTCTCCCGGACCAAGGACTCCAAAGGCTTCCGC 1797
DB 1759 ATGCGCGGATGGGTTCCTGATGCTGCTTCTCCCGGACCAAGGACTCTAAGGCAATCCGC 1818

QY 1798 CAGATGGGCATTTGATGATTTCCAGCAAGACAAACCGGGGACCCCAAGATGCCCTGAAACCT 1857
DB 1819 CAGATGGGCATTTGATGATTTCTAGCAAGACAAACCGGGGTGCCAAGATGCTCTGAAACCT 1878

QY 1858 GAGGATCAGGTGGATGATTTCTGAGCCGTGCCATTCATGCCCGCAGCATTTGATCAGCTG 1917
DB 1879 GAGATCAGGTGGATGATTTCTGAGCCGAGCCATCATGCCCGCAGCATTTGATCAGCTG 1938

QY 1918 CGGAAGCAGCATGTGCGCGCGGTTTGTCTCACCTTCCAGAGAGAGGATTTTGAGAGAAAG 1977
DB 1939 CGGAAGCAGCATGTGCGCGCGGTTTGTCTCACCTTCCAGAGAGAGGATTTTGAGAGAAAG 1998

Qy 1978 TACTCCGGAAGGTGGATCCCGCTTCGAGCCTACGTTGCTGTGCCCCCTGTGCTTTC 2037
Db 1999 TACTCCGGAAGGTGGATCCCGCTTCGAGCCTACGTTGCTGTGCCCCCTGTGCTTTC 2058
Qy 2038 TGTTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCTGATGCTTGGGAT 2097
Db 2059 TGTTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCTGATGCTTGGGAT 2118
Qy 2098 TATGCGACATCTTCTGCTGCTGCTAATCACCGTGTGATCTGTGCTGTGCTACTCCGT 2157
Db 2119 TATGCCACATCTTCTGCTGCTGCTAATCACCGTGTGATCTGTGCTGTGCTACTCCGT 2178
Qy 2158 GGTTCCTGTTCCCTAAGCCCTGCAACGCTGTGCCGAGCATGTGCCGTCAACGGCA 2217
Db 2179 GGTTCCTGTTCCCTAAGCCCTGCAACGCTGTGCCGAGCATGTGCCGTCAACGGCA 2238
Qy 2218 CATAGCACCGAGTTGGATCTTTCCGCTCTGCTGTGTTTACTTCTGCCATTGCCAAC 2277
Db 2239 CATAGCACCGAGTTGGATCTTTCCGCTCTGCTGTGTTTACTTCTGCCATTGCCAAC 2298
Qy 2278 ATGTTCACTGTAAACACACCCCATACGGAGCTGTGAGCCCGGATGCTGAATTTAACA 2337
Db 2299 ATGTTCACTGTAAACACACCCCATACGGAGCTGTGAGCCCGGATGCTGAATTTAACA 2358
Qy 2338 CCTGTGACATCACTGCTGCCACTGCGAGAGCTCAATTAATCTCTCTGGGCTGATGCT 2397
Db 2359 CCTGTGACATCACTGCTGCCACTGCGAGAGCTCAATTAATCTCTCTGGGCTGATGCT 2418
Qy 2398 CCCCTGTGAGGGACCATGCCACCTGCAAGCTTCTGAGGTGCTCATCGGGAACATG 2457
Db 2419 CCCCTGTGAGGGACCATGCCACCTGCAAGCTTCTGAGGTGCTCATCGGGAACATG 2478
Qy 2458 CTGCTGAGTCTCTTGGCCAGCTCTGCTTCTGTCACATCAGCAGCATCGGGAAGTTGCC 2517
Db 2479 CTGCTGAGTCTCTTGGCCAGCTCTGCTTCTGTCACATCAGCAGCATCGGGAAGTTGCC 2538
Qy 2518 ATGATCTTTGCTTGGGGCTCATCTAATTTGGTGTGCTTCTGCTGGGTCGCCCGCCGCC 2577
Db 2539 ATGATCTTTGCTTGGGGCTCATCTAATTTGGTGTGCTTCTGCTGGGTCGCCCGCCGCC 2598
Qy 2578 ATCTTTGACAACTATGACTACTGCTTGGCGTCCATGCTTGGCTTCTTCCAATGAGACC 2637
Db 2599 ATCTTTGACAACTATGACTACTGCTTGGCGTCCATGCTTGGCTTCTTCCAATGAGACC 2658
Qy 2638 TTTGATGGGCTGGACTGCTCCAGCTGTCAGGAGGCTGGCCCTCAATATATACCCCTGTG 2697
Db 2659 TTTGATGGGCTGGACTGCTCCAGCTGTCAGGAGGCTGGCCCTCAATATATACCCCTGTG 2718
Qy 2698 ATTCTGTGTTGTTGGCGCTGGCGCTGTATCTGCAATGCTCAGCAGGTGGAATCGACTGCC 2757
Db 2719 ATTCTGTGTTGTTGGCGCTGGCGCTGTATCTGCAATGCTCAGCAGGTGGAATCGACTGCC 2778
Qy 2758 CGCCTAAACTTCCCTGCAAACTACAGGCAACAGGGGAAAGAGGAGATGGAGAGCTA 2817
Db 2779 CGCCTAGACTTCCCTGGAAGCTACAGGCAACAGGGGAAAGAGGAGATGGAGAGCTA 2838
Qy 2818 CAGGCATACACCGGAGGCTGTGATAAATCTTGCCTCAAGGAGCTGGCGCCCACTTC 2877
Db 2839 CAGGCATACACCGGAGGCTGTGATAAATCTTGCCTCAAGGAGCTGGCGCCCACTTC 2898
Qy 2878 CTGGCCCGGAGCGCCGCAATGATGAATCTACTATCATAGTGTGATGTGTGCTGTT 2937
Db 2899 CTGGCCCGGAGCGCCGCAATGATGAATCTACTATCATAGTGTGATGTGTGCTGTT 2958
Qy 2938 ATGTTTGGCTCCATGGCAACTTCTCAGTCTCTATGTTGAGCTGGAGGCAACAAATGAG 2997
Db 2959 ATGTTTGGCTCCATGGCAACTTCTCAGTCTCTATGTTGAGCTGGAGGCAACAAATGAG 3018
Qy 2998 GGTGCGGAGTGGCTGCGGCTGCTCAACGAGATCATCGTGTGACTTTTGTGAGATTTATCAGC 3057
Db 3019 GGTGTCGAGTGGCTGCGGCTGCTCAACGAGATCATCGTGTGACTTTTGTGATGATTTATCAGC 3078
Qy 3058 GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACCATTTGTTAGCACCTACATGCTGCC 3117

Db 3079 GAGGAGCGGTTCCGGCAGCTGAAAAGATCAAGAGTATGATGCTACATGCTGCC 3138
Qy 3118 TCAGGGCTGAACGCCAGCACCTACGATCAGGTGGCCCGCTCCACATCCTGCTGCTGCT 3177
Db 3139 TCAGGGCTGAACGCCAGCACCTACGATCAGGTGGCCCGCTCCACATCCTGCTGCTGCT 3198
Qy 3178 GACTACGCGCATCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCCTTCAACAAT 3237
Db 3199 GACTACGCGCATCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCCTTCAACAAT 3258
Qy 3238 TTCAGATGAAGATTGGGCTGAACATGGCCCGAGTCTGCGAGGTTGTCATCGGGCTCGG 3297
Db 3259 TTCAGATGAAGATTGGGCTGAACATGGCCCGAGTCTGCGAGGTTGTCATCGGGCTCGG 3318
Qy 3298 AAGCCACAGTATGATCTGGGGAACACAGTGAATGCTCTAGTCTGATGACAGCAGC 3357
Db 3319 AAGCCACAGTATGATCTGGGGAACACAGTGAATGCTCTAGTCTGATGACAGCAGC 3378
Qy 3358 GGGTCCCGCAGCAATCCAGGTGACACGACCTGTACCAGGTTTCTAGCTGCCAAGGCC 3417
Db 3379 GGGTCCCGCAGCAATCCAGGTGACACGACCTGTACCAGGTTTCTAGCTGCCAAGGCC 3438
Qy 3418 TACCAGCTGGAGTGTGAGGGGTGTCGAAGGTGAAGGCAAGGGGAGATGACCACTAC 3477
Db 3439 TACCAGCTGGAGTGTGAGGGGTGTCGAAGGTGAAGGCAAGGGGAGATGACCACTAC 3498
Qy 3478 TTCCTCAATGGGGCCCCCAGCAGTTAACAGGCCCGCAGCCAAATTCAGCTGAAGGGACC 3537
Db 3499 TTCCTCAATGGGGCCCCCAGCAGTTAACAGGCCCGCAGCCAAATTCAGCTGAAGGGACC 3558
Qy 3538 AAGGTGGCACT 3549
Db 3559 AAGGTGGCACT 3570

RESULT 7

US-60-248-592-183
; Sequence 183, Application US/60248592
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000961
; CURRENT APPLICATION NUMBER: US/60/248,592
; CURRENT FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 3706
; TYPE: DNA
; ORGANISM: HUMAN
US-60-248-592-183

Query Match 88.7%; Score 3147; DB 68; Length 3706;
Best Local Similarity 96.9%; Pred. No. 0;
Matches 3257; Conservative 0; Mismatches 35; Indels 69; Gaps 2;
Qy 213 CCGAGGGCGGCCCGCAGCAAGGAGCTGGGGCTGGGGGAGTGGGCTGGGCTT 272
Db 346 CTGGGGGGCGGCCAGGCAAGGAGCTGGGGCTGGGGGAGTGGGCTGGGCTT 405
Qy 273 CGAGATACCGAGGTGAACAGCACAGCGGGGAGCTGAGTGGCGCCGACCGCT 332
Db 406 CGAGATACCGAGGTGAACAGCACAGCGGGGAGCTGAGTGGCGCCGACCGCT 465
Qy 333 GCCAGGAGTGGGCTATCTGCTGGCGCGTGTGTCAGGTTTCCAGTGAAGCAGTT 392
Db 466 GCCAGGAGTGGGCTATCTGCTGGCGCGTGTGTCAGGTTTCCAGTGAAGCAGTT 525
Qy 393 CCGTTGCGCCCAAGCTGGAGCGCTGTACAGCGGTACTTTTCCAGATGAACAGAGCAG 452

Db 526 CCGTTCGCCAAGCTGGAGCGCCTGTATACAGCGGTACTTCTCCAGATGAACACAGAGCAG 585
Qy 453 CCTCAGCGTGTGTGGGGTGTGGTGTCTCAGAGCGGTGTGTGGTGTCTTCCAAAGC 512
Db 586 CCTCAGCGTGTGTGGGGTGTGGTGTCTCAGAGCGGTGTGTGGTGTCTTCCAAAGC 645
Qy 513 CGCAGCGCGCGCGCTCAGCGTGTGTGGGACTGTGTGGCGGTGTGGCGCGCGCGTGT 572
Db 646 CGCAGCGCGCGCGCTCAGCGTGTGTGGGACTGTGTGGCGGTGTGGCGCGCGCGTGT 705
Qy 573 CGTGGGCTATGTGTGTGTATACCGGATAGCTTCGGCAGGACTTCATGTGGTGGT 632
Db 706 CGTGGGCTATGTGTGTGTATACCGGATAGCTTCGGCAGGACTTCATGTGGTGGT 765
Qy 633 GAGTAAGCTGTGTGGGACTGTGGGCGAGTGCAGGTGGGGCGCTTCGCGAGAGA 692
Db 766 GAGTACGTGTGTGGGACTGTGGGCGAGTGCAGGTGGGGCGCTTCGCGAGAGA 825
Qy 693 CCCGCGAGCGCGCTCTCGGGCGCTGTGTGGCGCTGTGTCTTATACATCGCATACAC 752
Db 826 CCCGCGAGCGCGCTCTCGGGCGCTGTGTGGCGCTGTGTCTTATACATCGCATACAC 885
Qy 753 GCTCTCCCATCGCATCGGGGTGTGGTGTCTCAGCGCGCTGGCGCTCTCCACCTTGCA 812
Db 886 GCTCTCCCATCGCATCGGGGTGTGGTGTCTCAGCGCGCTGGCGCTCTCCACCTTGCA 945
Qy 813 TTTGATCTTGGCTTGGCAACTTAACCGTGTGTATGCCCTCTCTGGAAGCAGCTCGGTGC 872
Db 946 TTTGATCTTGGCTTGGCAACTTAACCGTGTGTATGCCCTCTCTGGAAGCAGCTCGGTGC 1005
Qy 873 CAATGTGTGTCTGTCTGCACCAAGCTCATTTAGCATCTGCACACACTATCCAGAGA 932
Db 1006 CAATGTGTGTCTGTCTGCACCAAGCTCATTTAGCATCTGCACACACTATCCAGAGA 1065
Qy 933 GGTGTCTCAGCGCAGCGCTTTTACGAGAGCCCGAGTTACATCAGCGCGCTCCACCT 992
Db 1066 GGTGTCTCAGCGCAGCGCTTTTACGAGAGCCCGGTTTACATCAGCGCGCGCTCCACCT 1125
Qy 993 GCAGCATGAGAAATCGGAGAGCGCGCTGTCTGTGGTATTTGCCAGCAGCTGTC 1052
Db 1126 GCAGCATGAGAAATCGGAGAGCGCGCTGTCTGTGGTATTTGCCAGCAGCTGTC 1185
Qy 1053 CATGAGATGAGAAAGACATCAACAAAAAAGAGAC---ATGTTCCACAGATCTA 1109
Db 1186 CATGAGATGAGAAAGACATCAACAAAAAAGAGACATGATGTTCACAAAGATCTA 1245
Qy 1110 CATCAGAGCATGACAAATGTACGATCTGTGTGCAGACATTCAGGCGCTTCACAGCCT 1169
Db 1246 CATCAGAGCATGACAAATGTACGATCTGTGTGCAGACATTCAGGCGCTTCACAGCCT 1305
Qy 1170 GGCATCCAGTGCATCGCAGGAGCTGGTGCATGACCTGAATGAGCTCTTTGGCGCGTT 1229
Db 1306 GGCATCCAGTGCATCGCAGGAGCTGGTGCATGACCTGAATGAGCTCTTTGGCGCGTT 1365
Qy 1230 TGACAAGTGTCTGGGAGAAATCACTGCCTGAGGATCAAGATCTTTGGGGACTCTTACTA 1289
Db 1366 TGACAAGTGTCTGGGAGAAATCACTGCCTGAGGATCAAGATCTTTGGGGACTCTTACTA 1425
Qy 1290 CTGTGTGTACGGGTGCGGAGCGCGCGGCGGACCATGCCACTGCTGTGTGGAGATGGG 1349
Db 1426 CTGTGTGTACGGGTGCGGAGCGCGCGGCGGACCATGCCACTGCTGTGTGGAGATGGG 1485
Qy 1350 GGTAGACATGATTGAGGCACTCTCGCTGTGTACGTGAGGTGACAGGTGTGAATGTGAACAT 1409
Db 1486 GGTAGACATGATTGAGGCACTCTCGCTGTGTACGTGAGGTGACAGGTGTGAATGTGAACAT 1545
Qy 1410 GCGGTGGGATCCACAGCGGCGGTGTGACTGCGGCGTCTTGGCTTGGGAAATGSCA 1469
Db 1546 GCGGTGGGATCCACAGCGGCGGTGTGACTGCGGCGTCTTGGCTTGGGAAATGSCA 1605
Qy 1470 GTTCGATGTGTGTCATGATGTGACCTTGGCCAAACCATGGAAGCAGGAAGCGCGGC 1529
Db 1606 GTTCGATGTGTGTCATGATGTGACCTTGGCCAAACCATGGAAGCAGGAAGCGCGGC 1665

Qy 1530 TGGCGGCATCCATCATCTCGGGCAACACTGCAGTACTGAACGGGACTACGAAGTGA 1589
Db 1666 TGGCGGCATCCATCATCTCGGGCAACACTGCAGTACTGAACGGGACTACGAAGTGA 1725
Qy 1590 GCCAGGCGGTGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGACATGAGATTTTCCT 1649
Db 1726 GCCAGGCGGTGTGGCGAGCGCAACGCGTACCTCAAGGAGCAGACATGAGATTTTCCT 1785
Qy 1650 CATCTCGGCGCAGCGCAGAAAACGGAAGAGGAAAGGATGCTGCGCAAGCTGCAGCG 1709
Db 1786 CATCTCGGCGCAGCGCAGAAAACGGAAGAGGAAAGGATGCTGCGCAAGCTGCAGCG 1845
Qy 1710 GACTCGGCGCAACTCCATGGAAGGCGTGTGCCGATGGTTCCTCATCGTCTTCTC 1769
Db 1846 GACTCGGCGCAACTCCATGGAAGGCGTGTGCCGATGGTTCCTCATCGTCTTCTC 1905
Qy 1770 CCGSACCAAGGACTCCAAAGCGCTTCGCCAGATGGGCAATTCATGATTCAGCAAGACAA 1829
Db 1906 CCGSACCAAGGACTCCAAAGCGCTTCGCCAGATGGGCAATTCATGATTCAGCAAGACAA 1965
Qy 1830 CCGGGGCAACCAAGATGCCCTGAACCTGAGGATGAGGTGATGATTCCTGAGCCGTCG 1889
Db 1966 CCGGGGCAACCAAGATGCCCTGAACCTGAGGATGAGGTGATGATTCCTGAGCCGTCG 2025
Qy 1890 CATCGATCGCGCAGCATTTGATCAGCTGCGGAAGGACCATGTGCGCGGTTTTTGTCTAC 1949
Db 2026 CATCGATCGCGCAGCATTTGATCAGCTGCGGAAGGACCATGTGCGCGGTTTTTGTCTAC 2085
Qy 1950 CTTCAGAGAGAGATTTTGAGAAGAGTACTCCCGAAGGTGGATCCCGCTTCGGAGC 2009
Db 2086 CTTCAGAGAGAGATTTTGAGAAGAGTACTCCCGAAGGTGGATCCCGCTTCGGAGC 2145
Qy 2010 CTAGCTTGCCTGTGCCCTGTGTGCTTCTCATCTGCTTTCATCCAGCTTCTTAATTT 2069
Db 2146 CTAGCTTGCCTGTGCCCTGTGTGCTTCTCATCTGCTTTCATCCAGCTTCTCATCTT 2205
Qy 2070 CCCACATCCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGTGCTTAATC 2129
Db 2206 CCCACATCCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGTGCTTAATC 2265
Qy 2130 CGTCTCATCTGTGCTGTACTCTCTGCTTCTGCTTCTCCCTAAGGCGCTTCGACGCT 2189
Db 2266 CGTCTCATCTGTGCTGTACTCTCTGCTTCTGCTTCTCCCTAAGGCGCTTCGACGCT 2325
Qy 2190 GTCCCGCAGCATCTCGCTGCACGGGCACATAGCACCGCAGTTGGCATCTTTCCGCT 2249
Db 2326 GTCCCGCAGCATCTCGCTGCACGGGCACATAGCACCGCAGTTGGCATCTTTCCGCT 2385
Qy 2250 GCTTGTGTTTACTTCTGCCATTTGCCATGTTTCCCTGTAAACACACACCCCATACGAG 2309
Db 2386 GCTTGTGTTTACTTCTGCCATTTGCCATGTTTCCCTGTAAACACACACCCCATACGAG 2445
Qy 2310 CTGTGAGCGCGGATGCTGAATTTAAACCTGTGACATCACTGCTGCCACCTGCAGCA 2369
Db 2446 CTGTGAGCGCGGATGCTGAATTTAAACCTGTGACATCACTGCTGCCACCTGCAGCA 2505
Qy 2370 GCTCAATTTACTTCTCTGGCGCTGGATGCTCCCTGTGTGAGGGCACCACCTGCAG 2429
Db 2506 GCTCAATTTACTTCTCTGGCGCTGGATGCTCCCTGTGTGAGGGCACCACCTGCAG 2565
Qy 2430 CTTCCTCTGAGGTGCTTCAGCGGAACATGCTGCTGAGTCTCTTGGCCAGCTGTGCTTCT 2489
Db 2566 CTTCCTCTGAGTACTTTCATCGGAACATGCTGCTGAGTCTCTTGGCCAGCTGTGCTTCT 2625
Qy 2490 GCACATCAGAGCATCGGGAAGTTGGCCATGATCTTGTCTTGGGGCTCATCTATTGGT 2549
Db 2626 GCACATCAGAGCATCGGGAAGTTGGCCATGATCTTGTCTTGGGGCTCATCTATTGGT 2685
Qy 2550 GCTGCTTCTGCTGGTCCCGCAGCGCCATCTTTGACAACTATGACCTACTGCTTGGCT 2609
Db 2686 GCTGCTTCTGCTGGTCCCGCAGCGCCATCTTTGACAACTATGACCTACTGCTTGGCT 2745

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Qy 2610 CCATGGCTTGGCTTCTTCCAAATGAGACCTTTGATGGGCTGACTGTCCAGCTGCAGGAG 2669
Db 2746 CCATGGCTTGGCTTCTTCCAAATGAGACCTTTGATGGGCTGACTGTCCAGCTGCAGGAG 2805
Qy 2670 GGTGGCCCTCAAAATATATGACCCCTGTGATTCTGCTGTTTGGCTGGGCTGTATCT 2729
Db 2806 GGTGGCCCTCAAAATATATGACCCCTGTGATTCTGCTGTTTGGCTGGGCTGTATCT 2865
Qy 2730 GCATGCTCAGCAGTGAATCGACTGCCCGCTAAACTTCTCTGGAACACTACAGCAAC 2789
Db 2866 GCATGCTCAGCAGTGGAGTGCAGTCCCGCTAGACTTCTCTGGAACACTACAGCAAC 2925
Qy 2790 AGGGAAAAAGAGAGATGGAGGAGTACAGGCATACAAACGGAGGCTGCTGCATACAT 2849
Db 2926 AGGGAGAGAGAGAGATGGAGGAGTACAGGCATACAAACGGAGGCTGCTGCATACAT 2985
Qy 2850 TCTGCCAAGACGCTGGCGGCCACTTCTTCCCGCGGAGCGCGCAATGATGAACCTA 2909
Db 2986 TCTGCCAAGACGCTGGCGGCCACTTCTTCCCGCGGAGCGCGCAATGATGAACCTA 3045
Qy 2910 CTATCAGTCGTGTGAGTGTGGCTGTATTTTGGCTTCCATTTGCCAACTTCTCTGAGTT 2969
Db 3046 CTATCAGTCGTGTGAGTGTGGCTGTATTTTGGCTTCCATTTGCCAACTTCTCTGAGTT 3105
Qy 2970 CTATCTGAGCTGGAGCAAAATAGAGGTGCGGCTGCTGCGGCTCAACGAGAT 3029
Db 3106 CTATCTGAGCTGGAGCAAAATAGAGGTGCTGAGTGCCTGCGGCTCAACGAGAT 3165
Qy 3030 CATCGCTGACVTTTGATG----- 3047
Db 3166 CATCGCTGACVTTTGATGAGGTACTTTTCCAGTTGGTGGTGGCAGAGAGTGGGGGT 3225
Qy 3048 -----GATTATCAGCAGGAGGCGGTTTCGGCAGCTGGAATA 3083
Db 3226 ACTTGGAGACCAAGGATTTGGAATGGATTATCAGCAGGAGGCGGTTCCGGCAGCTGGAATA 3285
Qy 3084 GATCAAGACGATTTGGTAGCCTACATGGCTGCCTCAGGCGTGAACGCCAGCACCTAGCA 3143
Db 3286 GATCAAGACGATTTGGTAGCCTACATGGCTGCCTCAGGCGTGAACGCCAGCACCTAGCA 3345
Qy 3144 TCAGTGGCGCGCTCCACATCACTTGCCTGGCTGACTTACGCCATTCGGGCTCATGGAGCA 3203
Db 3346 TCAGTGGCGCGCTCCACATCACTTGCCTGGCTGACTTACGCCATTCGGGCTCATGGAGCA 3405
Qy 3204 GATGAAGCACATCAATGAGCCTCCTTCAACAATTTCCAGATGAAGATTGGGCTGAACAT 3263
Db 3406 GATGAAGCACATCAATGAGCCTCCTTCAACAATTTCCAGATGAAGATTGGGCTGAACAT 3465
Qy 3264 GGGCCCACTGCTGGCAGGTGTCATCGGGGCTCGGAAGCCACAGTATGACATCTGGGGAA 3323
Db 3466 GGGCCCACTGCTGGCAGGTGTCATCGGGGCTCGGAAGCCACAGTATGACATCTGGGGAA 3525
Qy 3324 CACAGTGAATCTCTAGTCTATGAGCAGCAGCGGGGTCCCGACCGAATCCAGGTGAC 3383
Db 3526 CACAGTGAATCTCTAGTCTATGAGCAGCAGCGGGGTCCCGACCGAATCCAGGTGAC 3585
Qy 3384 CACGACCTGTACAGGTTCTAGCTGCCAAGGGCTACAGCTGAGTGTCCAGGGGTGGT 3443
Db 3586 CACGACCTGTACAGGTTCTAGCTGCCAAGGGCTACAGCTGAGTGTCCAGGGGTGGT 3645
Qy 3444 CAAGTGAAGGCAAGGGGAGATGACCACTTCTCAATGGGGCCCGCAGCAGTTA 3503
Db 3646 CAAGTGAAGGCAAGGGGAGATGACCACTTCTCAATGGGGCCCGCAGCAGTTA 3705
Qy 3504 A 3504
Db 3706 A 3706
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RESULT 8
US-60-245-228-549
; Sequence 549, Application US/60245228
; GENERAL INFORMATION:

; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES
; FILE REFERENCE: CL000878
; CURRENT APPLICATION NUMBER: US/60/245,228
; CURRENT FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 630
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 549
; LENGTH: 3356
; TYPE: DNA
; ORGANISM: HUMAN
US-60-245-228-549

Query Match 88.6%; Score 3144.2; DB 68; Length 3356;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 3253; Conservative 0; Mismatches 33; Indels 69; Gaps 2;

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Qy 219 GGGGGGGCCAGGCAAGGCAAGGAGCTGGGGCTGGGGCAGTGGCCCTGGGCTTCGAGA 278
Db 2 GGGGGGGCCAGGCAAGGCAAGGAGCTGGGGCTGGGGCAGTGGCCCTGGGCTTCGAGA 61
Qy 279 TACGAGGTGACAACGACAGCGGGGCGAGCTGAGTGGCGCCGCGCGGTCGCCAG 338
Db 62 TACGAGGTGACAACGACAGCGGGGCGAGCTGAGTGGCGCCGCGCGGTCGCCAG 121
Qy 339 GAGTGGGGGATCTCTGCTGGCGCCCTTTTGTGTCAGGTGTTCCAGTGAAGCAGTTCGTTTC 398
Db 122 GAGTGGGGGATCTCTGCTGGCGCCCTGCTGTCAGGTGTTCCAGTGAAGCAGTTCGTTTC 181
Qy 399 GGCAGCTGAGCGCCCTGTACAGCGGTACTTTTTCAGATGAACAGAGAGCCTGAC 458
Db 182 GGCAGCTGAGCGCCCTGTACAGCGGTACTTTTTCAGATGAACAGAGAGCCTGAC 241
Qy 459 GCTGCTGTGGCGGTGCTGCTGCTCACAGCGGTGCTGCTGCTTTCAGAGCGCACC 518
Db 242 GCTGCTGTGGCGGTGCTGCTGCTCACAGCGGTGCTGCTGCTTTCAGAGCGCACC 301
Qy 519 CGCCCGCCCTCAGCGCTGCTATGTGGCCTGTTGGCCCTGTCGCCCGCCCTGTTTCGTGG 578
Db 302 CGCCCGCCCTCAGCGCTGCTATGTGGCCTGTTGGCCCTGTCGCCCGCCCTGTTTCGTGG 361
Qy 579 GCTCATGTGTGTGTAAACCGCATAGCTTCGCCAGAGCTCCATGTGGGTGGTGAATA 638
Db 362 GCTCATGTGTGTGTAAACCGCATAGCTTCGCCAGAGCTCCATGTGGGTGGTGAATA 421
Qy 639 CGTGTGCTGGCGCTTCTTGGCGGAGTGCAGTGGGGGCGCTTTCGAGCAGAGACCCGCG 698
Db 422 CGTGTGCTGGCGATCTTGGCGGAGTGCAGTGGGGGCGCTTTCGAGCAGAGACCCGCG 481
Qy 699 CAGCCCTCTCTCGGGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 758
Db 482 CAGCCCTCTCTCGGGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
Qy 759 CCCATCCGATGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
Db 542 CCCATCCGATGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
Qy 819 CTTGGCCTGGCAACTTAAACCGTGTGATGCTTCTCTGGAAGCAGCTCGGTGCAATGT 878
Db 602 CTTGGCCTGGCAACTTAAACCGTGTGATGCTTCTCTGGAAGCAGCTCGGTGCAATGT 661
Qy 879 GCTGCTGTCTCTGCAACCAAGCTATTAGCATCTGACACATATCCAGCAGAGGCTGTC 938
Db 662 GCTGCTGTCTCTGCAACCAAGCTATTAGCATCTGACACATATCCAGCAGAGGCTGTC 721
Qy 939 TCAGGCCAGGCTTTTCAGGAGACCCGAGTTTACATCAGGGCCGGCTCCACCTGCAGCA 998
Db 722 TCAGGCCAGGCTTTTCAGGAGACCCGAGTTTACATCAGGGCCGGCTCCACCTGCAGCA 781
Qy 999 TGAGAACTCGCAGCAGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1058
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Db	782	TGAGAAATCGCGAGAGCGGCTGCTGCTGCGTATTTGCCCCAGCAGCTTGGCCATCGGA	841
Qy	1059	GATCAAAAGAGACATCAACAACAAAAAGAAC---ATGTTTCCACAGATCTACATACA	1115
Db	842	GATCAAAAGAGACATCAACAACAAAAAGAGACATGATTTCCACAGATCTACATACA	901
Qy	1116	GAGCATGACAATGTTCAGCATCCTGTTTTCAGACATTTAGGGCTTTCACAGCCTGGCATC	1175
Db	902	GAAGCATGACAATGTTCAGCATCCTGTTTTCAGACATTTAGGGCTTTCACAGCCTGGCATC	961
Qy	1176	CCAGTGCACATCGCCAGAGCTGGTCATGACCCTGTAATGAGCTCTTTGCCCGGTTTGACAA	1235
Db	962	CCAGTGCACATCGCCAGAGCTGGTCATGACCCTGTAATGAGCTCTTTGCCCGGTTTGACAA	1021
Qy	1236	GCTGGCTCGCGAGAATCACTGCGTGAAGATCAAGATCTTTGGGGACACTTTACTACTGTGT	1295
Db	1022	GCTGGCTCGCGAGAACTACTGCGTGAAGATCAAGATCTTTGGGGACACTTTACTACTGTGT	1081
Qy	1296	GTCAGGGCTGCGGAGCGCGGCGCCGACCATGCCACATGCTGTGTGTGAGATGGGGGTAGA	1355
Db	1082	GTCAGGGCTGCGGAGCGCGGCGCCGACCATGCCACATGCTGTGTGAGATGGGGGTAGA	1141
Qy	1356	CATGATTTAGGCCATCTCGCTGGTACGTGAGTGCACAGGTGTGTAATGTGAACATGCGCGT	1415
Db	1142	CATGATTTAGGCCATCTCGCTGGTACGTGAGTGCACAGGTGTGTAATGTGAACATGCGCGT	1201
Qy	1416	GGGCATCCACAGCGGGCGCTGCACATGCGCGCGCTCCTTGCTTGCAGAAATGGCAAGTTTCTGA	1475
Db	1202	GGGCATCCACAGCGGGCGCTGCACATGCGCGCGCTCCTTGCTTGCAGAAATGGCAAGTTTCTGA	1261
Qy	1476	TGTTGTGTCCAATGATGTGACCTTGCCCAACACATGGAAGCAGGAAGCGGGGTGGCCG	1535
Db	1262	TGTTGTGTCCAATGATGTGACCTTGCCCAACACATGGAAGCAGGAAGCGGGGTGGCCG	1321
Qy	1536	CATCCACATCACTCGGGCACACTGCGTACCTGACCGGGGACACAGAGTGGAGCCAGG	1595
Db	1322	CATCCACATCACTCGGGCACACTGCGTACCTGACCGGGGACACAGAGTGGAGCCAGG	1381
Qy	1596	CCGTGTGTGGCAAGCGCAACCGGTACCTCAAGGAGCAGACATTTGAGACTTTCCCTCATCCT	1655
Db	1382	CCGTGTGTGGCGAGCGCAACCGGTACCTCAAGGAGCAGACATTTGAGACTTTCCCTCATCCT	1441
Qy	1656	GGGCGCCAGCCAGAAAGAGAGAGAAAGGCATGCTGGCCAAAGCTGCAGCGGATCTCG	1715
Db	1442	GGGCGCCAGCCAGAAAGAGAGAGAAAGGCATGCTGGCCAAAGCTGCAGCGGATCTCG	1501
Qy	1716	GGCCAACCTCCATGSAAGGGCTGATGCGCGATGGGTTCTCTGATCGTGCCTTCTCCCGGAC	1775
Db	1502	GGCCAACCTCCATGSAAGGGCTGATGCGCGATGGGTTCTCTGATCGTGCCTTCTCCCGGAC	1561
Qy	1776	CAAGGACTCCAAAGCCCTTCGCGCAGATGGGCATTTGATGATTTCCAGCAAGACAACCGGGG	1835
Db	1562	CAAGGACTCCAAAGCCCTTCGCGCAGATGGGCATTTGATGATTTCCAGCAAGACAACCGGGG	1621
Qy	1836	CACCAAGATGCCCCGTAACCTTGAGGATGAGTGTGATGAGTTCTGTAGCGGTGCCATCGA	1895
Db	1622	CACCAAGATGCCCCGTAACCTTGAGGATGAGTGTGATGAGTTCTGTAGCGGTGCCATCGA	1681
Qy	1896	TGCCCCGAGCATTTGATCAGCTGGGGAAGACCATGTGGCGCGGTTTGTGTCACCTTCCA	1955
Db	1682	TGCCCCGAGCATTTGATCAGCTGGGGAAGACCATGTGGCGCGGTTTGTGTCACCTTCCA	1741
Qy	1956	GAGAGAGATTTTGAAGAAGTACTCCCGGAAGGTGGATCCCGCTTTCGGAGCCTACGT	2015
Db	1742	GAGAGAGATTTTGAAGAAGTACTCCCGGAAGGTGGATCCCGCTTTCGGAGCCTACGT	1801
Qy	2016	TGCGTGTGCCCTGTGTGCTTCTGCTTTCATCTGCTTTCATCCAGCTTCTTAATTTTCCACCA	2075
Db	1802	TGCGTGTGCCCTGTGTGCTTCTGCTTTCATCTGCTTTCATCCAGCTTCTTAATTTTCCACCA	1861
Qy	2076	CTCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGTGCTAATACACCGTGTCT	2135
Db	1862	CTCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGTGCTAATACACCGTGTCT	1921

QY	2136	GATCTGCTGCTGATACCTCCTGCTGGTCTCTGTTTCCCTAAGGCCCTGCAACGCTCTGTCTCCG	2195
Db	1922	GAICTGTGCTGTGTACTCTCTGTTGGTCTCTGTTTCCCTAAGGCCCTGCAACGCTCTGTCTCCG	1981
QY	2196	CAGCAATTCTCCGCTACCGGCACATAGCACCGAGTTGGCATCTTTTCCGTCCTGCTGTGT	2255
Db	1982	CAGCAATGTCCGCTACCGGCACATAGCACCGAGTTGGCATCTTTTCCGTCCTGCTGTGT	2041
QY	2256	GTTTACTTCTGCCATTGCCAACATGTTCACTGTATAACCACACCCCATACAGAGCTGTGC	2315
Db	2042	GTTTACTTCTGCCATTGCCAACATGTTCACTGTATAACCACACCCCATACAGAGCTGTGC	2101
QY	2316	AGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCCACCTGCCACCTGCAGCACTCAA	2375
Db	2102	AGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCCACCTGCCACCTGCAGCACTCAA	2161
QY	2376	TTACTCTCTGGGCTGTGATGCTCCCTGTGTGAGGGCACCATGCCACCTGCAGAGTTTCC	2435
Db	2162	TTACTCTCTGGGCTGTGATGCTCCCTGTGTGAGGGCACCATGCCACCTGCAGAGTTTCC	2221
QY	2436	TGAGGTGTCCATCGGGAACATGCTGTAGTCTCTTTGGCCAGCTCTGTCTTCTCTGCGACAT	2495
Db	2222	TGAGTACTTCACTCGGGAACATGCTGTAGTCTCTTTGGCCAGCTCTGTCTTCTCTGCGACAT	2281
QY	2496	CAGCAGCATCGGAAGTTGGCCATGATCTTTGTCTTTGGGGCTCATCTATTGTGGTGTGCT	2555
Db	2282	CAGCAGCATCGGAAGTTGGCCATGATCTTTGTCTTTGGGGCTCATCTATTGTGGTGTGCT	2341
QY	2556	TCTGCTGGTCCCCAGCCGCCATCTTTGACAACTATGACCTACTGCTTTGGCGTCCATG	2615
Db	2342	TCTGCTGGTCCCCAGCCACCATCTTTGACAACTATGACCTACTGCTTTGGCGTCCATG	2401
QY	2616	CTTGGCTTCTTCCAATCAGACCTTTGATGGGCTGGAGTCTCCAGCTGCAGGAGGGTGGC	2675
Db	2402	CTTGGCTTCTTCCAATCAGACCTTTGATGGGCTGGAGTCTCCAGCTGCAGGAGGGTGGC	2461
QY	2676	CCTCAAAATATAGCCCTCTGATCTGCTGTGTTTGGCTGGCGCTGTATCTGCAATGC	2735
Db	2462	CCTCAAAATATAGCCCTCTGATCTGCTGTGTTTGGCTGGCGCTGTATCTGCAATGC	2521
QY	2736	TCACAGGTGAATCAGTCCCGCCTAACTTCCCTCGGAACTACAGGCAACAGGGGA	2795
Db	2522	TCAGCAGGTGAGTGCAGTCCCGCCTAGACTTCCCTCGGAACTACAGGCAACAGGGGA	2581
QY	2796	AAAAGAGAGATGGAGAGCTACAGGCATACAACCGAGGCTGTCATCAATCTTGC	2855
Db	2582	GAAGSAGAGATGGAGAGCTACAGGCATACAACCGAGGCTGTCATCAATCTTGC	2641
QY	2856	CAAGACGTGCGGCCACTTCTTGCCCGGAGCGCCGCAATGATGAACCTTACTATCA	2915
Db	2642	CAAGACGTGCGGCCACTTCTTGCCCGGAGCGCCGCAATGATGAACCTTACTATCA	2701
QY	2916	GTCTGTGAGTGTGTGGCTGTTATGTTTGGCTCTCATTTGCCAACTTCTCTGAGTCTATGT	2975
Db	2702	GTCTGTGAGTGTGTGGCTGTTATGTTTGGCTCTCATTTGCCAACTTCTCTGAGTCTATGT	2761
QY	2976	GGAGCTGGAGCAAAATCAGGGTCCCGAGTCCCTGCGGCTGCTCAACAGAGATCATCGC	3035
Db	2762	GGAGCTGGAGCAAAATCAGGGTCCCGAGTCCCTGCGGCTGCTCAACAGAGATCATCGC	2821
QY	3036	TCACTTTGATGA-----	3047
Db	2822	TGACTTTTGAATGAGTACTTTTCCAGTTGGCTGGTGGCAGAGAGTGGGGGTACTTGG	2881
QY	3048	-----GATTATCAGCGAGGAGCGGTTTCCGGCAGCTGGAAAGATCAA	3089
Db	2882	AGACCAGGATTGGAATGGATTATCAGCGAGGAGCGGTTTCCGGCAGCTGGAAAGATCAA	2941
QY	3090	GACGATTTGGTAGCACCTTACATGCTGCCTCAGGGTGTAAACGCCAGCACTTACGATCAGGT	3149
Db	2942	GACGATTTGGTAGCACCTTACATGCTGCCTCAGGGTGTAAACGCCAGCACTTACGATCAGGT	3001

Qy	3150	GGGGCGCTCCACATCACTGCTCCCTGGCTGCTACGCCATCGGGTCACTGGAGCAGATGAA	3209
Ds	3002	GGGGCGCTCCACATCACTGCTCCCTGGCTGCTACGCCATCGGGTCACTGGAGCAGATGAA	3061
Qy	3210	GCACATCAATGAGCAGCTCTTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGGGCC	3269
Ds	3062	GCACATCAATGAGCAGCTCTTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGGGCC	3121
Qy	3270	AGTCTGGCAGGTGCTATCGGGGCTCGGAAGCCACAGTATGACATCTGGGGGAACACAGT	3329
Ds	3122	AGTCTGGCAGGTGCTATCGGGGCTCGGAAGCCACAGTATGACATCTGGGGGAACACAGT	3181
Qy	3330	GAATGCTCTAGTCTATGAGACAGCAGGGGTCGCCAGCAGTATGACATCTGGGGGAACACAGT	3389
Ds	3182	GAATGCTCTAGTCTATGAGACAGCAGGGGTCGCCAGCAGTATGACATCTGGGGGAACACAGT	3241
Qy	3390	CCTGTACCAGGTCTAGTCTGCAAGGCTACACAGTGGAGTGCAGGGGTGGTCAAGT	3449
Ds	3242	CCTGTACCAGGTCTAGTCTGCAAGGCTACACAGTGGAGTGCAGGGGTGGTCAAGT	3301
Qy	3450	GAAGGGCAAGGGGAGATGACCACTACTTCTCAATGGGGGCCGCCAGCAGTTAA	3504
Ds	3302	GAAGGGCAAGGGGAGATGACCACTACTTCTCAATGGGGGCCGCCAGCAGTTAA	3356
RESULT 9			
US-60-360-207-5921			
; Sequence 5921, Application US/60360207			
; GENERAL INFORMATION:			
; APPLICANT: VENTER, J. Craig			
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF			
; FILE REFERENCE: CL001321			
; CURRENT APPLICATION NUMBER: US/60/360,207			
; CURRENT FILING DATE: 2002-03-01			
; NUMBER OF SEQ ID NOS: 47235			
; SEQ ID NO 5921			
; LENGTH: 5826			
; TYPE: DNA			
; ORGANISM: HUMAN			
US-60-360-207-5921			
Query Match 78.98; Score 2799.2; DB 80; Length 5826;			
Best Local Similarity 87.5%; Pred. No. 0;			
Matches 310; Conservative 0; Mismatches 433; Indels 11; Gaps 4;			
Qy	1	ATGTCATGGTTAGTGGCTCTGCTCCCTAAAGTGGATGAACGAAACACCTGGGGT	60
Ds	96	ATGTCATGGTTAGTGGCTCTGCTCCCAAGTGGATGAACGAAACACCTGGGGG	155
Qy	61	GAACGCAATGGCAGAGCTTCCGGCGCTGGGCTGAGTGGGAGGTGGTTCGTGACG	120
Ds	156	GAACGCAATGGCAGAGCTTCCGGCGCTGGGCTGAGTGGGAGGTGGTTCGTGACG	212
Qy	121	CCCGCTATATGAGTGGCTCCGGGATGACAGCCACCGCCACCGCCACCGCCCGCC	180
Ds	213	CCTGCTACATGAGTGGCTCCAGATGGGAGCCACCGCCACCGCCACCGCCCGCC	272
Qy	181	CCTGGTCCCGCTGGCAGGATGAGCCCTTCAATCGGGAGGGCGGCCAGGCAAGGCAAG	240
Ds	273	ACTGGTCCCGCTGGCAGGATGAGCCCTTCAATCAGGAGGGCGGCCAGGCGGTGTG	332
Qy	241	GAGCTGGGGCTGGGGCAGTGGGCTTGGGCTTCGAGGATACCGAGGTGACACGACAGC	300
Ds	333	GAGCTGGGGCTGGGGCAGTGGGCTTGGGCTTCGAGGATACCGAGGTGACACGACAGC	392
Qy	301	GGCGGAGCGGTGAGTGGCGCCGACGCGTGGCCAGGAGTGGCGATCTGCTGGCGC	360
Ds	393	GGC---ACAGCTGAAGTGGCAGCGGATACATCGGCTCGGAGCGGTCCGCTGCTGGCAC	449
Qy	361	CGTTTGGTGGAGGTGTTCCAGTCGAGCAGTTCGCTTCGGGCAAGCTGGAGCGGCTGTAC	420
Ds	450	CGGCTGTGCAAGGTGTTCCAGTCTAAGCAGTTCGCTCTGCCAAGCTGGAGCGGCTGTAC	509

Qy	421	CAGCGGTACTTTTCCAGATGAACAGAGAGCCCTGACGCTGCTGGTGGCGTGGTGGT	480
Ds	510	CAGCGGTACTTTTCCAGATGAACAGAGAGCCCTGACGCTGCTGGTGGCGTGGTGGT	569
Qy	481	CTGCTCAGAGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	540
Ds	570	CTGCTCAGAGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	629
Qy	541	GTGGCAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	600
Ds	630	GTGGCAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	689
Qy	601	CATAGCTTCCGCCAGGACTCCATGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	660
Ds	690	CACAGCTTCCGCCAGGACTCCATGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	749
Qy	661	GCAGTGCAGGTGGGGGGCTTTCGCAGCAGACCCGCGCGAGCCCTCTGCGGGCTCTGG	720
Ds	750	GCCGTGCAAGTGGGGGGCTTTCGCAGCAGACCCGCGCGAGCCCTCTGCGGGCTCTGG	809
Qy	721	TGCCCTGTGTTCTTGTATACATGCATACACGCTCCCTCCCATCCGATCGGGCTGCC	780
Ds	810	TGCCCTGTGTTCTTGTATACATGCATACACGCTCCCTCCCATCCGATCGGGCTGCC	869
Qy	781	GTCTCAGCGGCTGGGCTCTCCACCTTTGATTTGATTTGATTTGATTTGATTTGATTTG	840
Ds	870	GTCTCAGCGGCTGGGCTCTCTACTCTGATTTGATTTGATTTGATTTGATTTGATTTG	929
Qy	841	GGTATGCTTCCCTCTGGAAGCAGCTCGTGGCCATGTTGCTGCTGCTGCTGCTGCTGCT	900
Ds	930	AGCCAGCCCTTCCCTTGGGAAGCAGCTCGTGGTCTTAACGTTGCTGCTGCTGCTGCTG	989
Qy	901	GTCATTAGCATCTGCACACACTATCCAGCAGAGGTGTTCTCAGCGCAGGCTTTTCAGG	960
Ds	990	GCCATCGTGTCTGCACACACTACCTGCTGAGTGTCTCAGCGCAGGCTTTTCAGG	1049
Qy	961	ACCCGAGTTACATCCAGGCGCGCTCCACCTGTCAGCATGAGAAATCGCAGCAGGCGG	1020
Ds	1050	ACCCGAGTTACATCCAGGCGCGCTGCACCTGTCAGCATGAGAAATCGCAGCAGGCGG	1109
Qy	1021	CTGCTGCTGCTGGTATTCGCCCGCAGCAGCTTGCCTGGAGATGAAGAAGACATCAACA	1080
Ds	1110	CTGCTGCTGCTGGTATTCGCCCGCAGCAGCTTGCCTGGAGATGAAGAAGACATCAACA	1169
Qy	1081	AAAAAAGAGAC---ATGTTCCACAAGATCTACATACAGAGCATGCAATGTCAGCATC	1137
Ds	1170	AAAAAAGAGACATGATGTTCCATAAGATCTACATCCAGAGCATGATTAATGTCAGCATC	1229
Qy	1138	CTGTTTGAGCAGATTTAGGGCTTACCAGCTGGCATCCCATGTCAGTGGCAGGAGGTG	1197
Ds	1230	CTGTTTGAGCAGATTTAGGGCTTACCAGCTGGCATCCCATGTCAGTGGCAGGAGGTG	1289
Qy	1198	GTCATGACCTGAATGAGTCTTTTCCCGGTTTGAACAGCTGGCTGCGGAGATCACTGT	1257
Ds	1290	GTCATGACCTGAATGAGTCTTTTCCCGGTTTGAACAGCTGGCTGCGGAGATCACTGT	1349
Qy	1258	CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCGGAGGCGCGG	1317
Ds	1350	CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCGGAGGCGCGG	1409
Qy	1318	GCCGACATGCGGCTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCGCATCTCGGTG	1377
Ds	1410	GCAGATCAGCGGCTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCGCATCTCGGTG	1469
Qy	1378	GTAGCTGAGGTGACAGGTGTGAATGTAACATGCGCGTGGGCTGCAGAGCGGCGCGT	1437
Ds	1470	GTAGCTGAGGTGACAGGTGTGAATGTAACATGCGCGTGGGCTGCAGAGCGGCGCGT	1529
Qy	1438	CAGTGGCGGCTTGGCTTGGGAAATGCGAGTTCGATGTTGTTGTTGTTGTTGTTGTTG	1497
Ds	1530	CAGTGGCGGCTTGGCTTGGGAAATGCGAGTTCGATGTTGTTGTTGTTGTTGTTGTTG	1589
Qy	1498	CTGGCCAAACACATGGAAGCAGGAGCGGGCTGCGCCGATCCACATCACTCGGCGAACA	1557

Db 1590 CTGGCTAACACATGAGGCGGGGGCCGGCCGGCGCATCCACATCACTCGGGCTTACA 1649
QY 1558 CTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGCCGCTGTGTGCAAGCGCAACGCG 1617
Db 1650 CTGCAGTACTTGAACGGGGACTATGAGGTGGAGCCAGCCGCTGTGTGCAAGCGCAATGCG 1709
QY 1618 TACCTCAAGGAGCAGCACAATTGAGACTTTCTCTCATCTCGGGCCGACCCAGCAACGGA 1677
Db 1710 TACCTCAAGGAGCAGTGCATTGAGACCTTCTCTCATCTTGGCGCCAGCCAAAACGGA 1769
QY 1678 GAGGAGAAAGCATCTGGCCACAGCTCAGGGGACTCGGGCCAACTCCATGGAAAGGCGTG 1737
Db 1770 GAGGAGAAAGCCATGCTGGCCACAGCTTACGCGGACACGGGCCAACTCCATGGAAAGGACTG 1829
QY 1738 ATGCCCGGATGGGTTCCTGTGATCGTCCGCGACCAAGGACTCCAAGGCCCTTCGCG 1797
Db 1830 ATGCCCGGCTGGGTTCCTGACCGTGCCTTCCCGGACCAAGGACTCAAGGCATTCGCG 1889
QY 1798 CAGATGGGCATTTGATGATCCAGCAAAAGACAACCGGGCCACCAAGATGCCCTGAACCCCT 1857
Db 1890 CAGATGGGCATTTGATGATTTAGCAAAAGACAACCGGGTGCCCAAGATGCTCTGAACCCCT 1949
QY 1858 GAGATGAGTGGATGATGATTCCTGAGCCGTGCCATGCATGCCCGCAGCATTGATCAGCTG 1917
Db 1950 GAGATGAGTGGATGATGATTCCTGAGCCGTGCCATGCATGCCCGCAGCATTGATCAGCTG 2009
QY 1918 CGGAAGGACCATGTGCGCCGCTTTTCTCACCCTTCCAGAGAGAGGATTTTGAAGAAG 1977
Db 2010 CGTAAGGACCATGTGCGCCGCTTCTCTCACTTCCAGAGAGAGATCTTGAGAAG 2069
QY 1978 TACTCCCGAAGGTGGATGATGATTCCTGAGCCGTGCCAGCTTACGCTGTGCCCTTGGTCTTC 2037
Db 2070 TATTACGGAAAGTAGATCTCTGCTTCCGAGCCCTACGCTGCGCTTGGCCCTGCTGTTTT 2129
QY 2038 TGCTTCACTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCTGATGCTTGGGATT 2097
Db 2130 TGCTTCACTGCTTATCCAGCTCTCTGTGTTCCCATCTACTCCACCTGATCTCGGGATT 2189
QY 2098 TATGCCAGCATCTTCTGCTGCTGCTAATCACCGTGTGATCTGTGCTGTGCTGCTGCTGCT 2157
Db 2190 TATGCCGCTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2249
QY 2158 GGTTCCTGTTCCCTAAGGCCCTGCAAGCTCTGTCCCGCAGCATGTCCGCTCACGGGCA 2217
Db 2250 GGTTCCTTCTTCCCAAGGCCCTGCAAGGCCCTGTCCCGCAATATTGTCCGCTCACGGGTG 2309
QY 2218 CATAGCACCGCAGTTGGCATCTTTTCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2277
Db 2310 CACAGCACCGGCTGGAAATCTTCTCGGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2369
QY 2278 ATGTTACCTGTAAACACACCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACA 2337
Db 2370 ATGTTTACCTGTATACACCCCAATAGACCTGTCCGCGCGGATGCTGAATTTAACA 2429
QY 2338 CTTGCTGACATPACTGCTGCACTGCTGCAAGCTCAATTAATCTCTGGGCTGGATGCT 2397
Db 2430 CCAGCGGATGTACCGGCTGCACTGCTGCAAGCTCAATTAATCTCTGGGACTGGATGCT 2489
QY 2398 CCGCTGTGAGGGCACCATGCGCCACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2457
Db 2490 CCGCTGTGAGGGCACCAGCCACCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2549
QY 2458 CTGCTGAGTCTTCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2517
Db 2550 CTGCTGAGTCTTCTAGCCAGCTGCTGCTTCTTCTACACATCAGCAGCATCGGCAAGCTGCGC 2609
QY 2518 ATGATCTTTGCTGGGGCTCATCTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2577
Db 2610 ATGACCTTTCATCTGGGGTTCACCTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2669
QY 2578 ATCTTTTACACATGATGACTGCTGCTGGGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2637

Db 2670 ATCTTTGACAACTATGATCTACTGCTTTGGCGTCCATGGCTTGGCTTCTCTCAATGAGACC 2729
QY 2638 TTTGATGGCTGGACTGCTCAGCTGCAAGGAGGTGGCCCTCAAAATATATGACCCCTGTG 2697
Db 2730 TTTGATGGCTGGACTGCTCAGCTGCGGAGGTACGCTCAATATATGACCCCGTG 2789
QY 2698 ATTCTGCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2757
Db 2790 ATTCTGCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2849
QY 2758 CGCTTAACTTCTCTGGAACACTACAGCAACAGGGGAAAGAGAGATGGAGAGCTA 2817
Db 2850 CGCTGAGACTTCTCTGTTGGAAGTTACAGCAACAGGGGAGAGAGATGGAGAGCTA 2909
QY 2818 CAGCATACAAACCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2877
Db 2910 CAGCATACAAACCGGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2969
QY 2878 CTGGCCCGGAGCGCCCAATGATGAATCTCTACTATCAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 2937
Db 2970 CTGGCCCGGAGCGCCCAACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3029
QY 2938 ATGTTTCTCTTCCATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2997
Db 3030 ATGTTTCTCTTCCATCGCAATTTCTCGAGTTCTACGTTGAGCTCGAGGCAACACAGAG 3089
QY 2998 GGTCCGAGTGCCTGCGGCTGCTCAACGAGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3057
Db 3090 GGTCCGAGTGCCTGCGGCTGCTCAATGAGATCATCGAGATCTTGACGAGATCATCAGT 3149
QY 3058 GAGGAGCGGTTCCGGAGCTTGGAAAGATCAAGAGGATTTGGTAGCACCCTACATGGCTGCC 3117
Db 3150 GAGGAGAGATTTCCGGCAGTTGGAGAGATCAAGACCATCGGTAGCACCCTACATGGCCGCC 3209
QY 3118 TCAGGGCTGAAGCGACGACCTACGATCAGTGGCGCGCTCCACACACTGCTGCCCTGGCT 3177
Db 3210 TCTGGGCTAAATGCCACACCTATGACAGGTGCGCGCTCACACATCAGCGGCTGGCT 3269
QY 3178 GACTACCCCATGCGGCTCATGGAGCAGATGAAGCAGATCAATGAGCACTCTTCAACAAT 3237
Db 3270 GACTATGCCATGCGGCTCATGGAGCAGATGAACACATCAATGAACACTCTTTCAACAAT 3329
QY 3238 TCCAGATGAAGATTGGGCTGAACATGGGCCAGTCTGTCGCGAGGTGTCATCGGGCTCGG 3297
Db 3330 TCCAGATGAAGATTGGGCTGAACATGGGTTCGCGGTTTAGCAGCGCTCATTTGGGGCCCGA 3389
QY 3298 AAGCCACAGTATGACATCTGGGGAAACACAGTGAATGCTCTAGTCTGATGCGAGCAGCAG 3357
Db 3390 AAGCCACAGTATGACATCTGGGGAAATACCGTGAATGTTTCCAGTCTGATGCGAGCAGCT 3449
QY 3358 GGGTCCCGGACCGAATCCAGGTGACCCAGGACTGTACCAGGTTCTAGCTGCGCAAGGC 3417
Db 3450 GGAGTTCTTGACCGAATACAGGTGACTACGACCATATACCAGGTTCTAGCTGCGCAAGGC 3509
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Db 3510 TACAGCTGAGGTGTCAGGGGTGTCAGGTGAAGGAAAGGGGAGATGACCACCTAC 3569
QY 3478 TTCTCTAATGGGGCCCGCAGCAGTTAAGGGGCCAGC -- -CACAATAATTAGCTGAAGGGA 3535
Db 3570 TTCTCTAAGGGGCCCGCAGCAGTTAGCAGGTGCGAGCTGAGATTCACCGAAGGGA 3629
QY 3536 CCAAGTGGGCACT 3549
Db 3630 CCAAGTGGGCACT 3643

RESULT 10

US-08-538-815-11
; Sequence 11, Application US/08538815
; GENERAL INFORMATION:
; APPLICANT: Tang, Wei-Jen
; APPLICANT: Gilman, Alfred G.

;> TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLVL
;> TITLE OF INVENTION: CYCLASE AND USES THEREFOR
;> NUMBER OF SEQUENCES: 27
;> CORRESPONDENCE ADDRESS:
;> ADDRESSEE: Arnold, White & Durkee
;> STREET: P.O. Box 4433
;> CITY: Houston
;> STATE: Texas
;> COUNTRY: United States of America
;> ZIP: 77210
;> COMPUTER READABLE FORM:
;> MEDIUM TYPE: Floppy disk
;> COMPUTER: IBM PC compatible
;> OPERATING SYSTEM: PC-DOS/MS-DOS
;> SOFTWARE: PatentIn Release #1.0, Version #1.30
;> CURRENT APPLICATION DATA:
;> APPLICATION NUMBER: US/08/538,815
;> FILING DATE: Concurrently Herewith
;> CLASSIFICATION: 435
;> ATTORNEY/AGENT INFORMATION:
;> NAME: Highlander, Steven L.
;> REGISTRATION NUMBER: 37,642
;> REFERENCE/DOCKET NUMBER: UTSD:450
;> TELECOMMUNICATION INFORMATION:
;> TELEPHONE: (512) 418-3000
;> TELEFAX: (512) 474-7577
;> TELEX: N/A
;> INFORMATION FOR SEQ ID NO: 11:
;> SEQUENCE CHARACTERISTICS:
;> LENGTH: 4131 base pairs
;> TYPE: nucleic acid
;> STRANDEDNESS: single
;> TOPOLOGY: linear
;> MOLECULE TYPE: other nucleic acid
;> DESCRIPTION: /desc = "DNA"
US-08-538-815-11

Query Match 77.5%; Score 2751.2; DB 9; Length 4131;
Best Local Similarity 86.7%; Pred. No. 0;
Matches 3080; Conservative 0; Mismatches 463; Indels 11; Gaps 4;

Qy 1 ATGTCATGTTAGTGGCTCCTGCTCCCTAAAGTGGATGAACGGAACACGCTGGGGT 60
Db 56 ATGTCATGTTAGTGGCTCCTGCTCCCTAAAGTGGATGAACGGAACACGCTGGGGT 115
Qy 61 GAACGCAATGGCAGAACGCTGCGCGCGCTGCGCATCTGGGAGGCTGCTGCGACG 120
Db 116 GAACGCAATGGCAGAACGCTGCGCGCGCTGCGCATCTGGGAGGCTGCTGCGCG 172
Qy 121 CCCCGCTATATAGTGGCTCGGATGCGAGCCACCCAGCCACCCCTGCGGGGCC 180
Db 173 CCCCGCTACATAGTGGCTCAAGAAATGTGGAGCCACCCAGCCACCCCTGCGAGCTGC 232
Qy 181 CCTGGTCCCCCTGGCAGGATGAGCCCTTATCCGGAGGCGGCCAGGCAAGGGCAAG 240
Db 233 ACTGGTGGCTGGCAGGATGAGCCCTTATCCGGAGGCGGCCAGGCAAGGGCTG 292
Qy 241 CAGCTGGGGCTGCGGGAGTGGGCTTGGCTTCGAGGATACCGAGGTGACACACACAGCG 300
Db 293 GAGCTGGGGCTGCGGTGAGTGGCTTGGCTTTCGAGGATGAGGCTGAGGCTGAGGCTG 349
Qy 301 GCGGGAGCGGTGAGTGGGCGCCGACGCGGTGCGGAGGAGGCGGATGCTGCTGGCGC 360
Db 350 ATGGGACAGCTGAAGTGGCAGCCGACACATCGCTCAAGCGGCTGCTGCTGGCGAC 409
Qy 361 GCTTGGTGGAGGTGCTCCAGTCGAGGATGCTCCGTCGCGCAAGCTGGAGCGCTGTAC 420
Db 410 GCGTGGAGGAGGTGCTCCAGTCAAGCAGTTCGCTGCGGCAAGCTGGAGCGCTGTAC 469
Qy 421 CAGCGGTACTTTTCCAGATGAACACAGACAGCCCTGAGCGCTGCTGGTGGCGGTGCTGTG 480
Db 470 CAGCGGTACTTCTCCAGATGAACACAGACAGCCCTGAGCGCTGCTGCTGCTGCTG 529

Qy 481 CTGCTCACAGCGGTGCTGCTGGCTTTCCAAAGCCGACCCGCCGCCCTCAGCCCTGCTAT 540
Db 530 CTCCTCATGGCTGTACTGTTGACCTTCCACGCGCGCTGCCCTGCTCAGCCCTGCTAT 589
Qy 541 GTGGCACTGTTGGCTGTGCGCGCGCTGTTCTGGGGCTCATGGTGTGTGAACCG 600
Db 590 GTGGCCCTGCTGACTGCTGCGCTCGCTGCTTTTGTGGTACTCATGGTGTGTGAACCG 649
Qy 601 CATAGCTTCCGCCAGGACTCCATGTGGTGTGAGTAACGTGGTGTGCTGGGCTGCTGCG 660
Db 650 CATAGCTTCCGCCAGGACTCCATGTGGTGTGAGTGTGCTGGTGTGCTGGGCTCATCTAGCA 709
Qy 661 GCAGTCAGGTGCGGGGCGCTTCCAGCAGACGCGCGCAGCCCTCTGCGGGCTCTGCG 720
Db 710 GCGCTCAAGTGGGGGTGCGCTTGGCAGCAACCCAGCAGCCCTCAGCAGGCTTTGG 769
Qy 721 TGCCTGTGTTCTTTGTATACATGCATACAGCTCTCCGCCATCCCGATCGGGCTGCC 780
Db 770 TGCCTGTGTTCTTTGTATACATGCATACAGCTCTCCGCCATCCCGATCGGGCTGCC 829
Qy 781 GTCCTCAGCGGCTTGGCTCTCCACCTTGCATTGTGCTTTGGCTGGCACTTAACCGT 840
Db 830 GTGCTCAGTGGCTGGCTTTCACCTGCTATTTTGGCTGGCATCTCAACAAT 889
Qy 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTCTCTGTCACCAAC 900
Db 890 GGTGACCCCTTCTTGGAGCAGCTCGGTGCTTAACGTGGTGTCTCTCTGTCACCAAT 949
Qy 901 GTCATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGAG 960
Db 950 GCCATCGGTGTCTGCAGCAGCTACCCCGCTGAAGTGTCTCAGCGCCAGGCTTTTCAGAG 1009
Qy 961 ACCGCGAGTTACATCCAGCGCGCTCCACCTGCAGCATGAGAAATGCGCAGCAGGCGG 1020
Db 1010 ACCGCTGTTACATCCAGCGCGCTGCCTGCATGAGATGAGATGCGCAGCAGGAAACG 1069
Qy 1021 CTGCTGTGTCGGTATTGCCCGCAGCAGCTTGCATGAGATGAGAAAGAGATCAACACA 1080
Db 1070 CTGCTGTGTCGGTATTGCCCGCAGCAGCTTGCATGAGATGAGAAAGAGATCAACACA 1129
Qy 1081 AAAAAAGAGAC---ATGTTCCACAAGATCTACATACAGAGCATGACAATGTGACGATC 1137
Db 1130 AAAAAAGAGACATGATGTTCCACAAGATTTACATCCAGAGCATGACAATGTGACGATC 1189
Qy 1138 CTGTTTGCAGACATTGAGGGCTTCCACAGCTGGCATCCAGTGCATGCGCAGGAGCTG 1197
Db 1190 CTGTTTGCAGACATGAGGGCTTCCACAGCTGGCTCCAGTGCATGCGCAGGAACTG 1249
Qy 1198 GTCATGACCTGATGAGCTTTTGGCGCGTTCGACAGTGGCTGCGGAGAACTGCTGCG 1257
Db 1250 GTCATGACCTGATGAGCTTTTGGCGCGTTCGACAGTGGCTGCGGAGAACTGCTGCT 1309
Qy 1258 CTGAGGATCAAGATCTTGGGGAGCTGTTACTGCTGTCAGGGCTCCCGAGGCGCGG 1317
Db 1310 CTGAGGATCAAGATCTTGGAGACTGTTACTGCTGTCGGGGCTCCCGAGGCGCGG 1369
Qy 1318 GCCGACCATGCCCCACTGCTGTGAGATGGGGGTAGACATGATTGAGCGCATCTGCGTG 1377
Db 1370 GCAGACCATGCCACTGCTGTGAGATGGGGGTAGACATGATGAGGAGCCATCTGCGTG 1429
Qy 1378 GTAGTGAAGTGAAGTGAATGTGAACATGCGCGTGGGATCCACAGCGGGCGCGTG 1437
Db 1430 GTGGCTGAGGTGAAGGGGTGAATGTGAACATGCGCGTGGGATCCACAGGCGGCTGTA 1489
Qy 1438 CACTGCGCGCTTGGCTTGGGAAATGGCAGTTCGATGCTGCTCAATGATGTGAC 1497
Db 1490 CACTGCGGTGCTTGGCTTGGGAAATGGCAGTTCGATGCTGCTCAATGATGTGAC 1549
Qy 1498 CTGCGCAACCATGAGGAGGAGCGGGCTGCGCCCATCCACATCACTCGGCAACA 1557
Db 1550 CTGCGCAACCATGAGGAGGAGCGGGCTGCGCCCATCCACATCACTCGGCGCA 1609
Qy 1558 CTGAGTACCTGAACGGGGACTACAGTGGAGCGGCGGCTGTTGGCAAGCGCAACGCG 1617

Db 1610 CTGAGTACCTGAAAGGGGACTATGAGGTGAGCCAGCCGCTGGCGTGAGCGCAAGCGG 1669
QY 1618 TACCTCAAGGAGCAGCAGATTTGAGACTTTCTCATCTATCGGCGCAGCAGCAAGCGGAAA 1677
Db 1670 TACCTCAAGGAGCAGCAGATTTGAGACTTTCTCATCTATGAGGAGCAGCAGCAAGCGAAA 1729
QY 1678 GAGGAGAAAGCAGTCTGGGCAAGCTGAGCGGAGCTCGGCGCAACTCCATGGAAGGCGTG 1737
Db 1730 GAGGAGAAAGCAGTCTGGTCAAGCTGAGCGGAGCGGCGCAACTCCATGGAAGGAGTG 1789
QY 1738 ATGCGCGGATGGGTTCTGATGCTGCTTCTCCCGGAGCAGGAGCTCCAGGCGTTCCGC 1797
Db 1790 ATGCGCGGCTGGGTTCTGAGCGCTGCTTCTCCCGGAGCAGGAGCTCCAGGCAATCCGA 1849
QY 1798 CAGATGGGCAATGATTTCCAGCAAGACAAACCGGGGACCCCAAGATGCCCTGAACCCCT 1857
Db 1850 CAGATGGGCAATGATTTCCAGCAAGACAAACCGGGGACCCCAAGATGCCCTGAACCCCT 1909
QY 1858 GAGGATGAGTGGATGATTTCTGAGCGGTCGCCATGATGCCCGCAGCATTTGAGAAAG 1917
Db 1910 GAGGATGAGTGGATGATTTCTGAGCGGTCGCCATGATGCCCGCAGCATTTGAGAAAG 2029
QY 1918 CGGAGGAGCAGTGGCGCGGTTTCTGCTCAGCTTCCAGAGAGGATTTGAGAAAG 1977
Db 1970 CGTAAAGGAGCAGTGGCGCGGTTTCTGCTCAGCTTCCAGAGGAGGATTTGAGAAAG 2029
QY 1978 TACTCCGCGGAGTGGATTTCCCGGCTCGGAGCGCTTACGCTGCGCTGCTGCTGCTTC 2037
Db 2030 TATTACGGAAGTGGATTTCCCGGCTCGGAGCGCTTACGCTGCGCTGCTGCTGCTTC 2089
QY 2038 TGCTTATCTGCTTATCCAGCTTCTAATTTTCCACACATCCACCGCTGATGCTTGGGATT 2097
Db 2090 TGCTTATCTGCTTATCCAGCTTCTGATTTCCACACATCCACCGCTGATGCTTGGGATT 2149
QY 2098 TATGCGAGCAGTCTTCTGCTGCTTATCCAGCTGCTGATGCTGCTGCTGCTGCTGCT 2157
Db 2150 TATGCGGAGTCTTCTGCTGCTTATCCAGCTGCTGATGCTGCTGCTGCTGCTGCTGCT 2209
QY 2158 GGTCTCTGTTTCCCAAGGCGCTCAACGCTGCTGCGCGCAGCAATTTCCGCTCAGGGCA 2217
Db 2210 GGTCTCTTCTTCCCAAGGCGCTCAACGCTGCTGCGCGCAGCAATTTCCGCTCAGGGTG 2269
QY 2218 CATGAGCAGGAGTGGGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2277
Db 2270 CACAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2329
QY 2278 ATGTTACCTGTACACACACCCCATACGAGCTGCTGCGCGGAGTCTCAATTTAAACA 2337
Db 2330 ATGTTACCTGTACACACCCCATACGAGCTGCTGCGCGGAGTCTCAATTTAAACA 2389
QY 2338 CCTGCTGACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2397
Db 2390 CCGTCCGATGCTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2449
QY 2398 CCGTGTGAGGAGCAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2457
Db 2450 CCGTGTGAGGAGCAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2509
QY 2458 CTGCTGAGTCTCTTGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2517
Db 2510 CTGCTGAGTCTCTTGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2569
QY 2518 ATGATCTTTGCTTGGGCTCATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2577
Db 2570 ATGATCTTTGCTTGGGCTCATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2629
QY 2578 ATCTTTGACAACTATGACTTACTGCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2637
Db 2630 ATCTTTGACAACTATGACTTACTGCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2689
QY 2638 TTTGATGGCTGGACTCTGAGCTGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2697

Db 2690 TTGATGGGTGAGTCTCCAGCGCTAGGAGGCTAGGAGGCTCAAAATACATGACCCCTGTG 2749
QY 2698 ATTCTGCTGCTGTTGGCTGGCGCTGATCTGATGCTCAGCAGGTTGAATGACATGCC 2757
Db 2750 ATTCTGCTGCTGTTGGCTGGCGCTGATCTACACCAACAGGTTGAATCTACCGCC 2809
QY 2758 CGCTTAACTTCTCTGGAACATACAGGCAACAGGGAAGAGGAGATGGAGGAGCTA 2817
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QY 2818 CAGGCAATACACCGGAGGCTGCTGATTAACATTTGCGCAAGGAGCTGGCGGCCACTTC 2877
Db 2870 CAGGCTTACACCGGAGGCTGCTGATTAACATTTGCGCAAGGAGCTGGCTGCCACTTC 2929
QY 2878 CTGCGCGGAGGCGGCAATGATGAACTTACTATCAGTCTGCTGAGTGTGCTGCTGCT 2937
Db 2930 CTGCGCGGAGGCGGCAATGATGAACTTACTATCAGTCTGCTGAGTGTGCTGCTGCT 2989
QY 2938 ATGTTTCCCTCCATTTGCCAATTTCTCTGAGTTTCTATGAGCTGGAGGCAACAAATGAG 2997
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QY 2998 GGTCCCGAGTCTGCGGCTGCTCAACAGATCATGCTGCTGATGATGATGATGATGAT 3057
Db 3050 GGTCCCGAGTCTGCGGCTGCTCAACAGATCATGCTGCTGATGATGATGATGATGAT 3109
QY 3058 GAGGAGCGGTTCCGCGAGCTGGAAGATCAAGACGATTTGATGAGCTACATGCTGCTGCT 3117
Db 3110 GAGGAGCGGTTCCGCGAGCTGGAAGATCAAGACCATCGTAGCTTACATGCTGCTGCT 3169
QY 3118 TCAGGCTGAAAGCGGAGCAGCTAGGATCAGGTGGCGGCTCCACATCATGCTGCTGCTGCT 3177
Db 3170 TCAGGCTGAAAGCGGAGCAGCTAGGATCAGGTGGCGGCTCCACATCATGCTGCTGCT 3229
QY 3178 GACTTACCGCTGCGGCTGATGGAGCAGATGAAGCAGATCAATGAGCTCTCTTCAACAAT 3237
Db 3230 GACTTACCGCTGCGGCTGATGGAGCAGATGAAGCAGATCAATGAGCTCTCTTCAACAAT 3289
QY 3238 TTCAGATGAAGATTTGGCTGAAATGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3297
Db 3290 TTCAGATGAAGATTTGGCTGAAATGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3349
QY 3298 AAGCAGCAGTATGATCTGCGGAGCAGATGAATGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 3357
Db 3350 AAGCAGCAGTATGATCTGCGGAGCAGATGAATGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 3409
QY 3358 GGTCTCCCGAGCAGTCTGAGGCTGAGCAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3417
Db 3410 GGTCTCCCGAGCAGTCTGAGGCTGAGCAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3469
QY 3418 TACAGCTGAGTCTGAGGCTGAGCAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 3477
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QY 3478 TTCTTCAATGGGCGGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3535
Db 3530 TTCTTCAATGGGCGGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3589
QY 3536 CCAAGGTGGGCACT 3549
Db 3590 CCAAGGTGGGCACT 3603

RESULT 11

US-09-491-404-837
; Sequence 837, Application US/09491404
; GENERAL INFORMATION:
; APPLICANT: Tang, Yuanhua T.
; APPLICANT: Tillinghast, John
; APPLICANT: Sinku, Ankura
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Contigs Obtained

; TITLE OF INVENTION: From Various Libraries

; FILE REFERENCE: 785

; CURRENT APPLICATION NUMBER: US/09/491.404

; CURRENT FILING DATE: 2000-01-27

; NUMBER OF SEQ ID NOS: 3796

; SOFTWARE: pLSP_genes version 1.0

; SEQ ID NO 837

; LENGTH: 5353

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: sig_peptide

; LOCATION: (1669)...(1804)

; OTHER INFORMATION: this location contains the signal peptide sequence,

; OTHER INFORMATION: MLGIYASIFLLLLITVLICAVYSCGLSPKALQRLSRIVSRRAH, Run with SignalP

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (3)...(2946)

; OTHER INFORMATION: similar to gi2887419 in the genepept database release 114,

; OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters

US-09-491-404-837

Query Match 75.98; Score 2693.8; DB 18; Length 5353;
Best Local Similarity 93.18; Pred. No. 0;
Matches 2935; Conservative 1; Mismatches 33; Indels 182; Gaps 4;

Qy 422 AGCGGTACTTTTCCAGATGAACAGACGACGCTGCTGGTGGCGTGTGTTGTC 481

Db 1 AGCGGTACTTCTCCAGATGAACAGACGACGCTGCTGATGGCGGTGTGTTGTC 60

Qy 482 TGCTCACAGCGGTGCTGCTGGCTTTCCAAAGCCGACCGCCGCCCTCAGCCTGCCTATG 541

Db 61 TGCTCACAGCGGTGCTGCTGGCTTTCCACGCGCAGCCGCCCTCAGCCTGCCTATG 120

Qy 542 TGGCACTTGGCGCTGTCGCCCGCCCTGTTCTGGGGCTCATGGTGTGTAAACCGCG 601

Db 121 TGGCACTTGGCGCTGTCGCCCGCCCTGTTCTGGGGCTCATGGTGTGTAAACCGCG 180

Qy 602 ATAGCTCCGCGAGGACTCCATGTGGGTGTGAGTAAGCTGTGTGGGCATCTCTGGCGG 661

Db 181 ATAGCTCCGCGAGGACTCCATGTGGGTGTGAGTAAGCTGTGTGGGCATCTCTGGCGG 240

Qy 662 CAGTGCAGGTGCGGGCGCTTTCCGAGCAGACCGCGCAGCCCTCTCGGGGCTCTGGT 721

Db 241 CAGTGCAGGTGCGGGCGCTCTCGCAGCAGACCGCGCAGCCCTCTCGGGGCTCTGGT 300

Qy 722 GCCCTGTCTTGTATACATGCAATACAGCTCTCCCATCGCATGCGGGCTGCGG 781

Db 301 GCCCTGTCTTGTATACATGCGCTACAGCTCTCCCATCGCATGCGGGCTGCGG 360

Qy 782 TCCTCAGCGGCTGGCGCTCTCCACCTTGCAATTTGATCTTGGCCTGGCAACTTAACCGTG 841

Db 361 TCCTCAGCGGCTGGCGCTCTCCACCTTGCAATTTGATCTTGGCCTGGCAACTTAACCGTG 420

Qy 842 GTGATGCCCTTCCCTC-TGGAAGCAGCTCGGTGCCAATGTGCTGTCTCTGCACCAAC 900

Db 421 GTGATGCCCTTCCCTCTTGGAGGAGCTCGGTSCCAATGTGCTGTCTCTGCACCAAC 480

Qy 901 GTCATTAGCATCTGCACACACTATCCACGAGGTGTCTCAGCGCCAGCCCTTTCAGAG 960

Db 481 GTCATTAGCATCTGCACACACTATCCACGAGGTGTCTCAGCGCCAGCCCTTTCAGAG 540

Qy 961 ACCCGCAGTTACATCCAGGCGCGGCTCCACCTGCAAGCATGAGAATCGGCAGCAGGAGCGG 1020

Db 541 ACCCGCGTTACATCCAGGCGCGGCTCCACCTGCAAGCATGAGAATCGGCAGCAGGAGCGG 600

Qy 1021 CTGCTGCTGTGGTATTCGCCAGCAGCTTGCCATGGAGATGAAGAAGACATCAACACA 1080

Db 601 CTGCTGCTGTGGTATTCGCCAGCAGCTTGCCATGGAGATGAAGAAGACATCAACACA 660

Qy 1081 AAAAAAGAGAC---ATGTTCCACAGATCTACATACAGAGCATGACAATGTACGATC 1137

Db 661 AAAAAAGAGACATGATGTTCACAAAGATCTACATACAGAGCATGACAATGTACGATC 720

Qy 1138 CTGTTTGCAGACATTGAGGCTTTCACAGCCTGGCATCCAGTGCACATGCGCAGGAGCTG 1197

Db 721 CTGTTTGCAGACATTGAGGCTTTCACAGCCTGGCATCCAGTGCACATGCGCAGGAGCTG 780

Qy 1198 GTCATGACCCCTGAATGAGCTCTTTGCCGGTTTGACAAGCTGGGTGCGGAGAAATACATGCG 1257

Db 781 GTCATGACCCCTGAATGAGCTCTTTGCCGGTTTGACAAGCTGGGTGCGGAGAAATACATGCG 840

Qy 1258 CTGAGGATCAAGATCTTGGGGAGCTGTTACTACTGTGTGTCAGGGCTCCCGAGGCCCGG 1317

Db 841 CTGAGGATCAAGATCTTGGGGAGCTGTTACTACTGTGTGTCAGGGCTCCCGAGGCCCGG 900

Qy 1318 GCCGACCATGCCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTAGGCCATCTCGCTG 1377

Db 901 GCCGACCATGCCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTAGGCCATCTCGCTG 960

Qy 1378 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGATCCACAGCGGGCGCTG 1437

Db 961 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGATCCACAGCGGGCGCTG 1020

Qy 1438 CACTGCGCGCTCCTTGGCTTGGGAAATGCGAGTTCGATGTGTGTCCTCAATGATGTGACC 1497

Db 1021 CACTGCGCGCTCCTTGGCTTGGGAAATGCGAGTTCGATGTGTGTCCTCAATGATGTGACC 1080

Qy 1498 CTGCCCCAACCATGGAAGCAGGAGCGCGCTGGCCGCATCCACATCACTCGGGCAACA 1557

Db 1081 CTGCCCCAACCATGGAAGCAGGAGCGCGCTGGCCGCATCCACATCACTCGGGCAACA 1140

Qy 1558 CTGCACTACCTGAACGGGGACTAGCAAGTGAAGCAGCGCTGTGGCAAGCGCAACCGG 1617

Db 1141 CTGCACTACCTGAACGGGGACTAGCAAGTGAAGCAGCGCTGTGGCAAGCGCAACCGG 1200

Qy 1618 TACCTCAAGGAGCAGCATTGAGACTTTCTCTCATCTCTGGGCGCCAGCAGAAACGGGAA 1677

Db 1201 TACCTCAAGGAGCAGCATTGAGACTTTCTCTCATCTCTGGGCGCCAGCAGAAACGGGAA 1260

Qy 1678 GAGGAGAAAGCATGCTGGCCAAAGTGCAGCGGACTCGGGGCCAATCCATGAGAGGGGTG 1737

Db 1261 GAGGAGAAAGCATGCTGGCCAAAGTGCAGCGGACTCGGGGCCAATCCATGAGAGGGGTG 1320

Qy 1738 ATGCGCGATGGTTCCTGTGATGCTGCTCTCCGGGACCAAGGACTCCAAGGCTTCGCG 1797

Db 1321 ATGCGCGCTGGTTCCTGTGATGCTGCTCTCCGGGACCAAGGACTCCAAGGCTTCGCG 1380

Qy 1798 CAGATGGCATTTGATGATTCCAGCAACAGCAACCGGGGCCACCAAGATGCCCTGAACCT 1857

Db 1381 CAGATGGCATTTGATGATTCCAGCAACAGCAACCGGGGCCACCAAGATGCCCTGAACCT 1440

Qy 1858 GAGGATGAGGTGGATGAGTTCTGAGCGGTGCCATTCGATGCCCGCAGCATTTGATCAGGTG 1917

Db 1441 GAGGATGAGGTGGATGAGTTCTGAGCGGTGCCATTCGATGCCCGCAGCATTTGATCAGGTG 1500

Qy 1918 CGGAAGGACCATGTCGCCCGGTTTGTCTCACTTCCAGAGAGAGGATTTTGAAGAAG 1977

Db 1501 CGGAAGGACCATGTCGCCCGGTTTGTCTCACTTCCAGAGAGAGGATTTTGAAGAAG 1560

Qy 1978 TACTCCCGAAGGTGGATCCCGGTTTCGAGCCTACGTTGCTGTGCGCTGTGTCCTTC 2037

Db 1561 TACTCCCGAAGGTGGATCCCGGTTTCGAGCCTACGTTGCTGTGCGCTGTGTCCTTC 1620

Qy 2038 TGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCTGATGCTTGGGAT 2097

Db 1621 TGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCTGATGCTTGGGAT 1680

Qy 2098 TATGCCAGCATCTTCTGCTGCTGCTAATACCGGTGCTGATGTGTGTGTACTCTCTGT 2157

Db 1681 TATGCCAGCATCTTCTGCTGCTGCTAATACCGGTGCTGATGTGTGTGTACTCTCTGT 1740

Qy 2158 GGTTCCTGTTCCCTTAAGCCCTGCAAGCTGTCTCCCGCAGCATGTCGGCTCACGGGCA 2217

Db 1741 GGTTCCTGTTCCCTTAAGCCCTGCAAGCTGTCTCCCGCAGCATGTCGGCTCACGGGCA 1800

QY 2218 CATAGCACCAGTTGGCATCTTTTCCGTCCTGCTGTGTGTTTACTTCTGGCAATGGCAAC 2277
Db 1801 CATAGCACCAGTTGGCATCTTTTCCGTCCTGCTGTGTGTTTACTTCTGGCAATGGCAAC 1860
QY 2278 ATGTTCACTTGTAAACACACCCCATACGGAGCTGTGCAGGCCCGATGCTCAATTTAACA 2337
Db 1861 ATGTAC----- 1866
QY 2338 CCTGCTGACATCACTGCTGCGACCTGCAGAGCTCAATTACTCTCTGGGCTGGATGCT 2397
Db 1867 ----- 1866
QY 2398 CCCCTGTGTAGGGCACCATGCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATG 2457
Db 1867 -----TTTCATCGGGAACATG 1881
QY 2458 CTGCTGAGTCTCTTTGGCAGCTCTGTCTCTCGACATCAGCAGCATCGGGAAGTTGGCC 2517
Db 1882 CTGCTGAGTCTCTTTGGCAGCTCTGTCTCTCGACATCAGCAGCATCGGGAAGTTGGCC 1941
QY 2518 ATGATCTTTGTCTTTGGGCTCATCTATTGTTGGTGTCTTCTGCTGGGTGCCCCAGCCGCC 2577
Db 1942 ATGATCTTTGTCTTTGGGCTCATCTATTGTTGGTGTCTTCTGCTGGGTGCCCCAGCCGCC 2001
QY 2578 ATCTTTGACAACATGACCTACTGCTTTGGGCTCCATGCTTGGCTTCTTCCAAATGAGACC 2637
Db 2002 ATCTTTGACAACATGACCTACTGCTTTGGGCTCCATGCTTGGCTTCTTCCAAATGAGACC 2061
QY 2638 TTTGATGGCTGGACTGTCAGCTGTCAGGGAGGTGGCCCTCAATATATGACCCCTGTG 2697
Db 2062 TTTGATGGCTGGACTGTCAGCTGTCAGGGAGGTGGCCCTCAATATATGACCCCTGTG 2121
QY 2698 ATTCGTGTGTGTTGGGCTGGCGCTGTATCTGTCATGCTCAGCAGGTGGATGACCTGCC 2757
Db 2122 ATTCGTGTGTGTTGGGCTGGCGCTGTATCTGTCATGCTCAGCAGGTGGATGACCTGCC 2181
QY 2758 CGCTAAACTTCTCTGGAACACTCAGCAACACAGGGGAAAGAGAGATGGAGAGCTA 2817
Db 2182 CGCTAGACTTCTCTGGAACACTCAGCAACACAGGGGAGAGAGATGGAGAGCTA 2241
QY 2818 CAGGCATACACCGAGGCTGCTCATATAACATTCTGCCAAGGACGTGGGGCCCACTTC 2877
Db 2242 CAGGCATACACCGAGGCTGCTCATATAACATTCTGCCAAGGACGTGGGGCCCACTTC 2301
QY 2878 CTGGCCGGGAGCGCGCAATGATGAATCTACTATCAGTCGTGTGATGTGTGGCTGTT 2937
Db 2302 CTGGCCGGGAGCGCGCAATGATGAATCTACTATCAGTCGTGTGATGTGTGGCTGTT 2361
QY 2938 ATGTTTGCCTCCATTGGCAACTTCTCTGAGTTCTATCTGGAGCTGGAGGCAACAATGAG 2997
Db 2362 ATGTTTGCCTCCATTGGCAACTTCTCTGAGTTCTATCTGGAGCTGGAGGCAACAATGAG 2421
QY 2998 GGTGCCGAGTGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATG----- 3046
Db 2422 GGTGTCGAGTGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGGTCTCCTTG 2481
QY 3047 -----AGATTATACGCGAGGAGCGGTTCCGGCAGCTGGAAGATGCAAGACGATGG 3098
Db 2482 TGTGTTTCAGATTATCAGCGAGGAGCGGTTCCGGCAGCTGGAAGATGCAAGACGATGG 2541
QY 3099 TAGCACCTACATGCTGCTCAGGGCTGAACGCCAGCACCTACCATCAGTGGGCCGCTC 3158
Db 2542 TAGCACCTACATGCTGCTCAGGGCTGAACGCCAGCACCTACCATCAGTGGGCCGCTC 2601
QY 3159 CCACATCACTGCCCTGGCTGACTACGCCATCGCGCTCATGGAGCAGATGAAGACACATCAA 3218
Db 2602 CCACATCACTGCCCTGGCTGACTACGCCATCGCGCTCATGGAGCAGATGAAGACACATCAA 2661
QY 3219 TGAGCACTCCTTCAACAATTTCCAGATGAAGATTTGGCTGAACATGGGCCCGCAGTCGTGGC 3278
Db 2662 TGAGCACTCCTTCAACAATTTCCAGATGAAGATTTGGCTGAACATGGGCCCGCAGTCGTGGC 2721
QY 3279 AGGTGTATCGGGGCTCGGAAGCCACAGATGACATCTGGGGGAACACAGTGAATGTCTC 3338

Db 2722 AGGTGTATCGGGGCTCGGAAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTC 2781
QY 3339 TAGTCGTATGACAGCAGCGGGGTCCCGACCGAATCCAGTGACCGACCTGTACCA 3398
Db 2782 TAGTCGTATGACAGCAGCGGGGTCCCGACCGAATCCAGTGACCGACCTGTACCA 2841
QY 3399 GGTTCAGCTGCCAAGGGCTACCACTGAGTGTGCGAGGGGTGGTCAAGGTGAAGGCCAA 3458
Db 2842 GGTTCAGCTGCCAAGGGCTACCACTGAGTGTGCGAGGGGTGGTCAAGGTGAAGGCCAA 2901
QY 3459 GGGGGAGATGACCACTTACTTCTCAATGGGGGCCCGACAGCAGTTAACAGGGCCCGACAC 3518
Db 2902 GGGGGAGATGACCACTTACTTCTCAATGGGGGCCCGACAGCAGTTAACAGGGCCCGACAC 2961
QY 3519 AAATTACAGCTGAAGGGACCAAGGTGGGCATT 3549
Db 2962 AAATTACAGCTGAAGGGACCAAGGTGGGCATT 2992

RESULT 12
US-09-922-279-837
; Sequence 837, Application US/09922279
; GENERAL INFORMATION:
; APPLICANT: Tang, Yuanhua T.
; APPLICANT: Tillinghast, John
; APPLICANT: Sinku, Ankura
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: From Various Libraries
; CURRENT APPLICATION NUMBER: US/09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 3796
; SOFTWARE: pt_sp_genes Version 1.0
; SEQ ID NO 837
; LENGTH: 5353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1569)...(1804)
; OTHER INFORMATION: this location contains the signal peptide sequence,
; OTHER INFORMATION: MLGIYASIFLLLLITVLICAVYSGSLFPPKALQRLSRIVSRRAH, Run with Signal
; NAME/KEY: misc_feature
; LOCATION: (3)...(2946)
; OTHER INFORMATION: similar to g12887419 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
US-09-922-279-837

Query Match 75.9%; Score 2693.8; DB 34; Length 5353;
Best Local Similarity 93.1%; Pred.No. 0;
Matches 2935; Conservative 1; Mismatches 33; Indels 182; Caps 4;

QY 422 AGCGGTACTTTTCCAGATGAACACAGACGACCTGCTGGTGGCGGTGTGGTGC 481
Db 1 AGCGGTACTTTTCCAGATGAACACAGACGACCTGCTGATGATGCGGTGTGGTGC 60
QY 482 TGCTACAGCGGTGCTGCTGGCTTTTCCAAAGCCGACCGCCCGCTCAGCTGCCTATG 541
Db 61 TGCTACAGCGGTGCTGCTGGCTTTTCCAAAGCCGACCGCCCGCTCAGCTGCCTATG 120
QY 542 TGGCACTGTTGGCTGTGCGCGCCCTGTTCGTGGGCTCATGCTGTGTGAACCGGC 601
Db 121 TGGCACTGTTGGCTGTGCGCGCCCTGTTCGTGGGCTCATGCTGTGTGAACCGGC 180
QY 602 ATAGCTTCCCGCCAGGACTCCATGTGGGTGTGAGTGAACAGTGGTGGTGGCATCTCTGGCG 661
Db 181 ATAGCTTCCCGCCAGGACTCCATGTGGGTGTGAGTGAACAGTGGTGGTGGCATCTCTGGCG 240

QY 662 CAGTCAGGTCGGGGCGCTTTTCAGCAGAGACCCGCGCAGGCCCTCTCGGGGCTCTCGGT 721
Db 241 CAGTCAGGTCGGGGCGCTCTCGCAGCAGACCCGCGCAGGCCCTCTCGGGGCTCTCGGT 300
QY 722 GCCCTGTCTTTGTATACATCGCATACAGCTCCTCCCATCCGCGATCGGGGTCGGG 781
Db 301 GCCCTGTCTTTGTATACATCGCATACAGCTCCTCCCATCCGCGATCGGGGTCGGG 360
QY 782 TCCTCAGGGGCTGGGCTCTCCACCTTGTCATTTGCTGCTGGCCTGGCAACTTAACCGTG 841
Db 361 TCCTCAGGGGCTGGGCTCTCCACCTTGTCATTTGCTGCTGGCCTGGCAACTTAACCGTG 420
QY 842 GTGATGCTTCCCTC-TGGAAGCAGCTCGGTGCCAATGTGCTGTCTTCTCTGCAACAC 900
Db 421 GTGATGCTTCCCTC-TGGAAGCAGCTCGGTGCCAATGTGCTGTCTTCTCTGCAACAC 480
QY 901 GTCAATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCCTTTCAGGAG 960
Db 481 GTCAATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCCTTTCAGGAG 540
QY 961 ACCCGCAGTTACATCCAGGCGCGGCTCCACCTGCAAGCATGAGAATCGGCAGCAGGCGG 1020
Db 541 ACCCGCGGTTACATCCAGGCGCGGCTCCACCTGCAAGCATGAGAATCGGCAGCAGGCGG 600
QY 1021 CTGCTGCTGTGGGTATGCCCCAGACAGCTGTCATGAGATGAAAGACATCAACACA 1080
Db 601 CTGCTGCTGTGGGTATGCCCCAGACAGCTGTCATGAGATGAAAGACATCAACACA 660
QY 1081 AAAAAAGAGAC- --ATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAAGCATC 1137
Db 661 AAAAAAGAGACATGTTTCCACAAGATCTACATACAGAAGCATGACAATGTCAAGCATC 720
QY 1138 CTGTTTTCAGACATTTAGGGGCTTACCAGCCTGGCATCCAGTGCACTGCGCAGGAGCTG 1197
Db 721 CTGTTTTCAGACATTTAGGGGCTTACCAGCCTGGCATCCAGTGCACTGCGCAGGAGCTG 780
QY 1198 GTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAGCTGGCTGCGGAGAAATCACTGC 1257
Db 781 GTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAGCTGGCTGCGGAGAAATCACTGC 840
QY 1258 CTGAGGATCAGATCTTGGGGGACTTACTACTGTGTGTCAGGGCTGCCGAGGCCCGG 1317
Db 841 CTGAGGATCAGATCTTGGGGGACTTACTACTGTGTGTCAGGGCTGCCGAGGCCCGG 900
QY 1318 GCCGACCATGCCACTGCTGTGGAGATGGGGGTAGACATGATGAGGCCATCTCGCTG 1377
Db 901 GCCGACCATGCCACTGCTGTGGAGATGGGGGTAGACATGATGAGGCCATCTCGCTG 960
QY 1378 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCCGTGGGCATCCAGCGGGGCGGTG 1437
Db 961 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCCGTGGGCATCCAGCGGGGCGGTG 1020
QY 1438 CACTCGGCGCTCTTGGCTTGGGAAATGGCAATGTCGATGTGTGTCTCAATCATGTGACC 1497
Db 1021 CACTCGGCGCTCTTGGCTTGGGAAATGGCAATGTCGATGTGTGTCTCAATCATGTGACC 1080
QY 1498 CTGGCCAAACCATGGAAGCAGGAGCGGGGCTGGCGGATCCACATCACTCGGGCAACA 1557
Db 1081 CTGGCCAAACCATGGAAGCAGGAGCGGGGCTGGCGGATCCACATCACTCGGGCAACA 1140
QY 1558 CTGCAGTACCTGAACGGGACTACGAATGGAGCGAGCGCGGTGGGCAAGCGCAACGGG 1617
Db 1141 CTGCAGTACCTGAACGGGACTACGAATGGAGCGAGCGCGGTGGGCAAGCGCAACGGG 1200
QY 1618 TACCTCAAGGAGCAGCATTCAGACTTTTCCTCATCTTGGGCGCCAGCAGAAACGGAAA 1677
Db 1201 TACCTCAAGGAGCAGCATTCAGACTTTTCCTCATCTTGGGCGCCAGCAGAAACGGAAA 1260
QY 1678 GAGGAAAGAGGACTGTGGCCAAAGTGCAGCGGACTTCGGGCCAACTTCCATGGAAGGGGTG 1737
Db 1261 GAGGAAAGAGGACTGTGGCCAAAGTGCAGCGGACTTCGGGCCAACTTCCATGGAAGGGGTG 1320
QY 1738 ATGCCGCGATGGGTTCTCTGATCGCTTCTCCCGGACCAAGACTTCCAAGGCCCTTCGCG 1797

Db 1321 ATGCCGCGTGGGTTCTCTGATCGTGCCTTCTCCCGGACCAAGGACTTCCAAGGCCCTTCGCG 1380
QY 1798 CAGATGGGCATTTGATATCCAGCAAAAGACACACCGGGGACCCCAAGATGCCCTGAAACCT 1857
Db 1381 CAGATGGGCATTTGATATCCAGCAAAAGACACACCGGGGACCCCAAGATGCCCTGAAACCT 1440
QY 1858 GAGGATGAGGTGGATGAGTTCTGAGCGGTCATCTGATGCTGCGCCGACGATTCATCAGCTG 1917
Db 1441 GAGGATGAGGTGGATGAGTTCTGAGCGGTCATCTGATGCTGCGCCGACGATTCATCAGCTG 1500
QY 1918 CGAAGGACCATGTCGCGCGGTTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1977
Db 1501 CGAAGGACCATGTCGCGCGGTTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1978 TACTCCCGGAGGTCGATCCCGCTTCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2037
Db 1561 TACTCCCGGAGGTCGATCCCGCTTCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 2038 TGCTTCATCTGCTTCATCCAGCTTCTAAATTTTCCACACACTCCACCTGATGCTTGGGAT 2097
Db 1621 TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCACACACTCCACCTGATGCTTGGGATC 1680
QY 2098 TATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2157
Db 1681 TATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
QY 2158 GGTTCCTGTTCCCTTAAGGCGCTGCAAGCTGCTGCCGACGATTCGCGTCACGGGCA 2217
Db 1741 GGTTCCTGTTCCCTTAAGGCGCTGCAAGCTGCTGCCGACGATTCGCGTCACGGGCA 1800
QY 2218 CATAGCAGCGAGTTGGCATCTTTTCCGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2277
Db 1801 CATAGCAGCGAGTTGGCATCTTTTCCGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
QY 2278 ATGTTACCTGTAAACACACACCCCATACGGAGCTGTGACGCCGAGTGTGAATTTAACA 2337
Db 1861 ATGTAC----- 1866
QY 2338 CCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCAATTAATCTCTGCGGCTGGATGCT 2397
Db 1867----- 1866
QY 2398 CCCCTGTGTGAGGGACCATGCCACCTGCAGCTTTCTGAGGTGTCCATCGGAAACATG 2457
Db 1867-----TTCATCGGAAACATG 1881
QY 2458 CTGCTGAGTCTTTCGCGAGCTGCTCTCTTCCTGACATCAGCAGCATCGGGAAGTTGGCC 2517
Db 1882 CTGCTGAGTCTTTCGCGAGCTGCTCTCTTCCTGACATCAGCAGCATCGGGAAGTTGGCC 1941
QY 2518 ATGATCTTTGCTTGGGCTCATCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2577
Db 1942 ATGATCTTTGCTTGGGCTCATCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2001
QY 2578 ATCTTTTGACAACTATGACCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2637
Db 2002 ATCTTTTGACAACTATGACCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2061
QY 2638 TTTGATGGGCTGGACTGTCACCTGTCAGGGAGGTTGGCCCTCAAAATATATGACCCCTGTC 2697
Db 2062 TTTGATGGGCTGGACTGTCACCTGTCAGGGAGGTTGGCCCTCAAAATATATGACCCCTGTC 2121
QY 2698 ATTCTGCTGCTTTTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2757
Db 2122 ATTCTGCTGCTTTTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2181
QY 2758 CGCCTAAACTTCTCTGGAACATACAGGCAACAGGGGAAAAAGAGAGATGAGGAGCTA 2817
Db 2182 CGCCTAGACTTCTCTGGAACATACAGGCAACAGGGGAGAGAGATGAGGAGCTA 2241
QY 2818 CAGGATACACCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2877

Db 2242 CAGGCATACAAACGAGGAGCTGCTGCATAACATCTGCCAAGAGGAGCTGGGGCCCACTTC 2301
Qy 2878 CTGCCCCGGGAGCCGCAATGATGAATCTACTATCAGTCTGAGTGTGAGTGTGCTGTT 2937
Db 2302 CTGCCCCGGGAGCCGCAATGATGAATCTACTATCAGTCTGAGTGTGAGTGTGCTGTT 2361
Qy 2938 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCATGTGGAGCTGGAGGCAACAATGAG 2997
Db 2362 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCATGTGGAGCTGGAGGCAACAATGAG 2421
Qy 2998 GGTCCGAGTCCCTGGCGCTCTCAACGAGATCATGCTGACTTTGATG----- 3046
Db 2422 GGTCTGAGTCCCTGGCGCTCTCAACGAGATCATGCTGACTTTGATGAGGTCTCCTTG 2481
Qy 3047 -----AGATTATCAGCAGGAGGCGTTCGCGCAGCTGGAAGATCAAGAGGATTGG 3098
Db 2482 TGTGTTTCAGATTATCAGCAGGAGGCGTTCGCGCAGCTGGAAGATCAAGAGGATTGG 2541
Qy 3099 TAGCACCTTACATGCTGCTCAGGCTGAAGCCAGCACCTTACGATCAGTGGGCCGCTC 3158
Db 2542 TAGCACCTTACATGCTGCTCAGGCTGAAGCCAGCACCTTACGATCAGTGGGCCGCTC 2601
Qy 3159 CCACATCACTGCCCTGGCTGACTAGCCATCGGCTCATGGAGCAGATGAAGCACATCAA 3218
Db 2602 CCACATCACTGCCCTGGCTGACTAGCCATCGGCTCATGGAGCAGATGAAGCACATCAA 2661
Qy 3219 TGAGCACTCTTCAACAAATTTCCAGATGAAGATTGGGCTGAACATGGGCCCGAGTCGTGGC 3278
Db 2662 TGAGCACTCTTCAACAAATTTCCAGATGAAGATTGGGCTGAACATGGGCCCGAGTCGTGGC 2721
Qy 3279 AGGTGTCATCGGGCTCGGAAGCCACAGTATGACATCTGGGGGAACACAGTGAATGCTC 3338
Db 2722 AGGTGTCATCGGGCTCGGAAGCCACAGTATGACATCTGGGGGAACACAGTGAATGCTC 2781
Qy 3339 TAGTCTGATGACAGCAGGGGGTCCCGACCGAATCCAGTGACCGGACCTGTACCA 3398
Db 2782 TAGTCTGATGACAGCAGGGGGTCCCGACCGAATCCAGTGACCGGACCTGTACCA 2841
Qy 3399 GGTTCCTAGTCCCAAGGGCTACCAAGCTGGAGTGTGAGGGGTGCTCAAGTGAAGGCA 3458
Db 2842 GGTTCCTAGTCCCAAGGGCTACCAAGCTGGAGTGTGAGGGGTGCTCAAGTGAAGGCA 2901
Qy 3459 GGGGAGATGACCACTTCTTCTCAATGGGGGCCCCAGCAGTTAAAGGGCCCCAGGCCAC 3518
Db 2902 GGGGAGATGACCACTTCTTCTCAATGGGGGCCCCAGCAGTTAAAGGGCCCCAGGCCAC 2961
Qy 3519 AAATTTCAGTCAAGGACCAAGGTGGCACT 3549
Db 2962 AAATTTCAGTCAAGGACCAAGGTGGCACT 2992

RESULT 13
US-09-922-279A-837
; Sequence 837, Application US/09922279A
; GENERAL INFORMATION:
; APPLICANT: Tang, Yuanhua T.
; APPLICANT: Tillinghast, John
; APPLICANT: Sinku, Ankura
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 785
; CURRENT APPLICATION NUMBER: US/09/922,279A
; PRIOR FILING DATE: 2001-08-03
; PRIOR FILING DATE: 2000-01-25
; SOFTWARE: pt_sp_genes Version 1.0
; SEQ ID NO 837
; LENGTH: 5353
; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1669)...(1804)
; OTHER INFORMATION: this location contains the signal peptide sequence,
; OTHER INFORMATION: MLGIYASIFLLLLITVLICAVYSCGSLFPKALQLRSRIVSRRAH, Run with Signal
; NAME/KEY: misc_feature
; LOCATION: (3)...(2946)
; OTHER INFORMATION: similar to gi2887419 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
US-09-922-279A-837

Query Match 75.9%; Score 2693.8; DB 34; Length 5353;
Best Local Similarity 93.1%; Pred. No. 0;
Matches 2935; Conservative 1; Mismatches 33; Indels 182; Gaps 4;

Qy 422 AGCGGTACTTTTCCAGATGAACCCAGACGACCTGCTGCTGCGGTGCTGGTGC 481
Db 1 AGCGGTACTTTTCCAGATGAACCCAGACGACCTGCTGCTGCGGTGCTGGTGC 60
Qy 482 TGCTCAGACGGGTGCTGCTGCTTTTCCAAAGCCGACCCGCCCTCAGCCTGCCTATG 541
Db 61 TGCTCAGACGGGTGCTGCTGCTTTTCCAAAGCCGACCCGCCCTCAGCCTGCCTATG 120
Qy 542 TGGCACTGTTGGCTGTGCGGCCCTGTTCGTGGGGCTCATGGTGTGTAAACCGGC 601
Db 121 TGGCACTGTTGGCTGTGCGGCCCTGTTCGTGGGGCTCATGGTGTGTAAACCGGC 180
Qy 602 ATAGCTTCGCGCAGGACTTCCATGTGGTGTGTAGTAACAGTGTGCTGGCATCCTGGCGG 661
Db 181 ATAGCTTCGCGCAGGACTTCCATGTGGTGTGTAGTAACAGTGTGCTGGCATCCTGGCGG 240
Qy 662 CAGTGCAGGTGCGGGGCGCTTTCGACAGACCGCGCAGCCCTCTGCGGGCTCTGCT 721
Db 241 CAGTGCAGGTGCGGGGCGCTTTCGACAGACCGCGCAGCCCTCTGCGGGCTCTGCT 300
Qy 722 GCCCTGTGTTTGTATACATCCGATACAGCTCTCCCATCCGATCCGAGCTGGGCTGCCG 781
Db 301 GCCCTGTGTTTGTATACATCCGATACAGCTCTCCCATCCGATCCGAGCTGGGCTGCCG 360
Qy 782 TCCCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATTTGGGCTGGCACTTAAACCGTG 841
Db 361 TCCCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATTTGGGCTGGCACTTAAACCGTG 420
Qy 842 GTGATGCTTCTCTCT-TGGAAGACGCTCGGTGCCAATGTGCTGTGTTCTCTGCACCAAC 900
Db 421 GTGATGCTTCTCTCTTGGAGGAGCTCGGTSCCAATGTGCTGTCTCTGTCACCAACC 480
Qy 901 GTCAATTAGCATCTCCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 960
Db 481 GTCAATTAGCATCTCCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 540
Qy 961 ACCGCGAGTTACATCCAGGCGCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGAGCGG 1020
Db 541 ACCGCGAGTTACATCCAGGCGCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGAGCGG 600
Qy 1021 CTGCTGCTGTGGTATTGCCCCAGCAGCTTGCCTATGGAGATGAAGAAGACATCAACACA 1080
Db 601 CTGCTGCTGTGGTATTGCCCCAGCAGCTTGCCTATGGAGATGAAGAAGACATCAACACA 660
Qy 1081 AAAAAAGAGAC---ATGTTCCACAAGATCTACATACAGAAGCATGACAATGTGAGCATC 1137
Db 661 AAAAAAGAGACATGATGTTTCCACAAGATCTACATACAGAAGCATGACAATGTGAGCATC 720
Qy 1138 CTGTTTGCAGACATTGAGGGCTTCCAGCAGCTTCCCATGCCACTGCCAGGAGGCTG 1197
Db 721 CTGTTTGCAGACATTGAGGGCTTCCAGCAGCTTCCCATGCCACTGCCAGGAGGCTG 780
Qy 1198 GTCATGACCTGAAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGGGAGAACTACTGC 1257
Db 781 GTCATGACCTGAAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGGGAGAACTACTGC 840
Qy 1258 CTGAGGATCAAGATCTTGGGGGAGCTGTACTACTGTGTGTCAGGGCTGCCGGAGGCCGG 1317

Db 841 CTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTCTCAGGGCTGCCGGAGCCCGG 900
QY 1318 GCCGACCATGCCACTGCTGTGAGATGGGGTAGACATGATTGAGGCCATCTCGCTG 1377
Db 901 GCCGACCATGCCACTGCTGTGAGATGGGGTAGACATGATTGAGGCCATCTCGCTG 960
QY 1378 GTACCTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGCGCGTG 1437
Db 961 GTACCTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGCGCGTG 1020
QY 1438 CACTCGGCGCTTGGCTTGGGAAATGGCAGTTCGATGTGTGTCGAATGTGACC 1497
Db 1021 CACTCGGCGCTTGGCTTGGGAAATGGCAGTTCGATGTGTGTCGAATGTGACC 1080
QY 1498 CTGGCAACACATGGAAGAGCGCGCTGCCGATCCACATCACTCGGCAACA 1557
Db 1081 CTGGCAACACATGGAAGAGCGCGCTGCCGATCCACATCACTCGGCAACA 1140
QY 1558 CTGCACTACCTGAACGGGGACTACGAATGGAGCGCGGTGGCAAGCGCAACCGG 1617
Db 1141 CTGCACTACCTGAACGGGGACTACGAATGGAGCGCGGTGGCAAGCGCAACCGG 1200
QY 1618 TACCTCAAGGAGCAGCATGAGACTTTCCTCATCTCTGGGCGCCAGCCAGAAACGGAA 1677
Db 1201 TACCTCAAGGAGCAGCATGAGACTTTCCTCATCTCTGGGCGCCAGCCAGAAACGGAA 1260
QY 1678 GAGGAGAAAGGATGCTGGCCAAAGCTGCAGCGACTCGGCGCAACTCCATGGAAGGGCTG 1737
Db 1261 GAGGAGAAAGGATGCTGGCCAAAGCTGCAGCGACTCGGCGCAACTCCATGGAAGGGCTG 1320
QY 1738 ATGCGCGATGGTTCCTGATGCTGCTCCCGGACCAAGGATCCAAAGCGCTTCGCG 1797
Db 1321 ATGCGCGATGGTTCCTGATGCTGCTCCCGGACCAAGGATCCAAAGCGCTTCGCG 1380
QY 1798 CAGATGGCATGTGATTCAGAGAAAGACACCGCGGACCCAGAGATGCCCTGAACCT 1857
Db 1381 CAGATGGCATGTGATTCAGAGAAAGACACCGCGGACCCAGAGATGCCCTGAACCT 1440
QY 1858 GAGGATGAGGTGATGATCTCTGAGCGGTGCCATCGATCGCCGAGCATTTGATCAGCTG 1917
Db 1441 GAGGATGAGGTGATGATCTCTGAGCGGTGCCATCGATCGCCGAGCATTTGATCAGCTG 1500
QY 1918 CGGAAGGACATGTGCGCGGTTTGTGCTACCTTCCAGAGAGAGATTTGAGAGAG 1977
Db 1501 CGGAAGGACATGTGCGCGGTTTGTGCTACCTTCCAGAGAGAGATTTGAGAGAG 1560
QY 1978 TACTCCGGAAGTGTATCCCGCTTCGAGCGCTACGTTGCTGTGCGCTGTGCTCTC 2037
Db 1561 TACTCCGGAAGTGTATCCCGCTTCGAGCGCTACGTTGCTGTGCGCTGTGCTCTC 1620
QY 2038 TGCTTCATCTGCTCATCCAGCTTCTAATTTTCCACACTCCACCGCTGATGCTTGGGAT 2097
Db 1621 TGCTTCATCTGCTCATCCAGCTTCTAATTTTCCACACTCCACCGCTGATGCTTGGGAT 1680
QY 2098 TATGCGAGCATCTGCTGTGCTATATCAGCGTGTGATCTGTGCTGTGCTGTGCTGT 2157
Db 1681 TATGCGAGCATCTGCTGTGCTATATCAGCGTGTGATCTGTGCTGTGCTGTGCTGT 1740
QY 2158 GGTTCCTGTTCCCTAAGGCGCTGCAACGCTGTGCCGAGCATTTGCCGCTCACGGGA 2217
Db 1741 GGTTCCTGTTCCCTAAGGCGCTGCAACGCTGTGCCGAGCATTTGCCGCTCACGGGA 1800
QY 2218 CATAGACCGGAGTTGGCATTTTCCGCTGCTGTGTTTACTTCTGCCATTTGCCAAC 2277
Db 1801 CATAGACCGGAGTTGGCATTTTCCGCTGCTGTGTTTACTTCTGCCATTTGCCAAC 1860
QY 2278 ATGTTCACTGTAAACCAACCCCATACGGAGCTGTGAGCCCGATGCTGAATTAACA 2337
Db 1861 ATGTAC----- 1866
QY 2338 CTTGCTGACATCACTGCTGCCACCTGCAGCAGCTCAATTTACTCTCTGCGCGCTGGATGCT 2397
Db 1867 ----- 1866

QY 2398 CCCCTGTGTGAGGGCACCATGCCACCTGCAGCTTTCCTGAGGTGTCCATCGGAACATG 2457
Db 1867 -----TTTCATCGGGAACATG 1881
QY 2458 CTGCTGAGTCTCTTGGCAGCTCTCTCTCTGTCACATCAGCAGCATCGGAAGTTGGCC 2517
Db 1882 CTGCTGAGTCTCTTGGCAGCTCTCTCTCTGTCACATCAGCAGCATCGGAAGTTGGCC 1941
QY 2518 ATGATCTTGTCTTGGGCTCATCTATTTGGTGTCTCTCTCTGCTGGTCCCCCAGCCGC 2577
Db 1942 ATGATCTTGTCTTGGGCTCATCTATTTGGTGTCTCTCTCTGCTGGTCCCCCAGCCGC 2001
QY 2578 ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTCTTCCAAATGAGACC 2637
Db 2002 ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTCTTCCAAATGAGACC 2061
QY 2638 TTTGATGGCTGGACTGTCACCTGCTGAGGAGGGTGGCCCTCAAAATATATGACCCCTG 2697
Db 2062 TTTGATGGCTGGACTGTCACCTGCTGAGGAGGGTGGCCCTCAAAATATATGACCCCTG 2121
QY 2698 ATTCTGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2757
Db 2122 ATTCTGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2181
QY 2758 CGCCTTAACTTCTCTGGAACCTACAGGCAACAGGGGAGAGAGAGAGAGAGAGAGCTA 2817
Db 2182 CGCCTTAACTTCTCTGGAACCTACAGGCAACAGGGGAGAGAGAGAGAGAGAGCTA 2241
QY 2818 CAGGCAATCAACCGGAGGCTGCTGATTAACATTTGCCCAAGAGCTGGCGGCCCATCTC 2877
Db 2242 CAGGCAATCAACCGGAGGCTGCTGATTAACATTTGCCCAAGAGCTGGCGGCCCATCTC 2301
QY 2878 CTGGCCCGGAGCGCGCAATGATGAATCTACTATCAGTCTGTGAGTGTGCTGCTGT 2937
Db 2302 CTGGCCCGGAGCGCGCAATGATGAATCTACTATCAGTCTGTGAGTGTGCTGCTGT 2361
QY 2938 ATGTTTGGCTTCCATTTGCCAACTTCTCTGAGTTCTATGTGAGCTGGAGCAACAAATGAG 2997
Db 2362 ATGTTTGGCTTCCATTTGCCAACTTCTCTGAGTTCTATGTGAGCTGGAGCAACAAATGAG 2421
QY 2998 GGTGCGGAGTGGCTGGGCTGCTCAACGAGATCATCGTACTGCTGCTGCTGCTGCTG 3046
Db 2422 GGTGCGGAGTGGCTGGGCTGCTCAACGAGATCATCGTACTGCTGCTGCTGCTGCTG 2481
QY 3047 -----AGATTATCAGCGAGCGGTTCGCGAGCTGGAAAGATCAACAGCATTCG 3098
Db 2482 TGTGTTTTCAGATTATCAGCGAGCGGTTCGCGAGCTGGAAAGATCAACAGCATTCG 2541
QY 3099 TAGCACCTTACATGCTGCTCAGGGCTGAACGCCAGCAGCTACGATCAGGTGGCGGCTC 3158
Db 2542 TAGCACCTTACATGCTGCTCAGGGCTGAACGCCAGCAGCTACGATCAGGTGGCGGCTC 2601
QY 3159 CCACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3218
Db 2602 CCACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2661
QY 3219 TGAGCACTTCTTCAACAATTTCCAGATGAAGATTTGGGCTGAACATGGGCGCCAGTCTG 3278
Db 2662 TGAGCACTTCTTCAACAATTTCCAGATGAAGATTTGGGCTGAACATGGGCGCCAGTCTG 2721
QY 3279 AGGTGTATCGGGGTTCGGAAGCCACAGTATGACATCTTGGGGGAAACACAGTGAATGTCT 3338
Db 2722 AGGTGTATCGGGGTTCGGAAGCCACAGTATGACATCTTGGGGGAAACACAGTGAATGTCT 2781
QY 3339 TACTGCTATGAGACAGCAGCGGGGTCCCCACCGAATCCAGGTGACCCAGGAGCTGTACCA 3398
Db 2782 TACTGCTATGAGACAGCAGCGGGGTCCCCACCGAATCCAGGTGACCCAGGAGCTGTACCA 2841
QY 3399 GGTTCCTAGCTGCCAAGGGCTACAGCTGAGTGTGCGAGGGTGGTCAAGTGAAGGGCAA 3458
Db 2842 GGTTCCTAGCTGCCAAGGGCTACAGCTGAGTGTGCGAGGGTGGTCAAGTGAAGGGCAA 2901

QY 3459 GGGGAGATGACCACTTCTCTCAATGCGGGCCCGAGGTTTAAACAGGCCAGCCAC 3518
Db 2902 GGGGAGATGACCACTTCTCTCAATGCGGGCCCGAGGTTTAAACAGGCCAGCCAC 2961

QY 3519 AAATTGAGCTGAAGGACCAAGGTGGCACT 3549
Db 2962 AAATTGAGCTGAAGGACCAAGGTGGCACT 2992

RESULT 14
US-09-472-667-3
: Sequence 3, Application US/09472667
: GENERAL INFORMATION:
: APPLICANT: Hammond, H. Kirk
: APPLICANT: Insel, Paul A.
: APPLICANT: Ping, Peipei
: APPLICANT: Post, Steven R.
: APPLICANT: Gao, Melhua
: TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
: FILE REFERENCE: 22002056722
: CURRENT APPLICATION NUMBER: US/09/472,667
: CURRENT FILING DATE: 1999-12-27
: PRIOR APPLICATION NUMBER: PCT/US99/02702
: PRIOR FILING DATE: 1999-02-09
: PRIOR APPLICATION NUMBER: US 09/008,097
: PRIOR FILING DATE: 1998-01-16
: PRIOR APPLICATION NUMBER: US 09/021,773
: PRIOR FILING DATE: 1998-02-11
: PRIOR APPLICATION NUMBER: US 08/924,757
: PRIOR FILING DATE: 1997-09-05
: PRIOR APPLICATION NUMBER: PCT/US97/15610
: PRIOR FILING DATE: 1997-09-05
: PRIOR APPLICATION NUMBER: US 08/708,661
: PRIOR FILING DATE: 1996-09-05
: PRIOR APPLICATION NUMBER: US 60/048,933
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: 60/058,209
: PRIOR FILING DATE: 1996-09-05
: PRIOR APPLICATION NUMBER: PCT/US96/02631
: PRIOR FILING DATE: 1996-02-27
: PRIOR APPLICATION NUMBER: US 08/396,207
: PRIOR FILING DATE: 1995-02-28
: PRIOR APPLICATION NUMBER: US 08/485,472
: PRIOR FILING DATE: 1995-06-07
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 1812
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-472-667-3

Query Match 51.0%; Score 1808.4; DB 18; Length 1812;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 636 TAACCTGGTGTGGGCATCCTGGCGCAGTGCAGTCCGGGGCGCTTTTCGCAGCAGACCC 695
Db 3 TAACCTGGTGTGGGCATCCTGGCGCAGTGCAGTCCGGGGCGCTTTTCGCAGCAGACCC 62

QY 696 GCGCAGCCCTCTGCGGGCCTCTGGTGCCTGTGTTCTTTGTATACATCGCATACAGCT 755
Db 63 GCGCAGCCCTCTGCGGGCCTCTGGTGCCTGTGTTCTTTGTATACATCGCATACAGCT 122

QY 756 CCTCCCCATCGCATCGGGCTGCGCTTCCTCAGCGGCTGGGCTCTCCACCTTGCATTT 815
Db 123 CCTCCCCATCGCATCGGGCTGCGCTTCCTCAGCGGCTGGGCTCTCCACCTTGCATTT 182

QY 816 GATCTTGGCTTGGCACTTAACCTGTGTGATGCTTCTCTGGAAGCAGCTCGGTGCAA 875
Db 183 GATCTTGGCTTGGCACTTAACCTGTGTGATGCTTCTCTGGAAGCAGCTCGGTGCAA 242

QY 876 TGTGCTGCTGTCTCTGTCACCAACGCTATTAGCATCTGCACACACTATATCCAGCAGAGT 935
Db 243 TGTGCTGCTGTCTCTGTCACCAACGCTATTAGCATCTGCACACACTATATCCAGCAGAGT 302

QY 936 GTCTCAGCGCCAGCCCTTTTCAGGAGACCCGAGTTACATCCAGGCCGGCTCCACCTGCA 995
Db 303 GTCTCAGCGCCAGCCCTTTTCAGGAGACCCGAGTTACATCCAGGCCGGCTCCACCTGCA 362

QY 996 GCATGAGAATCGGCAGCAGGCGGCTGCTGCTGCGGTATTCGCCCAGCAGCTTGGCAT 1055
Db 363 GCATGAGAATCGGCAGCAGGCGGCTGCTGCTGCGGTATTCGCCCAGCAGCTTGGCAT 422

QY 1056 GGAGATGAAAGAGACATCAACACAAAGAGAGACATGTTCCACAAAGATCTACATACA 1115
Db 423 GGAGATGAAAGAGACATCAACACAAAGAGAGACATGTTCCACAAAGATCTACATACA 482

QY 1116 GAAGCATGACAATGTGAGCATCTGTTTGGAGACATTTGAGGGCTTTCACGAGCCTGGCATC 1175
Db 483 GAAGCATGACAATGTGAGCATCTGTTTGGAGACATTTGAGGGCTTTCACGAGCCTGGCATC 542

QY 1176 CCAGTGCACCTGCGCAGGAGCTGCTGATGACCTGAATGAGCTCTTTCGCCGGTTTGACA 1235
Db 543 CCAGTGCACCTGCGCAGGAGCTGCTGATGACCTGAATGAGCTCTTTCGCCGGTTTGACA 602

QY 1236 GCTGGCTGCGGAGAAATCACTGCTGAGGATCAAGATCTTGGGGAGCTGTTACTACTGT 1295
Db 603 GCTGGCTGCGGAGAAATCACTGCTGAGGATCAAGATCTTGGGGAGCTGTTACTACTGT 662

QY 1296 GTCAGGGCTGCGGAGGCCCGGGCCGACCATGCCACTGCTGTGTGAGATGGGGGTAGA 1355
Db 663 GTCAGGGCTGCGGAGGCCCGGGCCGACCATGCCACTGCTGTGTGAGATGGGGGTAGA 722

QY 1356 CATGATTGAGGCCATCTCGCTGGTGTGAGGTGACAGGTGTGAATGTGAACATGCGCGT 1415
Db 723 CATGATTGAGGCCATCTCGCTGGTGTGAGGTGACAGGTGTGAATGTGAACATGCGCGT 782

QY 1416 GGGCATCCAGCGGGCGCGTGCACCTGCGGCGTCTTGGCTTGGGAAATGGCAGTTGCA 1475
Db 783 GGGCATCCAGCGGGCGCGTGCACCTGCGGCGTCTTGGCTTGGGAAATGGCAGTTGCA 842

QY 1476 TGTGTGTGTCCAATGATGTGACCTGGCCAAACACATGGAAGCAGGAGCCGGCTGGCCG 1535
Db 843 TGTGTGTGTCCAATGATGTGACCTGGCCAAACACATGGAAGCAGGAGCCGGCTGGCCG 902

QY 1536 CATCCACATCACTCGGCAACACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1595
Db 903 CATCCACATCACTCGGCAACACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 962

QY 1596 CCGTGTGGCAAGCGCAACCGCTACCTCAAGGAGCAGCAGCATTTGAGACTTTCTCATCCT 1655
Db 963 CCGTGTGGCAAGCGCAACCGCTACCTCAAGGAGCAGCAGCATTTGAGACTTTCTCATCCT 1022

QY 1656 GGGCGCCAGCAGAAACGGAGAAAGAGGATGAGTGTGCTGCGCAAGCTGCAGCGGACTCG 1715
Db 1023 GGGCGCCAGCAGAAACGGAGAAAGAGGATGAGTGTGCTGCGCAAGCTGCAGCGGACTCG 1082

QY 1716 GGGCAACTCCATGGAAGGCTGATGCGCGATGGGTTCCTGATGCTGCTTCTCCCGGAC 1775
Db 1083 GGGCAACTCCATGGAAGGCTGATGCGCGATGGGTTCCTGATGCTGCTTCTCCCGGAC 1142

QY 1776 CAAGGACTCCAAAGCCCTTCGCGCAGATGGGCATTTGATGATTCAGCAAGAACACCGGG 1835
Db 1143 CAAGGACTCCAAAGCCCTTCGCGCAGATGGGCATTTGATGATTCAGCAAGAACACCGGG 1202

QY 1836 CACCCAGAGTGCCTGAACCTTGAGGATGAGTGTGATGAGTGTGATGAGTGTGATGAGT 1895
Db 1203 CACCCAGAGTGCCTGAACCTTGAGGATGAGTGTGATGAGTGTGATGAGTGTGATGAGT 1262

QY 1896 TGCCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCGCGGTTTGTGCTCACTTCCA 1955
Db 1263 TGCCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCGCGGTTTGTGCTCACTTCCA 1322

QY 1956 GAGAGAGGATTTTGGAGAAGAGTACTCCCGGAAGGTGGATTCGCCGCTTCGGAGCCTACGT 2015

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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 22:29:24 ; Search time 604.737 Seconds
(without alignments)
9128.329 Million cell updates/sec

Title: US-09-750-240-5

Perfect score: 3549

Sequence: 1 atgtcatggttttagtgccct.....aaggaccagggtgggcact 3549

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2850587 seqs, 777717511 residues

Total number of hits satisfying chosen parameters: 5701174

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_New.*

- 1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2799.2	78.9	5826	6	US-10-144-771-5921
2	1531.4	44.8	4349	6	US-10-144-771-19529
3	1060.2	29.9	1386	1	PCT-US02-36759-83
4	505.2	14.2	3518	6	US-10-121-911A-2
5	473.4	13.3	6196	1	PCT-US02-34621-1
6	473.4	13.3	6196	6	US-10-282-942-1
7	459	12.9	4008	7	US-60-436-643-3039
8	452.4	12.7	2731	6	US-10-305-720-1344
9	432.4	12.2	5124	6	US-10-144-771-18424
10	428	12.1	3357	6	US-10-338-044-2053
11	425.2	12.0	4633	6	US-10-144-771-16338
12	410.8	11.6	3458	6	US-10-144-771-3825
13	397.4	11.2	3820	6	US-10-144-771-855
14	362.8	10.2	3756	6	US-09-724-676-11592
15	362.8	10.2	3756	6	US-09-724-676A-11592
16	346	9.7	2253	5	US-10-144-771-16113
17	339	9.6	2949	5	US-09-724-676-11593
18	339	9.6	2949	5	US-09-724-676A-11593
19	338.2	9.5	4079	6	US-10-305-720-1412
20	338.2	9.5	5370	5	US-09-724-676-11576
21	338.2	9.5	5370	5	US-09-724-676A-11576
22	338.2	9.5	5680	5	US-09-724-676-11577
23	338.2	9.5	5680	5	US-09-724-676A-11577
24	320.6	9.0	3158	6	US-10-144-771-14946
25	308.6	8.7	1661	6	US-10-144-771-15361
26	284.4	8.0	1180	6	US-10-277-802-11
					Sequence 5921, Ap
					Sequence 19529, A
					Sequence 83, Appl
					Sequence 2, Appl
					Sequence 1, Appl
					Sequence 1, Appl
					Sequence 3039, Ap
					Sequence 1344, Ap
					Sequence 18424, Ap
					Sequence 2053, Ap
					Sequence 16338, A
					Sequence 3825, Ap
					Sequence 855, App
					Sequence 11592, A
					Sequence 11592, A
					Sequence 16113, A
					Sequence 11593, A
					Sequence 11593, A
					Sequence 1412, Ap
					Sequence 11576, A
					Sequence 11576, A
					Sequence 11577, A
					Sequence 11577, A
					Sequence 14946, A
					Sequence 15361, A
					Sequence 11, Appl

RESULT 1
US-10-144-771-5921
; Sequence 5921, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTNER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CLO01321
; CURRENT APPLICATION NUMBER: US/10/144.771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 5921
; LENGTH: 5826
; TYPE: DNA
; ORGANISM: HUMAN
; US-10-144-771-5921

Query Match 78.9%; Score 2799.2; DB 6; Length 5826;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 3110; Conservative 0; Mismatches 433; Indels 11; Gaps 4;

Qy	1	ATGTCATGTTAGTGGCTCTCGTCCCTAAAGTGGATGAACGGAACAGCCCTGGGGT	60
Db	96	ATGTCATGTTAGTGGCTCTCGTCCCTAAAGTGGATGAACGGAACAGCCCTGGGGT	155
Qy	61	GAACGCAATGGGACAGACGGTTTCGGGGCGCGTGGCACTCGGGCAGGTGCTTCTGCAG	120
Db	156	GAACGCAATGGGACAGACGG---CCACGCCACGCGAATCGAGCCAGTGGCTTCTGC	212
Qy	121	CCCGCTATATGAGTGGCTCGGGATGACAGCCACCCAGCCGCCCTCGGGGCCCC	180
Db	213	CCTCCTACATGAGTGGCTCAAGATGGGAGCCACCCAGCCGCCCTCGGAGCTCAC	272
Qy	181	CCTCGGTCCCTCGGAGGATGACCCCTTCATCCGGAGGGCGGCCAGGCAAGGCAAG	240
Db	273	ACTCGGTCCCTCGGAGGATGACCCCTTCATCAGAGGGCGGGCGGGCAGGGGTGTG	332
Qy	241	GAGCTGGGGTGGGGCAGTGGCCCTTGGGCTTCGAGGATACCGAGGTGACACACAGG	300
Db	333	GAGCTGGGGTGGGGCAGTGGCCCTTGGGCTTCGAGGATGAGGTGACACACAGG	392
Qy	301	GGCGGAGGCTGAGTGGCGCCCGCGGTGGCCAGGAGTGGGATCTCTGCTGGCGC	360
Db	393	GGC---ACAGCTGAAGTGGCAGCCCGGATACATCGCCTCGAGAGCGGTCCTGCTGG	449
Qy	361	CGTTGGTGCAGTGTTCAGTCAAGAGTTCCTTCCGTCGAGGAGTGGAGCGCTGTAC	420
Db	450	CGGCTGTGAGTGTTCAGTCAAGAGTTCCTTCCGTCGAGGAGTGGAGCGCTGTAC	509
Qy	421	CAGCGGTACTTTTCCAGATGAACGAGACGCTGACGCTGCTGCTGGGCTGCTGGTG	480

Sequence 588, App
Sequence 11582, A
Sequence 11582, A
Sequence 11583, A
Sequence 11583, A
Sequence 11586, A
Sequence 11586, A
Sequence 11587, A
Sequence 11587, A
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Sequence 11587, A
Sequence 11581, A
Sequence 11581, A
Sequence 23772, A
Sequence 23772, A
Sequence 11594, A
Sequence 11594, A
Sequence 11595, A
Sequence 11595, A
Sequence 11584, A

ALIGNMENTS

Db 510 CAGCGTACTTCTCCAGATGAACACAGAGAGCCTACGCTGCTCATGGCGGTGCTGGTG 569
QY 481 CTGCTCAGCGGTGCTGGCTTTCCAAAGCGGCACCCCGCCCTCAGCCCTGCGCTAT 540
Db 570 CTGCTCATGGCTGTACTGTGTGACTTTCCAGCTGCGGCTGCCAGCCCTCAGCCCTGCTTAC 629
QY 541 GTGGCACTGTGGGCTGTGGCGGCGCTGTCTGTGGGGCTCATGTGTTGTTAAACCGG 600
Db 630 GTGGCGCTGTGACCTGTGCTCTGTCTTTTGTGTACTCATGTGTGTGTAAACCGA 689
QY 601 CATAGCTTCGCCAGGACTCCATGTGGGTGGTGAATGAATGAGTGGTGGGATCCCTGGCG 660
Db 690 CACAGCTTCGCCAGGACTCCATGTGGGTGGTGAATGAGTGGTGGGATCCCTAGCA 749
QY 661 GCAGTGAAGTTCGGGGCGCTTTCGACAGAGACCCCGGAGCCCTCTGCGGGCTCTGG 720
Db 750 GCGGTGAAGTTCGGGGTGGCTGGCAGCAATCCACAGAGCCCTCGCGGGGCTTTGG 809
QY 721 TGCCCTGTGTTGTTATACATGCGATACAGGCTCTCCCAATCGCATGCGGGCTGCC 780
Db 810 TGCCCGCTGTGTTGTTGTTATACATGCGATACAGGCTCTCCCAATCGCATGCGGGGCT 869
QY 781 GTCTCAGCGGCTGGGCTTCACCTTCATTTGATTTGGCTGGCAACTTAACCGT 840
Db 870 GTACTCAGCGGCTGGGCTTCCTACTCTGATTTGATTTGGCTGGCAACTTAACCGT 929
QY 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGCTGTGTTCTCTGACCAAC 900
Db 930 AGCGACCCCTTCTTGAAGCAGCTCGGTGCCAATGCTGTGTTCTCTGACCAAT 989
QY 901 GTCATTAAGCATTCGACACACTATTCAGAGAGAGTGTCTCAGCGCCAGGCTTTTCAGGAG 960
Db 990 GCCATCGGTGTGACACACTACCTTGTGAGTGTCTCAGCGCCAGGCTTTTCAGGAG 1049
QY 961 ACCGCGAGTTACATCCAGGCGCGCTCCACTGCGAGATGAGATCGGAGGAGCGG 1020
Db 1050 ACCGAGGTTACATCCAGGCGCGCTCCACTGCGAGATGAGATCGGAGGAGCGG 1109
QY 1021 CTGCTGCTGTGCTGTTATGCCCCAGCAGCTTGCATGAGATGAAGAGAGCATCAACACA 1080
Db 1110 CTGCTGCTATCGGTGTGCCCCAGCAGCTTGCATGAGATGAAGAGAGCATCAACACA 1169
QY 1081 AAAAAAGAAC ---ATGTTCCACAGATCTACATACAGAGCATGACATGTCAGCATC 1137
Db 1170 AAAAAAGAGACATGATGTTTCCATTAAGATCTACATCCAGAGCATGATATGTCAGCATC 1229
QY 1138 CTGTTTCAGACATTTAGGGCTTCCAGCAGCTGGCATCCCACTGCGAGGAGCTG 1197
Db 1230 CTGTTTCGGACATTTAGGGCTTCCAGCAGCTGGCTCCCACTGCGAGGAGCTG 1289
QY 1198 GTCATGACCTGATGAGCTCTTTGCCCCGTTTGAACAGCTGGCTGGGAGATFCACTGC 1257
Db 1290 GTCATGACCTGATGAGCTCTTTGCCCCGTTTGAACAGCTGGCTGGGAGATFCACTGT 1349
QY 1258 CTGAGGATCAAGATCTTGGGGGAGCTTACTACTGCTGTGTCAGGCTGCGGAGCGCCGG 1317
Db 1350 CTGAGGATCAAGATCTTGGGGGAGCTTACTACTGCTGTGTCAGGCTGCGGAGCGCCGG 1409
QY 1318 GCCAGCATGCCACTGCTGTGTGGAGATGGGGTAGACATGATTTAGAGGCTATCTCGCTG 1377
Db 1410 GCAGATCACGCCACTGCTGTGTGGAGATGGGGTAGACATGATTCGAAGCCATCTCGCTG 1469
QY 1378 GTAGGTGAGGTGACAGGTGTGAATGTGAACATGCGCTGGGATTCACAGCGGGCGGCTG 1437
Db 1470 GTGGGTGAGGTGAACAGGTGTGAACATGCGTGGGATTCACAGCGGGAGCTG 1529
QY 1438 CACTGCGGCTCTTGGCTTGGGAATGCGAGTTCATGTGTTGGTCCATGATGTGACC 1497
Db 1530 CATTTGGGCTGCTTGGCTTGGGAATGCGAGTTCATGTGTTGGTCCAAACGATGTGACC 1589
QY 1498 CTGCGCAACACATGGAAGAGGAGCGGCTGGCGGCTCCACATCACTTCGCGGCAACA 1557

Db 1590 CTGGCTAACCAACATGAGAGCGCGGGGGCGGCGCATTCACATCACTTCGGGCTACA 1649
QY 1558 CTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGCGCTGGTGGCAAGCGCAACGCG 1617
Db 1650 CTGCAGTACTTGAACGGGGACTATGAGTGGAGCCAGCGCTGGTGGTGAACGAATGCG 1709
QY 1618 TACCTCAAGGAGCAGACATTTGAGACTTTCTCATCTGCGGCGCCAGCCAGAAACGAAA 1677
Db 1710 TACCTCAAGGAGCAGTGCATTTGAGACCTTCTCATCTTGGCGCCAGCAAAAACGAAA 1769
QY 1678 GAGGAGAAAGGATGCTGGGCCAAGCTCAGGGGACTCGGGCCAACTCATGGAAGGCTG 1737
Db 1770 GAGGAGAAAGGATGCTGGGCCAAGCTTTCAGGGAGACAGGGCCAACTCATGGAAGGACTG 1829
QY 1738 ATGCCGCGATGGGTTCCTGATCGCTTCTCCCGGACCAAGGACTTCCAAAGGCTTCCGC 1797
Db 1830 ATGCCGCGATGGGTTCCTGATCGCTTCTCCCGGACCAAGGACTTCTAAGGCATTCGCG 1889
QY 1798 CAGATGGGCAATTTGATGATTTCCAGAAAGACAAACCGGGGACCCCAAGATGCCCTGAACCCCT 1857
Db 1890 CAGATGGGCAATTTGATGATTTTCAGCAAGACAAACCGGGGTGCCCAAGATGCTCTGAACCCCT 1949
QY 1858 GAGGATGAGTGGATGATTTCTGAGCGGTGCCATGATGCCGAGCATTTGATCAAGCTG 1917
Db 1950 GAGATGAGTGGATGATTTCTTGGCGGAGCCATGATGCCGAGCATCGACCAACTG 2009
QY 1918 CGAAGGACCATGTCGCCCGGTTTTTGTCTCACCTTCCAGAGAGAGGATTTTGAGAAGAAG 1977
Db 2010 CGTAAGGACCATGTCGCCCGGTTCTCTGCTCACCTTCCAGAGAGAGGATTTTGAGAAGAAG 2069
QY 1978 TACTCCGGGAAGTGGATCCCGGCTTCGGAGCCTACGTTGCCTGTGGCTTGTGGCTTTC 2037
Db 2070 TATTCAGGGAAGTAGATCTCTCGCTTCGGAGCCTACGCTGCTGCTGCTGCTGCTGCTGCT 2129
QY 2038 TGCTTCACTGCTTTCATCCAGCTTCTAAATTTTCCACACTCCACCTGATGCTTGGGAT 2097
Db 2130 TGCTTCACTGCTTTCATCCAGCTTCTGTTGCCATCTCCACCTGATGCTGCGGAT 2189
QY 2098 TATGCCAGCATCTTCCTGCTGCTGCTAAATCACCGTGTGATGCTGCTGCTGCTGCTGCTGCT 2157
Db 2190 TATGCCGCTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2249
QY 2158 GGTCTCTGTTTCCCTTAGGCGCTGCAAGCTGCTGCCCGAGCATTTGCCCTCACGGCA 2217
Db 2250 GGTCTCTTCTTCCCGCAAGCGCTGCAAGCGCTGCTGCCGCAATATTTGCCCTCACGGGTG 2309
QY 2218 CATAGCACCGCAGTTGGCATCTTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2277
Db 2310 CACAGCACCGCGGTGGATCTTCTCGGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2369
QY 2278 ATGTTCACTGTAAACACACACCCCATAGGAGCTGTGCGACCGCGGATGCTGAATTTAAACA 2337
Db 2370 ATGTTTACCTGTAAACACACACCCCATAGGAGCTGTGCGCGCGGATGCTGAATTTAAACA 2429
QY 2338 CTTGCTGACATCACTGCTGCCACTGCGAGCTCAATTAATCTCTGCGGCTGCTGCTGCTGCTGCT 2397
Db 2430 CCAGCGGATGCTACCGCTGCCACTTACAAAGCTCAATTAATCTCTGCGGACTGCTGCTGCT 2489
QY 2398 CTTGCTGAGGAGCAGCATGCCACCTGCGAGCTTTCTGAGGTGCTGCTGCTGCTGCTGCTGCTGCT 2457
Db 2490 CTTGCTGAGGAGCAGCATGCCACCTGCGAGCTTTCTGAGTACTTCTGCTGCGGAGCTG 2549
QY 2458 CTGCTGAGTCTTTGGGCGCTGCTGCTTCCGACATACAGAGCATCGGGAAGTGTGGCC 2517
Db 2550 CTGCTGAGTCTTTAGCGAGCTGCTGCTTCTACACATACAGAGCATCGGGAAGTGTGGCC 2609
QY 2518 ATGATCTTCTTGGGCTCATCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2577
Db 2610 ATGACCTTCTTGGGCTTACCTACTTGGGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2669
QY 2578 ATCTTTGACAACTATGACCTACTGCTTGGGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2637
Db 2670 ATCTTTGACAACTATGATGCTGCTTGGGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2729

QY	2638	TTTGTATGGCTGGACTTCCACTCGAGGAGGTGGCCCTCAAAATATATGACCCCTGTG	2697
Db	2730	TTTGTATGGCTGGACTTCCACCACTGTGGGAGGTTAGCGCTCAAAATATATGACCCCGTGTG	2789
QY	2698	ATTCTGCTGGTGTTCGCTGGCGTGTATCTGCAATGCTCAGCAGGTGGAAATCAGCTGCC	2757
Db	2790	ATTCTGCTGGTGTTCGCTGGCACTGTATCTGCATGCACAACTGGAATCGACTGCC	2849
QY	2758	CGCCTAAACTTCTCTGGAACATACAGGCACACAGGGGAAAAGAGGAGATGGAGAGCTA	2817
Db	2850	CGCCTGGACTTCTCTGTGGAAGTTACAGGCACACAGGGGAGAAGGAGGAGATGGAGAGCTA	2909
QY	2818	CAGGCATCAACCGGAGGCTGCTGATACACTTCTGCCCCAAGGACGTGGCGGCCCACTTC	2877
Db	2910	CAGGCATCAACCGGAGGTGCTGATACACTTCTCCCAAGGACGTGGCGGCCCACTTC	2969
QY	2878	CTGGCCGGGAGCGCGCAATGAACTCTACTATCAGTCTGTGAGTGTGTGGCTGTT	2937
Db	2970	CTGGCCGGGAGCGCGCAACGATGAGTGTACTACCACTGCTGTGAATGTGTGGCTGTC	3029
QY	2938	ATGTTTGGCTCCATTTGCCAACTTCTGAGTTCATGTGGAGCTGGAGGCAAACTAG	2997
Db	3030	ATGTTTGGCTCCATTCGCCAAATTTCTCGGAGTTCTACGTGGAGCTCGAGGCAAACTAG	3089
QY	2998	GGTCCGAGTGCTGGCGTCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC	3057
Db	3090	GGCGTGGAGTGCTGGCGTCTCAATGAGATCATCGCAGACTTTGACGAGATCATCAGT	3149
QY	3058	GAGGAGGGTTTCGGCAGCTGGAAAGATCAAGACGATTTGTTAGCACTACATGGCTGCC	3117
Db	3150	GAGGAGAGATTTCCGGCAGTTGGAGAAGATCAAGACCATCGGTAGCACCTACATGGCGGCC	3209
QY	3118	TCAGGCTGAACGCCAGCACTACGATCAGGTGGCGCGCTCCACATCATCTGCGCTGGCT	3177
Db	3210	TCTGGGCTAAATGCCAGCACTATGACCAGGTTCGGCCGCTCACACATCACGGCGCTGGCT	3269
QY	3178	GACTACGCCATCGGCTCATATGAGCAGATGAAGCACATCAATGAGCACTCTCTCAACAAT	3237
Db	3270	GACTATGCCATCGGCTCATATGAGCAGATGAAGCACATCAATGAGCACTCTCTTCAACAAT	3329
QY	3238	TTCCAGATGAAGATTTGGCTGAACATGGGCCAGTCGTGGCAGGTGTATCGGGGCTCGG	3297
Db	3330	TTCCAGATGAAGATCGGGTTGAACATGGCTCGGTTGTAGCAGCGCTCATTTGGGGCCGA	3389
QY	3298	AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCAGC	3357
Db	3390	AAGCCACAGTATGACATCTGGGGAATACCGTGAATGTTTCCAGTCGTATGGACAGCACT	3449
QY	3358	GGGGTCCCGACCGAATCCAGGTGACCGGACCTGTACCAAGTTCTAGCTGCCAAGGGC	3417
Db	3450	GGAGTTCTTGACCGAATACAGGTGACTACGGACCTTATACCAAGTTCTAGCTGCCAAGGGC	3509
QY	3418	TACCAGCTGGAGTGTACGGGCTGTCAAGGTGAAGGCAAGGGGGAGATGACCACTAC	3477
Db	3510	TACCAGCTGGAGTGTGAGGGGTGTCAAGGTGAAGGAAAAGGGGGAGATGACCACTAC	3569
QY	3478	TTCTCTAAATGGGGGCCCGCAGCACTTAAACAGGGCCCGAGC--CACAAATTCAGCTCAAGGGA	3535
Db	3570	TTCTCTAAACGGGGGCCCGCAGCACTTACGAGATGACGAGCTGAGATTCACCAAGGGA	3629
QY	3536	CCAAGTTGGCACT	3549
Db	3630	CCAAGTTGGCACT	3643

RESULT 2

RESULT 2
 US-10-144-771-19529
 ; Sequence 19529, Application US/10144771
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig
 ; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
 ; FILE REFERENCE: CL001321

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: CURRENT APPLICATION NUMBER: US/10/144,771
:
: CURRENT FILING DATE: 2002-05-15
:
: NUMBER OF SEQ ID NOS: 47235
:
: SEQ ID NO 19529
:
: LENGTH: 4349
:
: TYPE: DNA
:
: ORGANISM: HUMAN
:
: FEATURE:
:
: NAME/KEY: misc_feature
:
: LOCATION: (1)...(4349)
:
: OTHER INFORMATION: n = A,T,C or G
:
: US-10-144-771-19529

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Query Match	44.83;	Score 1591.4;	DB 6;	Length 4349;
Best Local Similarity	70.7%;	Pred. No. 0;		
Matches 222;	Conservative 0;	Mismatches 871;	Indels 48;	Gaps 6;
Qy	345	CGCATCTCTGCTGGCGCGCTTTGGTGTCAAGTCTTCCAGTGAAGCAGTATCCGTTGCGGCCAA	404	
Db	123	GGGCGCTGCTGCCTGGCCTTGCTGCAGATATCCGCTCTAAGAAGTTCGCGTCGGACAA	182	
Qy	405	GCTGAGGCGCTGTACACAGCGGTACTTTTTCAGATGAACACAGACAGCCTGACGCTGCT	464	
Db	183	ACTGAGCGCTGTACACAGCGCTACTTCTTCGCGCTGAACACAGACAGCTCTCACATGCT	242	
Qy	465	GGTGGCGGTGCTGTGCTGTCTACAGCGGTGCTGCTGGCTTTTCCAAGCGCACCGGCCG	524	
Db	243	CATGGCGCTGCTGTGCTGTGTGCGCTGGTCATGCTGGCTTTTCCACGGCGCGGCCGCC	302	
Qy	525	CCCTACAGCTGCCATGTGGCACTGTGGCGTGTGGCGCGCCCTGTGTTGGGGCTCAT	584	
Db	303	GCTCATAGATACCTACCTTGGCGGTGTGGCAGCTGCTGTGGCGGTGATCTTATCATGGC	362	
Qy	585	GGTGGTGTAAACCGCATAGCTTCCGCCACGAGCTTCCATGTGGGTGGTGAAGTGAAGTGCT	644	
Db	363	CGTGTCTGAACCGTGCAGCGTTTCCACAGAGACCATAGGCGCTGGCGCTGCTATGCGCT	422	
Qy	645	GCTGGGCATCTGGCGGAGTGCAGGTGGGGGCGCTTTCGACAGACACCGCGCAGCGCC	704	
Db	423	CATTGCAAGTGTGTGGCGGTCCAGTAGTGGGCGTGTGTGTCACAGCCACGACGAGCGC	482	
Qy	705	CTCTGCGGGCCTGTGGTCCCTGTGTCCTTTGTATATACATCGCATACAGCTTCTCCCAT	764	
Db	483	CTCGAGGGCATCTGTGTGGACCGTGTCTTCATCTATACCATCTACACCTTGTGCTGT	542	
Qy	765	CCGATGCGGGCTGCCGTCTCAGCGGCTGGGCGCTCTCCACCTTGCAATTGATCTTGGC	824	
Db	543	CGCATGAGGCTGCGGTGCTCAGCGGGTGTCTTCTGTGGCTCTCCACTTGGCCATCTC	602	
Qy	825	CTGGCACTTAACCGTGTGTATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCT	884	
Db	603	TCTGCACACCAACTCCCAGGACAGTGTCTCTGTAACAGAGCTGTGCTCAATGTCTCAT	662	
Qy	885	GTTCCTCTGCACCAAGTCATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCG	944	
Db	663	CTTCTCTGCACCAACATTTGGGTGTGTGCATCTACTACCAGCTGAGTCTCCCAGAG	722	
Qy	945	CCAGGCGTTTCAGGAGACCCGAGTTACATCCAGGCGCGCTCCACCTGACGATGAGAA	1004	
Db	723	ACAGGCGTTCCAGGAGACCCGGAGTGTATCCAGGCTCGGCTCATTTCCAGCGGGAGAA	782	
Qy	1005	TCGGCAGCAGGCGGCTGCTGCTCGGTATTGCCCCAGCAGCTTGCCATGGAGATGAA	1064	
Db	783	CCAGCAACAGAGGCGTCTCTGTCTGTCTTCTCCCGGTCTATGTGGCCATGGAGATGAA	842	
Qy	1065	AGAAGCATCAACACAAAAAAGA ---CATGTTCACAAGATCTACATACAGAGCA	1121	
Db	843	AGCAGACATCAACGCCAAGCAGGAGATATGATGTTCACAAGATCTACATCCAGAGCA	902	
Qy	1122	TGACAATGTACATCTCTGTTTGACAGCATTTAGAGGCTTACCAGCTGGCATCCCACTG	1181	
Db	903	TGACAATGTAGCATCTCTGTTTGTGACATCGAGGGTTTACCAGCTGGCTTCCCACTG	962	

Qy 1182 CACTGCCAGAGAGCTGTCTACATGACCCCTGAATGAGCTCTTTGCCGGTGTGACAAAGCTGGC 1241
Db 963 TACTGCCCAAGAACTGGTCTATGACCCCTCAATGAGCTCTTCCGCCGCTTGGACAAAGTTGGC 1022
Qy 1242 TGGGAGAAATCACATGCCCTGAGGATCAAGATCTTGGGGAGCTGTACTACTGTGTGTGAG 1301
Db 1023 TGGGAGAAATCACATGGTTTACGGATTAAGATCTTCCGCGGATGTGTACTACTGCGTCTCGGG 1082
Qy 1302 GCTCCGAGGCGCGGCGGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGAT 1361
Db 1083 GCTGCCCTGAAGCCAGAGCCGACCATGCCACTGCTGTGGAGATGGGAATGGACATGAT 1142
Qy 1362 TGAGGCCATCTCGCTGTGTAGCTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCAT 1421
Db 1143 CGAGGCCATCTCGTTGGTCCGGAGGTGACAGGGGTGAACGTGAACATGCGCGTGGGAAT 1202
Qy 1422 CCACAGGGGCGGTGCACATGCCGCGCTTGGCTTCCGGAATGGCAGTTTCGATGTGTG 1481
Db 1203 TCACAGGGGAGAGTACACTGCGGTGTCTTGGTCTCAGAAAGTGGCAATTCGACGTGTG 1262
Qy 1482 GTCCAATGATGTACCTTGGCCAAACCATGGAAGCAGGAAGCGCGGTGCCCGCATCCA 1541
Db 1263 GTCTAAGATGTACTCTGGCCAAACCATGGAAGCTGGTGGCAAGGCGGCGCCCATCCA 1322
Qy 1542 CATCACTCGGGCAACATCTGCAGTACCTGAACGGGGACTACGAAGTGAAGCAGCGCCGTGG 1601
Db 1323 CATCACAAGGCCACACTCAACTACCTGAATGGGGACTATGAGGTGAAGCAGGCTGTGG 1382
Qy 1602 TGGCAAGCGAACCGTACCTCAAGGAGCAGCATTTGAGACTTTCCTCATCTCCCTGGGCGC 1661
Db 1383 TGGCGATGCAATGCCCTTACCTCAAGGAGCAGCATTTGAGACTTTCCTCATCTTCCTGAGCTG 1442
Qy 1662 CAGCGAGAAACGGAAGAGGAGGAGCTGTGCCAAGCTGACGGGAGCTCGGGGCAA 1721
Db 1443 TACCAGAAGCGGAAGAGAGAGGCCATGATCGCCAAAGATGAACCCGACAGAAACCAA 1502
Qy 1722 CTCCATGGAAGGGCTGATGCCCGATGGGTCTCTGTATGCTGTCCTTCTP-----C 1769
Db 1503 CTCCATGGACACAAATCCGCTCTACTGGGAGCGCGCGCCCTTCTACAACTCTTGGG 1562
Qy 1770 CCGGACCAAGGACTTCAAGGCTTCCGCCAGATGGGCAATGATGATTTCCAGCAAGACAA 1829
Db 1563 CGCAACCAAGTGTCAAGAGAGATGAAGAGATGCTTGCCTATGCTGCGCTGGTTC 1622
Qy 1830 CCGGGGACCCAGATGCCCTGAACCTGAGGATGAGGTGATGATGATCTCTGAGCCGTGC 1889
Db 1623 CAGGAATGCCCGAAGAGTGGAAACCCAGAGGATGAAGTGGACGAGTTTCTGGGTGCGGC 1682
Qy 1890 CATCGATGCCGAGCATTTGATCAGCTGCGGAAGGACCATCTGCGCGGTCTTGTCTCAC 1949
Db 1683 CATCGATGCCAGGAGCATTCGACAGACTGCGCATCTGAACAGCTCGCGAAGTTCTCTGAC 1742
Qy 1950 CTTCCAGAGAGAGATTTTGAAGAAGTACTCCCGGAAGTGGATCCCGCTTTCGGAGC 2009
Db 1743 CTTCAGGAGCCGACTTAGAAGAAGTACTCCAAGCAGGTGATGACCGATTTGGTGC 1802
Qy 2010 CTAGCTTGCCTGTGCCCTGTGTGCTTCTGCTCATCTGCTTCATCCAGCTTCTTAATTT 2069
Db 1803 CTATGTGCCCTGCGCCTCGCTTGTCTTCTCTCATCTGCTTTGTCAGATCAACATTTG 1862
Qy 2070 CCCACATCCACCTGATGCTTGGATTTATGCCAGCATCTTCTGCTGCTGTCTAATCAC 2129
Db 1863 GCGCCATCTCCTGTTCATGCTGAGTTTCTTACCTGCTGCTGTGCTGCTGCTTGGT 1922
Qy 2130 CGTGTGATCTGTGCTGTACTCCTGTGGTTCTCTGTTCCCTAAGCCCTTGAACCTCT 2189
Db 1923 GGTCTTTGTGCTGTGATCTATGCTGTG-----TGAGACACT 1961
Qy 2190 GTCCCGCAGCATTTGCGCTACGGGCACATAGACCCGAGTGGCATCTTTTCCGCTCT 2249
Db 1962 CTCAGGAAGATAGTGGGATCCAAAGAGACAGCACCTTGTGCGGGGTATTCACCATCAC 2021
Qy 2250 GCTTGTGTTTACTTCTGCCATTGCCACATGTTCCACTGTAAACCAACCCCATACGAG 2309

Db 2022 CCTGGTCTTCTCGGCTTTTGTCAACATGTTTCATGTGCAACTCTAAGAACCTTGTGGG 2081
Qy 2310 CTGTGACCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCCCTGCCACCTGACGCA 2369
Db 2082 CTGCTGGCAGAGAGACAAACATCACGGTGAACCAAGTCAACGCATGTCTATGTGATGGA 2141
Qy 2370 GC-----TCAAATTACTCTCTGGGCTTGGATGTCTCCCTGTGTGAGGGCCACCATGCCAC 2423
Db 2142 GTCGGCTTCACTACAGCCTGGCGACGAGCAGGGCTTCTGTGGCAECCGCCACCCAA 2201
Qy 2424 CTGAGCTTTCTGAGGTGTCATCGGGAACATGCTGCTGAGTCTTGTGGCAGCTCTGT 2483
Db 2202 CTGCAACTTCCAGAGTACTTCACTACAGCTGCTGCTCAGCCTGCTGGCCTGCTCCGT 2261
Qy 2484 CTTCTCCACATCAGCAGCATCGGGAAGTTGGCCATCATCTTGTCTTGGGGCTCATCTA 2543
Db 2262 GTTCTCCAGATCAGCTGCAATGGAAGCTGGTGTCTCATGCTGGCCATTTGAGTTTCACTA 2321
Qy 2544 TTTGGTCTGCTTCTGCTGGGTCCCCCAGCGGCCATTTTGAACAATATGACCTACTGCT 2603
Db 2322 T---GTCTCATCTGTGGAGTGGCCGCGCTCACACTCTTCGACAACGCTGACCTTCTGGT 2378
Qy 2604 TGGGCTCCATGGCTTGGCTTCTTCCAAATGAGACCTTTGATGGGCTGGACGTGCCAGTGC 2663
Db 2379 CACGCCCAATGCCATAG---ACTTCAGCAACAAGCGGACCTCCCAAGTGGCCTGAGCATGC 2435
Qy 2664 AGGAGGCTGGCCTCAATATATGACCTGTGATCTGCTGGTGTTCGCTGGCTGGCGCT 2723
Db 2436 ACCAAGTGGCGTGAAGTGGTGACGCCCATCATCTCTGCTCTGCTGCTGGCTCT 2495
Qy 2724 GTATCTGCTCAGCAGGTGAAATGACTGCGCGCTAAACTTCTCTGGAACATACA 2783
Db 2496 GTATCTGATGCCAGCAGGTGGAGTCCACTGCTCGCTTGACTTCTCTGGAACATGCA 2555
Qy 2784 GGCACAGGGGAAAGAGAGATGGAGAGCTACAGGCATACACCGAGGCTGTGCTCA 2843
Db 2556 GGCACAGAGAGAGAGAGAGATGGAGAGCTGCAAGCCCTACAATCGGCGCTGTGCTCA 2615
Qy 2844 TAACATTTCTGCCAAGGACGTGGCGGCCACTTCTTGGCGGAGCGCGCAATGATGA 2903
Db 2616 CAACATTTCTGCCAAGGACGTGGCTGCCACTTCTTGGCGGAGCGCAATGACGA 2675
Qy 2904 ACTCTACTATCAGTGTGAGTGTGGCTGTGTATGTTTGGCTCCATTTGCCAACTTCTC 2963
Db 2676 GCTGTACTACCAATGCTGCGAGTGTGGTGTCTATGTTTGGCTTCCATTTGCCAACTTCTC 2735
Qy 2964 TGAGTCTTATGTGAGCTGGAGCAAACTAGGGTGGCGAGTGGCTGGCGCTGTCTCAA 3023
Db 2736 CGAATTTATGTAGAGCTAGAGCCAACTAGAGGGCTGAGTGGCTTACGGCTGTCTCAA 2795
Qy 3024 CGAGATCATCGCTGACTTTGATGAGATTATCAGCGAGAGCGGTTCGCGAGCTGGAAAA 3083
Db 2796 TGAGATCATCGACATTCGATGAGATCATCAGTGAAGATCGGTTCAAGCGAGCTGGAAAA 2855
Qy 3084 GATCAAGACGATTGGTAGCACCCTACATGGCTGCTCAGGGCTGAACCCAGCAGCTACGA 3143
Db 2856 GATCAAGACCATAGGCAAGCACCCTACATGGTGTCTTGGCTTCAACGACTCCACATGA 2915
Qy 3144 TCAGTGGGCGGCTCCACACATCACTGCGCTGGCTGAGCTACGCCATGCGGCTCATGGAGCA 3203
Db 2916 CAAGGCAAGCAAGCCACATCAAGGCTATTGCAAGCTTTCGCTATGAAGCTGATGGACCA 2975
Qy 3204 GATGAAGCAGCATCAATGAGCACCCTTTCAACAATTTCCAGATGAAGATTGGCTGAACAT 3263
Db 2976 AATGAAGTACATCAATGAGCACCCTTTCAACAATTTCCAGATGAAGATTGGCTCAACAT 3035
Qy 3264 GGGCCAGTGTGGCAGGTGTCTATCGGGGCTCGGAAGCCACAGTATGACATCTGGGGGAA 3323
Db 3036 TGGACCTGTATGGCTGGAGTCTATTTGGGGCTCGCAAGCCCTCAGTATGACATCTGGGGCA 3095
Qy 3324 CACAGTCAATGTCTCTAGTGTATGGACAGCAGCGGGGTCCCGCAAGTATCCAGGTGAC 3383

Db 3096 TACAGTGAATGGCCAGCCGATATGACAGCACTGGGTGCTGACCCATCCAGGTAC 3155
Qy 3384 CACGACCTGTACCAAGTTCTAGCTGCCAAGGCTTACCAGCTGGAGTGTGCGAGGGGTGCT 3443
Db 3156 TACAGATATGTACCAAGTGTCTGGCGCCACACATACCAGCTGGAGTCCCGGGGTGCT 3215
Qy 3444 CAAGTGAAGGCCAAGGGGA 3464
Db 3216 CAAGGTCAAGGCCAAGGAAGA 3236

RESULT 3

PCT-US02-36759-83

; Sequence 83, Application PC/TUS0236759

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: DUGGAN, Brendan M.

; APPLICANT: YANG, Junning

; APPLICANT: GIEZEN, Kimberly J.

; APPLICANT: LEE, Soo Yeun

; APPLICANT: TANG, Y. Tom

; APPLICANT: AZIMZAI, Yalda

; APPLICANT: WALIA, Narinder K.

; APPLICANT: WARREN, Bridget A.

; APPLICANT: BARROSO, Ines

; APPLICANT: BECHA, Shanya D.

; APPLICANT: YUE, Henry

; APPLICANT: LEHR-MASON, Patricia M.

; APPLICANT: THANGAVELU, Kavitha

; APPLICANT: LEE, Sally

; APPLICANT: EMERLING, Brooke M.

; APPLICANT: KABLE, Amy E.

; APPLICANT: KHARE, Reena

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: GANDHI, Ameena R.

; APPLICANT: TRAN, Uyen K.

; APPLICANT: RICHARDSON, Thomas W.

; APPLICANT: MARQUIS, Joseph P.

; APPLICANT: LAL, Preeti G.

; APPLICANT: FORSYTHE, Ian J.

; APPLICANT: LEE, Ernestine A.

; APPLICANT: SWARNAKAR, Anita

; APPLICANT: KALLICK, Deborah A.

; APPLICANT: GRIFFIN, Jennifer A.

; APPLICANT: ELLIOTT, Vicki S.

; APPLICANT: GORVAD, Ann E.

; APPLICANT: HAFALIA, April J.A.

; APPLICANT: ISON, Craig H.

; APPLICANT: JIN, Pei

; APPLICANT: JIANG, Xin

; APPLICANT: JACKSON, Alan

; APPLICANT: BHATIA, Umesh

; APPLICANT: BURRILL, John D.

; APPLICANT: BLAKE, Julie J.

; APPLICANT: HO, Ann

; APPLICANT: ZHENG, Wenjin

; APPLICANT: GAO, Jing

; TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS

; FILE REFERENCE: PF-1279 PCT

; CURRENT APPLICATION NUMBER: PCT/US02/36759

; CURRENT FILING DATE: 2002-11-13

; PRIOR APPLICATION NUMBER: US 60/333,097

; PRIOR FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: US 60/335,274

; PRIOR FILING DATE: 2001-11-15

; PRIOR APPLICATION NUMBER: US 60/340,542

; PRIOR FILING DATE: 2001-12-14

; PRIOR APPLICATION NUMBER: US 60/342,166

; PRIOR FILING DATE: 2001-12-18

; PRIOR APPLICATION NUMBER: US 60/347,580

; PRIOR FILING DATE: 2002-01-11

; PRIOR APPLICATION NUMBER: US 60/348,687

; PRIOR FILING DATE: 2002-01-14

; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PERL Program
; SEQ ID NO 83
; LENGTH: 1386
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7506194CB1
PCT-US02-36759-83

Query Match

29.9%; Score 1060.2; DB 1; Length 1386;

Best Local Similarity 97.5%; Pred. No. 1.5e-232;

Matches 1077; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 ATGTCATGGTTAGTGGCTCCTGGTCCCTAAAGTGAATGAACGGAAACACAGCTGGGGT 60
Db 25 ATGTCATGGTTAGTGGCTCCTGGTCCCTAAAGTGAATGAACGGAAACACAGCTGGGGT 84
Qy 61 GAACGCAATGGGCAGAACGCTTCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
Db 85 GAACGCAATGGGCAGAACGCTTCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 144
Qy 121 CCCGCTATATGAGCTGCTCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180
Db 145 CCCGCTATATGAGCTGCTCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 204
Qy 181 CTGGTGGCTTGGCAGGATGACGCTTTCATCCGAGGGGGCGGCCAGGAAGGCAAG 240
Db 205 CTGGTGGCTTGGCAGGATGACGCTTTCATCCGAGGGGGCGGCCAGGAAGGCAAG 264
Qy 241 GAGCTGGGGCTCGGGCAGTGGCCCTTGGGCTTCGAGGATACCGAGGTGACACACAGCG 300
Db 265 GAGCTGGGGCTCGGGCAGTGGCCCTTGGGCTTCGAGGATACCGAGGTGACACACAGCG 324
Qy 301 GCGGGACGCTGAGGTGGCGCGCACCGTGGCCAGAGTGGCGATCTCTGCTGGCGC 360
Db 325 GCGGGACGCTGAGGTGGCGCGCACCGTGGCCAGAGTGGCGATCTCTGCTGGCGC 384
Qy 361 CGTTGGTGCAGGTGTTCCAGTCCGAAGCAGTTCCTTCGGCCAACTCGAGCGCTGTAC 420
Db 385 CGTGGTGCAGGTGTTCCAGTCCGAAGCAGTTCCTTCGGCCAACTCGAGCGCTGTAC 444
Qy 421 CAGCGGTACTTTTCCAGTGAACACAGACAGCTGACGCTGCTGGTGGCGGTGCTGGTG 480
Db 445 CAGCGGTACTTTTCCAGTGAACACAGACAGCTGACGCTGCTGATGCGGTGCTGGTG 504
Qy 481 CTGCTCACAGCGGTGCTGCTGGCTTTCCAGCGCCACCGCCGCCCTCAGGCTGCCTAT 540
Db 505 CTGCTCACAGCGGTGCTGCTGGCTTTCCAGCGCCACCGCCGCCCTCAGGCTGCCTAT 564
Qy 541 GTGGCAGTGTGGCTGTGGCGCCGCTGTTCGTGGGGCTCATGGTGGTGTAAACCGG 600
Db 565 GTGGCAGTGTGGCTGTGGCGCCGCTGTTCGTGGGGCTCATGGTGGTGTAAACCGG 624
Qy 601 CATAGCTTCCGCCAGGACTCCATGTGGTGGTGAAGTGAACGCTGCTGGGATCTCTGGCG 660
Db 625 CATAGCTTCCGCCAGGACTCCATGTGGTGGTGAAGTGAACGCTGCTGGGATCTCTGGCG 684
Qy 661 GCAGTGCAGGTGGGGGCGCTTTCGACAGACAGCCGCGAGCCCTCTGCGGGGCTCTGG 720
Db 685 GCAGTGCAGGTGGGGGCGCTTTCGACAGACAGCCGCGAGCCCTCTGCGGGGCTCTGG 744
Qy 721 TGCCCTGTGTTCTTGTATACATCGCATACAGGCTCTCCCATCCGATCGGGCTGCC 780
Db 745 TGCCCTGTGTTCTTGTATACATCGCATACAGGCTCTCCCATCCGATCGGGCTGCC 804
Qy 781 GTCCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATCTTGGCTGGCAACTTAACCGT 840
Db 805 GTCCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATCTTGGCTGGCAACTTAACCGT 864
Qy 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTTCTCTGCAACCAAC 900
|||||

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Db 865 GGTGATGCTTCTCTCGAAGCAGCTCGGTGCCAATGTGCTGTCTCTCTCGTGCACCAAC 924
Qy 901 GTCAATTAGCATCTGCACACACTATCCAGCAGAGGTGCTCAGCGCCAGGCTTTTCAGGAG 960
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 925 GTCATTGGCATCTGCACACACTATCCAGCAGAGGTGCTCAGCGCCAGGCTTTTCAGGAG 984
Qy 961 ACCGCGAGTTACATCCAGGCGCGGCTCCACCTGCAGCATGAGAAATCGGCAGCAGGCGG 1020
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 985 ACCGCGGTTACATCCAGGCGCGGCTCCACCTGCAGCATGAGAAATCGGCAGCAGGCGG 1044
Qy 1021 CTGCTGCTGTCGGTATTGGCCAGCAGCTTGCCATGAGATGAAGAAGACATCAACACA 1080
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1045 CTGCTGCTGTCGGTATTGGCCAGCAGCTTGCCATGAGATGAAGAAGACATCAATGAG 1104
Qy 1081 AAAAAGAAGACATGTTCCACAAGA 1105
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1105 CACTCCTTCAACATTTCCAGATGA 1129

RESULT 4
US-10-121-911A-2
: Sequence 2, Application US/10121911A
: GENERAL INFORMATION:
: APPLICANT: Kapeller-Libermann, Rosana
: APPLICANT: Chun, Miyoung
: TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE
: FILE REFERENCE: 035800/246627
: CURRENT APPLICATION NUMBER: US/10/121.911A
: CURRENT FILING DATE: 2003-02-05
: PRIOR APPLICATION NUMBER: US 09/412,210
: PRIOR FILING DATE: 1999-10-05
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 3518
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (0)...(0)
: OTHER INFORMATION: 21529 adenylate cyclase
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (247)...(3480)
US-10-121-911A-2
Query Match 14.2%; Score 505.2; DB 6; Length 3518;
Best Local Similarity 50.0%; Pred. No. 1.7e-105;
Matches 1560; Conservative 0; Mismatches 1488; Indels 72; Gaps 9;

Qy 435 CCAGATGAACAGAGCAGCCTGACGCTGCTGGTGGCGGTGCTGTGCTCAGCAGCGGT 494
Db 318 CCAGCAGTACCCTGCTGCTGCTGCTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 377
Qy 495 GCT----GCTGGCTTTCCAGCCGACCCGCCCTCAG--CCTGCCATGTGGCACT 548
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 378 GCTCGCAGTGGCTTGGCCAGCAGCGGAGGAGCTGACCTCAGACCCGAGCTTCTTGACCAC 437
Qy 549 GTTGGCTGTGCCCGCGCTTCTGTTGGGCTCATGGTGGTGTGTAACCGGCATAGCTT 608
    || || || || || || || || || || || || || || || || || || || ||
Db 438 TGTGCTGTGGCGCTGGGCGCTTCTCGTGTGCTGTGGGCTCGCTTCCCGGGAGACGG 497
Qy 609 CCGCAGGACTTCCATGTGGTGTGAGTAACGTGTGCTGGGCATCTTGGCGGAGTGA 668
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 498 ACTGACGCTGGACGCTGCCCTGTCCGGCTTGGTATGGTTCGCTGTAGCGCTAGG 557
Qy 569 GGTGGGGGCGCTTTGGAGCAGACCCGCGAGCCCTCTGCGGGCCCTCTGGTGCCCTGT 728
    || || || || || || || || || || || || || || || || || || || ||
Db 558 CCAGCGCTTCTGTTTCCCGGGGCGGTGGTGGGCGCTGGGACCAAGGTGTCCTATTCT 617
Qy 729 GTTCTTTGTATACATACAGCTTCTCCCATCCGATCCGATCGCGTCCGCTCAG 788
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 618 CTTCGTATCTTACGGGATGTCATGCTGCCCTTGGGCATGCGGGACGCCCGCTCGC 677
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Qy 789 CGGCTTGGGCTCTCCACCTTGCATTTGATCTTGGCCTGGCAA-----CTTAACC 838
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 678 GGGCTCGCTCTCTCACTCTCGCATCTGCTGGCTCTGCTCGGCTGTATCTTGGGCGACAGCC 737
Qy 839 GTGGTGTGCTTCTCTCTG--GAAGCAGCTCGGTGGTCCAATGCTGCTCTCTCTGCAC 896
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 738 GGACTCAGCGCTGCACTGCTGCGCGATTTGGCAGCAACGCACTGCTGCTGCTGCGG 797
Qy 897 CAAGCTCATTAGCATTCACACACTATCCAGCAGAGGTGCTCTCAGCGCCAGGCTTTCA 956
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 798 GAAGCTGGCAGGAGTGTACCACAGGCGCTGATGGAGCGCCCTGCGGGCCAGGTTCCG 857
Qy 957 GGAGACCCGAGTTACATCCAGGCGCGCTCCACCTGCAGCATGAGAAATCGGCAGCAGGA 1016
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 858 GGAGGCATCTCAGCTCCCTGCACCTCAGCGCGGCTGGACACCGAAGAAGCACCAGA 917
Qy 1017 CGGCTGCTGCTGCTGGTATTGCCCAGCAGTTCATGCGATGAGATGAAGAAGACATCAA 1076
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 918 ACACCTTCTCTTGTCCATCTCTTCCCTACCTGGCGCGAGATGAAGCAGAGATCAT 977
Qy 1077 CACAA-----AAAAAGAAGACATGTTCCACAAGAT 1106
    || || || || || || || || || || || || || || || || || || || ||
Db 978 GGACGCTCGAGCAGCAGGGGTACGCGCCAGAGACACTAACATTTCCACAGCCT 1037
Qy 1107 CTACATACAGAAGCATGACAATGTACGATCCTGTTTGCAGACATTTAGGGCTTTCACAG 1166
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1038 CTATGTCAAGAGGCACCGAGGAGTCAGCGTCTGTATGCTGACATCGTGGGCTTTCAGCG 1097
Qy 1167 CTTGGCATCCAGTGCACCTCGCAGGAGCTGGTCATCACCTGAATGAGCTCTTTGGCCG 1226
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1098 GCTGGCCAGCAGGTTCCTCCCTAAGGAGCTGGTCTCATGCTCAATGAGCTCTTTGGCAA 1157
Qy 1227 GTTTGACAAGCTGGCTCGGAGATCACTGCCTGAGGATCAAGATCTTTGGGGACTGTTA 1286
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1158 GTTCGACCATTTGCCAAGGAGCATGAATGATCGCGATCAAGATCTCGGGGACTGTTA 1217
Qy 1287 CTACTGTGTGAGGCTCGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1346
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1218 CTACTGTGCTCTGGGCTGCCACTCTCACTGCCAGACCATGCCATCAACTCGCGGCGCAT 1277
Qy 1347 GGGGTAGACATGATTGAGGCCATCTCGTGGTACGTGAGGTGACAGTGTGAATGTGA 1406
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Db 1278 GGGCTGACATGTGCCGGGCCATCAGAAACTCGGGCAGCCACTGGCTGGGACTCAA 1337
Qy 1407 CATCGCTGGGCTATCCACAGCGGCGGTGCACTCGGGGTCTCTGGCTTGGGGAATG 1466
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1338 CATCGCTGGGCTGCACTCAGGCGAGCTACTGTGTGGAGTCACTCGGGCTGCAGAAAGTG 1397
Qy 1467 GCAGTTCGATGTGTGGTCCCAATGATGTGACCTGGCCCAACCATGGAAGCAGGAGCGG 1526
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1398 GCAGTACGAGCTTTGGTCACTGATGTACACTGGCTTAACCATGGAAGCGCGGTGT 1457
Qy 1527 GGCTGGCGCATCCACATCACTCGGCAACACTGCAGTACTGAAACGGGACTACGAAGT 1586
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1458 ACCAGGCGAGTGCATACAGGGGCTACCTGGCGCTGCTGGCAGGGGCTTATGCTGT 1517
Qy 1587 GGAGCCAGGGCGTGGTGGCAAGCGCAACCGGTACTCAAGAGCAGCAGCATTTGAGACTTT 1646
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1518 GGAGACGCGGCTGAGCATCGGACCCCTACCTTCGGGAGCTAGGGGAGCCTACCTA 1577
Qy 1647 CCTCATCTTGGGCGCCAGCCAGAAACGGAAGAGAGGAGCATGTGGCCAAAGCTGCA 1706
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1578 TCTGGTCACTCATCCAGCGGCGAGAGGAGGATGAAGAAGGCGCACTGCAGGAGGCTTGCT 1637
Qy 1707 GCGGACTCGGCGCAACTCCATGGAAGGCTGATGCCCGATGGGTCTTCTGATCGTCTT 1766
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1638 GTCTCTCTTGGGGCTCAAGATGCGTCCATCACTGCTGATGACCCGTTACCTGGAGTC 1697
Qy 1767 CTCCCGGACCAAGGACTCCCAAGGCTTCCCGCAGATGGGATTTGATGATTTCCAGCAAGA 1826
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1698 CTGGGGGCGCACAAGCCTTTTGGCCACTGAGCCACGAGACAGCCCTGTGTCCACCTC 1757
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Qy	1827	CAACGGGGACCCAGATGCCCTG--AACCTGAGGATGAGGTGGA-TGAGTTCTCTGAG	1881
Db	1758	CACCCCTCTCCGGGAGAAGACCTTGGCTTCCCTTCAGCACCCAGTGGAGCCCTGGATCGGAG	1817
Qy	1884	CCGTGCATCGATGCCCGCAGCATTTGATCAGCTGCGGAAGAACCATGTGCGCGGTTTTT	1943
Db	1818	CCGTACCCCGGGGACTAGATGAACTGGACACCGGGGATGCCAAGTTCTTCCAGGT	1877
Qy	1944	GCTCACCTTCCAGAGAGAGATTTTGAAGAAGTACTCCCGGAAGTGGATCCCQCCTT	2003
Db	1878	CATTGAGCAGCTCAACTCGCAGAAACAGTGAAGAGCAGTCGAAGGACTTCAACCCACITGAC	1937
Qy	2004	CGAGGCTTACGTTGCTGTGCCCTGTGGTCTTCTGTCTTCATCTGTCTTCAFCACAGTCTCT	2063
Db	1938	ACTGTACTTTCAGAGAAGAGATGGAGAAAGATACGAGACTCTCTGCAATCCCGCGCTT	1997
Qy	2064	AATTTTCCCACTCCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCGTGTGCTGTCT	2123
Db	1998	CAATACTATGAAGCCTGCACCTTCTGGTTTTCTTCCAACATTCATATCCAGATGCT	2057
Qy	2124	AATCACCGTCTGATCTGTGCTGTACTCTCTGTGGTTCTCTGTTCCTTAAGGCCCTGCA	2183
Db	2058	AGTGACAAACAGGCCCCAGCTCTGCCATCAG--TATAGCATCACTTTTCTCTCTT	2114
Qy	2184	ACGTCTGTCCCGCAGCATTTGCTCGCTCAGGGGCATAGACACGCGAGTTGGCATCTTTTC	2243
Db	2115	CCTCCTCATCTTTTGTCTCTCAGAGACCCTGATGAGGTGTGTCTCTGAAAGGCC	2174
Qy	2244	CGTCTGCTGTGTTTTACTTCTTGCCATTTGCCAATGTTTCACTTAAACACACCCCAT	2303
Db	2175	CAGATGCTGCATGCTGCTGCCACTGTGTGGCCTGTGTGGCCACACAGCAGGACTGAG	2234
Qy	2304	ACGGAGCTGTGCAGCCCGGATGCTGAAATTTAAACACCTCTGACATCACTGTGCCACCT	2363
Db	2235	AATAGCTTGGGCACGCCACCATCTCTCTGTCTTCCCATGGCCATTACCAAGCTGTT	2294
Qy	2364	GCAGCAGCTCAATTAATCTCTTGGGCTGGATGCTCCCCCTGTGTGAGGGCACCATGCCAC	2423
Db	2295	CTTCTTTCCAAACATCATAGACTGTGCCCTTTCCAGCTGCCAATGTGTCTCCATGATTC	2354
Qy	2424	CTCAGCTTTCTGAGGTGTCCATCGGGAACATGCTGCTGAGTCTCTTGGGCCAGCTCTGT	2483
Db	2355	CAACCTCTCTGGGAGCTCCCTGGGTCTGTGCTCTCATAGTGTCCATACTCCATGCA	2414
Qy	2484	CTTCTCTGCACATCAGCAGCATCGGAAGTTGGCCATGATCTTTGTCTTGGGGCTCATCTA	2543
Db	2415	CTGTGCACGCTGGGCTTCTCTCTGTGCTCCCTCTTCTGCACATGAGCTTCGAGCTGAA	2474
Qy	2544	TTTGGTGTGCTTCTGCTGGGTCCCCCAGCGGCCATCTTTGACAACATATGACCTTACTGTCT	2603
Db	2475	GCTGCTGCTGCTCTGCTGGGTGGCGCATCTGCTCCCTCTTCTCTGTGCACTCCCATGC	2534
Qy	2604	TGGGTCCATGGCTTGGCTTCTTCCAATGAGACCTTTGATGGGTGGACTGTCCAGCTGC	2663
Db	2535	CTGGCTGTGGAATGCTCATGCTCCGCTCTATCTGGGCCCCCTTGGACTCCAGGCCCGG	2594
Qy	2664	AGGAGGGTGGCCCTCAAAATATATACCCCTGTGATCTGCTGGTGTGTTTGGCGTGGCGCT	2723
Db	2595	AGTGTGAAGGAGCCCAACTGATGGTGTCTATCTCTTCTTCATCTTCTTCTTCCCT	2654
Qy	2724	GTATCTGCATGCTCAGCAGGTGGAATCGACTGCCCGCTAAACTTTCCTCTGGAAACTACA	2783
Db	2655	CCTTGTCTGGCTCGCCGAATAGTACTACTTGCCTGGACTTCTCTGTGGAAGAAGAA	2714
Qy	2784	GGCAACGGGGAAGAGAGATGGAGGAGCTACAGGCATACAAACGGGAGGCTGTGCA	2843
Db	2715	GCTGAGGACGAGGAGGAGACAGACGATGGAGAACCCTGACTCGGGCTCTTGGG	2774
Qy	2844	TAACTTCTGCCCAAGAGCTGCGGCCACCTTCTGTGCCGGGAGCGCCGAATGATGA	2903
Db	2775	GACGTGCTCCCTGACAGCTGGCCCCCAGTTTCAATGGCCAGAAACCGGCGCAACGAGA	2834
Qy	2904	ACTCTACTATCAGTCTGTGAGTGTGTGCTGTTATGTTTGTCTCTCAATTTGCCAACTTCTC	2963

Db	2835	TCCTACACAGCTCCTATGAATGGCTTGTCTCTTCGCGCTCAGTCCAGACATTTCAA	2894
Qy	2864	TGAGTTCTATGTGGAGCTGGAGGCAACAATGAGGGTGCCGAGTGCCTGCGGCTGCTCAA	3023
Db	2895	GGAGTTCTACTCTGAATCCAAACATCAATGAGGCGCTAGAGTCTCTGAGGCTGCTCAA	2954
Qy	3024	CGAGATCATCGCTGACTTTTGATGAGATTATCAGCCAGAGCGGTTCCGGCAGCTGGAAAA	3083
Db	2955	TGAGATAAATTTTGTGATTTTTGATGAGCTGCTCTCCAAGGCCCAAGTTCAAGTGGGGTGGAGAA	3014
Qy	3084	GATCAAGACGATTGTTAGCACCTACATGCTGCTCCCTCAGGGCTGAAGCGCCAGCAC-	3137
Db	3015	GATCAAGACCATCGGCAGCACCTACATGCGACCCACAGGCTTAAATGCCACCTCTGGACA	3074
Qy	3138	-----CTACGATCAGGTGGGCGCTCCCCACATCACTGCCCTGGCTGACTACGC	3185
Db	3075	GGATGCAACAACAGGATGCTGAACGGAGCTGCAAGCCACCTATGGTGGAATTTGC	3134
Qy	3186	CATCGGCTCATCGAGCAGATGAACACATCAATCAGACACTCCTTCAACAATTTCCAGAT	3245
Db	3135	CGTGGCCCTGGGCTTAAGCTGACGTCAACAAGAGATCATTCACAACATTTCCCGCT	3194
Qy	3246	GAAGATTGGGCTGAACATGGGCCAGTCGTGGCAGGTGTCAATCGGGGCTCGGAAGCCACA	3305
Db	3195	GCGAGTGGGGTTGAACCATGGACCCGTAGTACCTGGAGTTATTGGGCCCCAGAAGCCGA	3254
Qy	3306	GTATGACATCTGGGGAAACACAGTGAATGCTCTAGTCTGTATGACAGCAGCGGGTCC	3365
Db	3255	ATATGACATTTGGGGCAACACAGTGAACGTGGCCAGCCGATGGAGAGTACAGGAGTCT	3314
Qy	3366	CGACCGAATCCAGGTGACCAACGACCTGTACCAGGTTCTAGCTGCCAAGGCTACCAGCT	3425
Db	3315	TGGCAAAATCCAGTGACTCAGGAGACAGCATGGGCCCTACAGTCCCTGGGCTACACCTG	3374
Qy	3426	GGAGTGTGAGGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACCACTACTTCTCTCAA	3485
Db	3375	CTACAGCGGGGTGTCATCAAGGTGAAAGGCAAAAGGGCAGCTCTGCACCTACTTCTCTGAA	3434
RESULT 5			
PCT-US02-34621-1			
; Sequence 1, Application PC/TUS0234621			
; GENERAL INFORMATION:			
; APPLICANT: Silos-Santiago, Inmaculada			
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE			
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PAIN DISORDERS USING 980			
; FILE REFERENCE: MP101-240			
; CURRENT APPLICATION NUMBER: PCT/US02/34621			
; CURRENT FILING DATE: 2002-10-29			
; PRIOR APPLICATION NUMBER: 60/335,047			
; PRIOR FILING DATE: 2001-10-31			
; NUMBER OF SEQ ID NOS: 2			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 1			
; LENGTH: 6196			
; TYPE: DNA			
; ORGANISM: Homo sapien			
PCT-US02-34621-1			

	Query Match	13.3%;	Score 473.4;	DB 1;	Length 5196;
	Best Local Similarity	49.8%;	Pred. No. 3.9e-98;		
	Matches 1562;	Conservative 0;	Mismatches 1496;	Indels 81;	Gaps 11;
QY	460	CTGCTGGTGGCGGTCTGGTCTGCATCACAGGGTGTCTGTGGCTTTCACAGCCGACCC	519		
DB	380	CTGTGTGGTGGCGGCACATSCCTGGCGTGGCCCTCATCATTCATGGCTTCAGCCAGGGGAC	439		
QY	520	GGCCGCCCTCAGCCTGCCTATGTGGCACTGTTGGCTGTGGCGCGCCCTGTTCGTGGGG	579		
DB	440	CCCTCCAGACACAGCGCATTCGTGGGCATGGGTTCTCGTGTGTGGCGGTGTTCGCGCC	499		
OY	580	CTCATGTGGTGTGTAAACGGGCAVAGCTTCGCCACAGGACTCCATGTGGTGGTGTAGTAAC	639		

Db 3491 GGGCTGGGGCTGAACTGAG 3509

RESULT 7

US-60-436-643-3039
; Sequence 3039, Application US/60436643

; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic Inc.

OTHER INFORMATION: Genbank Accession No M80550

US-60-436-643-3039

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Query Match      12.9%; Score 459; DB 7; Length 4008;
Best Local Similarity 50.8%; Pred. No. 6.5e-95;
Matches 1370: Conservative 0; Mismatches 1240; Indels 87; Gaps
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OV 852 CCTCTGGAA GCAGCTCGGTGCCAATGTGCTGCTCTGCACCAACGTATTAGCAT 911

Db 624 CCTGTTCTGGCAGATACTGGCCAAATGTGATCATTTTCTGGGAACCTTGGGGGAGC 683

07 912 CTGCAACACTATTCCAGGCACGCCCTCCTCACCGCCCGAATTA 071

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[illegible]

24 lanes of gel electrophoresis results. Lanes 1-4 are molecular weight markers. Lanes 5-24 show various DNA bands. Lanes 5-8 are labeled 'A', 9-12 'B', 13-16 'C', 17-20 'D', 21-24 'E'.

[illegible][illegible][illegible]

Db 1983 CATCTTCATCTCTTTGTCTGCTTCCGTGGACAGCTTTTGCAATGACGAAAAAGGCCTC 2042
QY 2247 CTTGCTTTGTTTACTTCTGCCATTGCCAATGTTCACTGTAACACACACCCGCCATACG 2306
Db 2043 CACCTCTCATCTGGCTTTTGAATCATCAGGCATCATCGCCACCGCCCATGGCCACG 2102
QY 2307 GAGCTGTGCAGCCGGATGCTGAATTTAACACCTGCTGACATCAGTCCCTGGCCACCTGCA 2366
Db 2103 GATCTCCCTCACAAATGCTCACACCGCTTATCATACTAACCATGGCTGTGTTCACATGTT 2162
QY 2367 GCAGCTCAATTTACTCTGGCCCTGGATGCTCCCTGTGTGGGGACCATGCCACCTG 2426
Db 2163 TTTCTGAGCAACTCTGAGAGACACCCCTCCACATGCCAATACATCAATGCAACGT 2222
QY 2427 CAGCTTTCTGAGGTGTCCATCGGGAACATGCTGCTGAGTCTCTTGGCCAGCTCTGTCTT 2486
Db 2223 TTTCTGTCGGGATAACACAGCGTCGATTTCTTCATGCTCGAAACTGTGTTTTCTCCCGTA 2282
QY 2487 CTTGCACATCAGCAGNATCGGGAAGTTGGCCATGATCTTTGCTTTGGGGCTCATCTATTT 2546
Db 2283 CTTTCATATACAGCTGCATCTCGGGCTTGATCTCTGCTCGCTTTTCTGAGGGTGAACATA 2342
QY 2547 GGTGCTGCTTCTGCTGGTCCCGCCAGCCGCTATCTTTGACAACTATGACCTACTGCTTGG 2606
Db 2343 TGAGTTAAAAATGTTAATCATGATGGGCACCTCGGGGTACACACCACTTACTTCCA 2402
QY 2607 CGTCCATGCGCTTGGCTTTCTTCCAAATGAGACCTTTGATGGGCTGGACTGTCCAGCTCGAG 2666
Db 2403 CACCCATGCC---CATGTTCTGGATGCGTACAGCCAGGCTCTGTTTCAGAGACAGGCAT 2459
QY 2667 GAGGTGGCCCTCAATATATAGCCCTGTGATTTCTGCTGGTGTGTCGGTGGCGGTGGTA 2726
Db 2460 TTGGAAGACCTGAAGACCATGGGCTCCGCTGCTCACTCTCCATATTTCTACACGCTGCT 2519
QY 2727 TCTGCACTGCTCAGCAGTGAATCGACTGCTCCCGCTAAACTTCTCTGGAACACTACAGGC 2786
Db 2520 GGTCTTGGGCAGACAGTAGTAATTAATCTAGTTAGATCTTCTGTGGAAGACAAGTT 2579
QY 2787 AACAGGGGAAAAAGAGATGAGGAGCTACAGGCATACAAACCGGAGGCTGTGTCATAA 2846
Db 2580 CAAAAAGAGCGGAGAGATGAACACCATGGAGAACCTAAATCGAGTGTGCTGGAGAA 2639
QY 2847 CATCTGCCAAGAGCTGGCGCCCACTTCTGGCCGGAGCGCCGCAATGATGAAT 2906
Db 2640 CGTGTCTTCTGACAGCTGGCTGAACACTTCTCGGCGAGAGGCTGAAAAATGAGGAGCT 2699
QY 2907 CTACTATCAGTCTGTGAGTGTGCTGTATGTTTGCCTCCATTCGCAACTTCTCTGA 2966
Db 2700 GTACCACCACTCTACGACTGTCTCTGTCTGTCATGTTTGCCTCCATTCGCGACTTCRAGGA 2759
QY 2967 GTTCTATGGAGCTGGAGGCAACAAATGAGGTGCGGAGTGTGCTGGCGTGTCTCAACGA 3026
Db 2760 GTTCTACAGAGTCAAGTGTGAACAAGGAAGGCTTGGAAATGCTGCGGCTCTGAAATGA 2819
QY 3027 GATCATCGCTGACTTTGATCAGATTATCAGCGAGGAGCGGTTCCGGCAGCTGGAAGAAT 3086
Db 2820 GATCATTTGCTGACTTTGATGATCTGCTTTCTAAGCCCAAAAGTTTCAGTGGTGTGAAAAGAT 2879
QY 3087 CAAGAGATTGGTAGCACCTTACATGCTGCTCAGGCTGAACGCCAGCACCTACGATCA 3146
Db 2880 CAAGACCATTTGGGAGCACATACATGGCAGCCACGGGACTGAGTGCCATACCCAGCCAGGA 2939
QY 3147 GTTGGGCT-----GCTCCCACTACACTGCCCCCTGGCTGAGTACGCGCAT 3188
Db 2940 GCAGGCCCAAGAACCTGAGCGTTCAGTACATGACATAGGCACCATGTTGGGTTTGATGA 2999
QY 3189 GCGGCTCATGAGCAGATGAGCACATCAATGAGCACTCTCTTCAACAAATTTCCAGATGA 3248
Db 3000 TGCCCTTGGTGGGAAACTTGATGCCATCAATAAGCACTCTCTCAACGACTTCAAACTGGC 3059
QY 3249 GATTGGGCTGAACATGGGCCAGTTCGTGGCAGGTGTCTATCGGGGCTCGGAAGCCACAGTA 3308
Db 3060 AGTGGGTATCAACCATGGGCTCTAATAGCTGGCGTCATAGGGGCTCAAAAGCCACAGTA 3119

QY 3309 TGACATCTGGGGAAACACACAGTGAATGTCTAGTCTGATGGACAGACGGGGTCCCCGA 3368
Db 3120 TGACATCTGGGGAAACACTGTCAACGTGGCCAGCAGAAATGACAGACCGGGTCTCTGGA 3179
QY 3369 CCGAATCCAGGTACACAGGACCTGTACAGGTCTTACAGTTCGCCAAGGCTTACCAGCTGGA 3428
Db 3180 CAAAATACAGGTGACTGAGGAGACAGCCTCATCTTTCGACAGCGTTGGCTACACGTGTAC 3239
QY 3429 GTGTGAGGGGTGTCAAGGTGAAGGCAAGGGGAGATGACCACTTACTTCTCTCAA 3485
Db 3240 ATGTCGAGGTATCATCAATGTGAAGGGAAGGGGACCTGAAGACATATTTGTGAAA 3296

RESULT 8
US-10-305-720-1344
; Sequence 1344, Application US/10305720
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Express
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1344
; LENGTH: 2731
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No: g349268
US-10-305-720-1344

Query Match 12.7%; Score 452.4; DB 6; Length 2731;
Best Local Similarity 52.3%; Pred. No. 1.8e-93;
Matches 1274; Conservative 0; Mismatches 1046; Indels 114; Gaps 8;

QY 1064 AAGAAGACATCAACACAAAAAAGAACATGTTCCACAAGATCTACATACAGAACGATG 1123
Db 1 AAGAGGACTTCTTGAGCCCTCGAGAGGATTTCCACAAGATTTACATCAGAGGCAG 60
QY 1124 ACAATGTACAGATCTGTTTTCAGACATTTAGGGCTTTCACAGCCTGGCATCCAGTGC 1183
Db 61 ACAATGTAGCATCTGTTTGTGTCATCGTGGGTTTTCAGGGGCTTGGCATCCAGTGC 120
QY 1184 CTGGCAGGAGCTGGTCATGACCTGAATGAGCTCTTTGCCCGTTTGACAAGCTGGCTG 1243
Db 121 CAGCCAGGAGCTGGTGAACACTCTCAATGAGCTCTTTCGCAAGTTTCGATGAATTAGCCA 180
QY 1244 CGGAGATCACTGCTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGC 1303
Db 181 CGGAGAACCATCTGCGCCGCATCAAGATTTCTGGGGACTGCTACTACTGCGTGGGCC 240
QY 1304 TGCGGAGGCCCGGGCCGACCATGCCACACTGCTGTGTGGAGATGGGGGTGAGCATGATG 1363
Db 241 TCACCCAGCCCAAGACTGACCATGCCCACTGCTGTGTGGAGATGGGACTCGACATGATG 300
QY 1364 AGGCCATCTCGCTGGTACGTGAGGTGACAGTGTGAATGTGAACATCGGCTGGGCATCC 1423
Db 301 ATACCATCATCTGTGGCTGAAGCCACCGAGGTGGATCTGAACATCGGCTGGGTCTGC 360
QY 1424 ACAGCGGGCGTGCATCTGGGGCTCTCTTGGCTTTCGGAATAGGCAGTTGATGTGTGGT 1483
Db 361 ACAGGGCAGGGTCTCTGTGGTCTCTGGCTTTCGCAAGTGGCAGTACGACGTGTGGT 420
QY 1484 CCAATGATGTACCTTGGCCCAACCATGGAAGCAGGAAGCCGGGCTGGCCGATCCACA 1543
Db 421 CCAATGATGTGACCTTGGCCCAATGTCATGGAAGCCGCTGGCCCTGCCAGGAAGTTTATA 480
QY 1544 TCACTCGGGCAACACTGCACTACCTACCTGAAACGGGACTACGAAGTGGAGCCAGGCGCTG 1603

Db 481 TCACAAAGACGACCTAGCTGCTTGAATGGGACTACGAGGTAGAACCAGGTTACGGAC 540
Qy 1604 GCAAGCCCAACGCGTACTCAAGGAGCAGCACATTTGAGACTTTCTCATCTCTGGCGCCA 1663
Db 541 ATGAGAGGAACAGTTCTTGAAGAACTCATACATCGAAACCTTTTATTTGTCGCATCCC 600
Qy 1664 GCCAGAAACGGAAGAGAGAAAGGCGATGCTGGCCAAAGCTGCAGCGGACTCGGGCCAAC 1723
Db 601 ATCCCGAAAGATATTTCCAGGCGTATCTCTCAGATATAAAA-----CCGCGCAAAA 654
Qy 1724 CCATGGAAGGCTGATGCGCGGATGGGTTCTGTATGCTGCTTCTCCGGGACCAAGACT 1783
Db 655 GGATGAAGTTCAAGACTGTCTGTACTGTGTGTGTCAGCTCATCGACTGCGCGAAATGT 714
Qy 1784 CCAAGGCTTTCCGCGCAGATGGCATTTGATGATTCACGAAAGCAACCGGGGCCCAAG 1843
Db 715 TCAAGCGGAGATCCCTTCTCCNAATGTATGACTCGGAGGACA----- 760
Qy 1844 ATGCCCTGAACCCCTGAGGATGAGTGGATGATTTCTTGAGCGGTGCCATCGATCCCGCA 1903
Db 761 -----TGACAAAGCGGAGGCGATTAGAAGACGCTCGGAAAACTCAGAAACCGCTCA 812
Qy 1904 GCATTGATCAGCTCGGGAAGACCATGTGCGCGGTTTGTGCTCACCTTCCAGAGAGAG 1963
Db 813 TCTTTTCTTACCAACG-----TTGTCTACACCAACCCCGGGCACTC 852
Qy 1964 ATTTTGAGAAAGTACTCCCGGAAGGTGGATCCCGCTTCCGGAGCGCTAGCTTGCCTGTG 2023
Db 853 CGGTCAACAGGTACATCAGCGGCTCTTAGAAGCCCGCCAGACAG---AGCTGGAGATGG 909
Qy 2024 CCCTGTGGTCTTGTCTTCACTGCTTCATPCCAGCTTCTTAATTTCCACACTCCACCC 2083
Db 910 CAGACCTGAACCTTTTACCTGAAGTACAAACATGTGCAAGCGGACGAAAGTACCACC 969
Qy 2084 TGATGCTTGGATTTATGCCAGCATCTCTGCTGCTTAATCAACCGTCTGATCTGTG 2143
Db 970 AGCTTCAGGACGAGTATTTCAACGAGCGGTTGTCTCACCCCTCATCTGCTGCTGCTTAT 1029
Qy 2144 CTGTGTACTCCTGTGGTCTCTGTTCCTTAAGGCCCTGCAACGCTCTCCCGCAGCATG 2203
Db 1030 TTGGCTTGTCTACCTTCTAATATCCACAGAGTGTGGTCTGCTCTCC----- 1080
Qy 2204 TCCGCTCAGGGCACATAGCAGCGAGTTGGCATCTTTTCCGCTGCTGCTGTGTTACTT 2263
Db 1081 -----TGCTAGTATTCTGCATCTGCTTCTGCTGGCGCT 1113
Qy 2264 CTGCATTGCCAACATGTTCACTGTAAACACACACCCCATACGAGCTGTGCACCCGGA 2323
Db 1114 GTGTCTGTACCTGCACATCACCAGGTCAGTGTTTTCCAGGGTGCCTGACGATTCAGA 1173
Qy 2324 TGCTGAATTTAACAACCTGCTGACATCACTGCCTGCCACCTGCACAGCTCAATTTACTCTC 2383
Db 1174 TTCGACTGTCTGTGTTTTCATAGTGTCTTAATCTACTAGTAGGCCCAAGGTTGTG 1233
Qy 2384 TGGCCCTGGATGTCCTCCCTGTGTGAGGGCACCATGCCCCACCTGTCAGGTTTCTCAGGTGT 2443
Db 1234 TGTGGGCTGCCTGCTTGGGCTTGGAGCTTCCAAAGCCCAACAGTTCCCTGCTGCTCTT 1293
Qy 2444 CCATCGGGAACATGCTGCTGATCTCTTGGCCAGCTCTGTCTTCTGCACATCAGACGA 2503
Db 1294 CGTCTGGGGCGACG-----GCACAGCCCTGGCCACCCCTGCCCTGCGAGTCT 1340
Qy 2504 TCGGGAAGTTGGCCATGATCTTGTCTTGGGCTCATCTATTGGTGTGCTTCTGCTGG 2563
Db 1341 ACACACCATGCCCTGCTGCTGCTGGTGGGACCCCTCCCGCTAGCCATATTTTCCGG 1400
Qy 2564 GTCCCCCAGCGGCATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTT 2623
Db 1401 GTGTCTCTTGTGCAAAATGATCTGCTCTCCGGGCTCACCAAGTCTCTACATCCTGTT 1460
Qy 2624 CTTCCAATGAGACCTTTGATGGGTGGACTGTCTCCAGCTTGAGGGAGGCTGCCCTCAAT 2683

Db 1461 CTGAGGCTCAGCGGATACACCAGG-----ACTGGGGGTGGTCCGCTCTCCGGCGCAGCT 1515
Qy 2684 ATATGACCCCTGTGATTCTGCTGGTGTGGTCTGGCGCTGTATCTGATGCTCAGCAGG 2743
Db 1516 ACGAGCCGATTGTGGCCATCTCTCTTCTCTGTGCGCTGGCCTGCTGATGCCAGCAGG 1575
Qy 2744 TGAATCGACTGCCCGCTAAACTTCTCTTCTGAAACTACAGGCAACAGGAAAAAGAGG 2803
Db 1576 TGGACATCAGGCTGAGGCTGGACTTACCTTCTGGCGCACAGCAGAGGAGGAGCAGAGG 1635
Qy 2804 AGATGGAGGAGCTACAGGCATACAAACCGAGGCTGCTGCTGATCAATCTTGCCTCAAGGAGG 2863
Db 1636 ACATGGAGAAGGTGAAGCTGGACAACAGGCGCATCTCTTCAACCTCTGCGGCCACG 1695
Qy 2864 TGGCGGCCACTTCTGCGCCGGGAGCGCCCAATGATGAACCTCTACATCATCAGTCTGCTG 2923
Db 1696 TCGCCAGCACTTCTCATGTCCAAACCTCGGAACATCGACTCTACTACCAGTCTACT 1755
Qy 2924 AGTGTGGCTGTATGTTTGCCTCCATTTGCCAACTTCTCTGAGTCTATGTGGAGCTGG 2983
Db 1756 CCCAGGTGGGCTCATGTTTGCCTCCATCCCACTTCAATGACTTCTACATCGAGCTGG 1815
Qy 2984 AGGCAACAATGAGGTCGCCAGTGCCTGCGGCTGCTCAACGAGATCATCTGACTGACTTTG 3043
Db 1816 ACGCAACAACATGGGCTGGAGTGTCTGCGGCTTCTCAACGAGATCATCTGCCGACTTTG 1875
Qy 3044 ATGAGATTATCAGCGAGGAGCGGTTCCGGCAGCTTGGAAAGATCAAGAGATTGTTAGCA 3103
Db 1876 ACGAGCTCATGGAANAAGACTTTTACAAGGACATAGAAAGATCAAGACCATCGGGAGCA 1935
Qy 3104 CCTACATGGCTGCCTCAGGGCTGAACGCC-----AGCACCTTACGATCAGSTGGGCC 3154
Db 1936 CCTACATGGCGCTGTGGGCTAGCGCCACCTCGGGGACCAAGGCTAAGAAGTCCATCT 1995
Qy 3155 GCTCCCATCACTGCTGCCCTGCTGACTAGCCATCGGCTCATGAGCAGATGAGACACA 3214
Db 1996 CTTCCACCTGAGCAGCTGCGGACTTTGCCATTTGAGATGTTTGACCTTCTGGATGAAA 2055
Qy 3215 TCAATGAGCACTCCTTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGGCCAGTCG 3274
Db 2056 TCAACTACCACTCTTACAACGACTTTGTCTCCGAGTTGGCATCAATCTTGGCCTGTGG 2115
Qy 3275 TGGCAGTGTCTATCGGGCTCGGAAGCCACAGTATGAGATCTGGGGGAACAGTGAATG 3334
Db 2116 TGGCTGAGTGTATTTGGGCTCGCAGGCCCACTAGACATCTGGGGAACACAGTCAACG 2175
Qy 3335 TCTCTAGTGTATGGACAGCACGGGGTCCCGCCGAGTCCAGTGAACACGAGCTGT 3394
Db 2176 TGGCCAGTCGGATGGATAGCACAGGGTCCAGGGCAGAAATCCAGTGAAGTCC 2235
Qy 3395 ACCAGTTCTAGCTGCCAAGGGCTACCAGCTGGAGTGTGCGAGGGTGTCAAGGTGAAGG 3454
Db 2236 ACCGCTGCTGAGAAGGTGCCCCCTACCATTGTTGTCGCGAGGCAAGTCAAGTGTCAAGG 2295
Qy 3455 GCAAGGGGAGATACCACTACTTCTCTCAATGG 3488
Db 2296 GCAAGGCGAGATGTGACATACTTCTTAGAAGG 2329

RESULT 9

US-10-144-771-18424
; Sequence 18424, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 18424
; LENGTH: 5124
; TYPE: DNA
; ORGANISM: HUMAN

US-10-144-771-18424

Query Match 12.2%; Score 432.4; DB 6; Length 5124;
Best Local Similarity 51.1%; Pred. No. 8.6e-89;
Matches 1434; Conservative 0; Mismatches 1221; Indels 149;

5; 12;

Qy	853	CTCTGGAAGCAGCTCGGTCGCCAATGTGCTGTCTCTCTGCACCAACAGTCATTTAGCATC	912
Db	1136	CTGGGGTCGAGCTCTCGGCCAATCCGGTTATCTCTTGGTGGGAACTTCACGGGTGC	1195
Qy	913	TGCACACACTATCCACGACAGGTGTCTCAGCCGACAGGCTTTTCAGGAGACCCGACGTTAC	972
Db	1196	TTCCACACAGCAGCTGCAGACGGCTCCAGGGATCTCTTTATCTACACCGTCAATATGC	1255
Qy	973	ATCCAGGCGCGGCTCCACCTGCAGCATGAGATCGGCAGCAGGAGCGGCTGCTCTCTCG	1032
Db	1256	ATCCAGATCCGTCGGAAGCTTCGTGTGGAGAAGCCAGCAGGAGAACCTGCTTCTCTGCA	1315
Qy	1033	GTATTGCCCCAGCACGTTGCCATGGAGATGAAGAAGACATCA-----	1075
Db	1316	GTGCTCCAGCACACATCTCCATGGGTATGAAGCTGGGCATCATTTGAGCGCCTCAAAAG	1375
Qy	1076	-----ACACAAAAAAGAACATGTTTCCACAAGATCTACATACAGAAGCAT	1122
Db	1376	GGTGGTCACGACACTACATGCCGACACAACTTTACAGCTCTATGTCAAGCGCAC	1435
Qy	1123	GACAATGTACAGCATCTGTTTGAGACATTTAGGCGCTTTACACGCTTATGTCAAGCGCAC	1182
Db	1436	CAGAAATGTACAGCATCTGTATGCAGACATCGTGGGCTTTACAGAGCTGGCCAGCGACTGC	1495
Qy	1183	ACTGCGCAGGAGCTGCTCATGACCTGTAATGAGCTTTTGCCCGGTTTGACAAGCTGGCT	1242
Db	1496	TCTCCCAAGGAGCTGTGTGGTGTCTCAACGAGCTGTTTGGGAAGTTTGACACGATTGCT	1555
Qy	1243	CGCGAGAATCACTCCCTGAGGATCAAGATCTTTGGGGAGCTGTACTACTGTGTCTCAGG	1302
Db	1556	AAGGCCAATGAGTGCAATCGGATCAAGATCCTGGGTGACTGTTACTACTGGTGTCAAGC	1615
Qy	1303	CTGCCGAGGCCCGGCGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGATT	1362
Db	1616	CTGCCCGTGTGCTGGCCACATATGCCCGCAACTCTGTAAGATGGGTCTGGACATCTGC	1675
Qy	1363	GAGGCCATCTCGTGTAGTGAAGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATC	1422
Db	1676	GAGGCCATTAAACAGTGGCTGAGGCCACGCGCTGGACATCAGCATGCCGTGGGCAATT	1735
Qy	1423	CACAGCGGCGCTGCACTCGCGGCTCTTGCTTGCAGAAATGGCAGTTTCGATGTGTGG	1482
Db	1736	CACCTCCGGGAATGTGTATCTGGGGTCACTCGGGCTCCGTAAGTGGCAGTATGATGTGG	1795
Qy	1483	TCCAATGATGTACCTTGCCCAACCATGGAAGCAGGAAGCCGGCTGGCCGATCCAC	1542
Db	1796	TCCCATGATGTGCTTGGCCCAACAGATGAGGACAGCTGGAGTCCCTTGGCCGGGTGCAC	1855
Qy	1543	ATCACTCGGCAACACTTGCAGTACCTGAAACGGGACTACGAAGTGGAGCCAGGCGCTGGT	1602
Db	1856	ATCACAGGCAACATTGAATCACCTGGACAGGCAATACGAGGTGGAGATGGGCATGGG	1915
Qy	1603	GGCAAGCGCAACCGGTACCTCAAGGAGCAGCACATTGAGACTTTCTCAWCTTGGGCGCC	1662
Db	1916	GAGCAGCGAGACCCCTATCTGAAAGAGATGAACATCCGAACCTACCTGGTGATCGATCC	1975
Qy	1663	AGCCAGAAACGGAAGAGGAGAAGGCATGCT-----GGCCAAGCTGCACGCGACT	1713
Db	1976	CGGAGCAGCAGCACCCACCCACCCAGCCACCACTCTTCCAAGCCCCAGGGGACGCAACT	2035
Qy	1714	CGGGCCAACCTCCAATGGAAGGGCTGATGCGCGCATGGGTTCCTGTAGTCTGTCCTCCCG	1773
Db	2036	CTGAAGATGCGGGCTTCAGTGCCTGTAACCCCTATCTGGAGTCTTGGGGGCAACGAAG	2095
Qy	1774	ACCAGGACTTCCAAAGCGCTTTCGCCAGA---TGGGCATTGATGATTCAGCAAAAGACAAC	1830
Db	2096	CCCTTTGCACACCTCAACCAACCGGAGAGTGTGAGCAGCAGTGAGACCCCATCTCCAAT	2155

QY	1831	CGGGGCACCCAGATGCCCT-----	1851
Db	2156	GGACGGAGCAGAAAGCCATTCTCTGCGTCGACACCGCTGCCCTGATAGAGTGCATCC	2215
QY	1851	-----GAACCTGAGGATGAGTGCATGTTCTCTGAGCCGTGCATCGATCGCGCA	1903
Db	2216	CCCAAGGCGCTTGGAAAGATGACTGTGATGACAGATGCTGTACGCCATTGAGGGTCTCA	2275
QY	1904	GCATTGATCAGTGCG-----GAAGACCATGTGCGCCGTTTTTGTCTCACCTTCC	1954
Db	2276	GCTCCACAGGCCCTGCTGCTCCAACTCTGACTTCCACACTTTGGTCCCATCTTCT	2335
QY	1955	AGAGAGAGATTTTGAGAGAAGTACTCCCGGAAGTGGATCCCGCTTCGGAGCCTACG	2014
Db	2336	TGGAGAAGGCTTTTGAGCGTAGTACCGCTGTGTGCCATTCGCCCGGGCTCGGTACGACT	2395
QY	2015	TTGCGCTGCGCCCTGTTGGTCTTCTGCTTCACTCTGCTTCATCCAGCTCTTAATTTCCAC	2074
Db	2396	TCGCGTGTGCCAGCCTTGCTTCGCTGTGATCCTGTGTGCCACCTCTTAGTGATGCCCA	2455
QY	2075	ACTCCACCCTGATGCTTGGGATTTATGCCAGATCTTCCTGTCTGTCTGAATCACCGTGC	2134
Db	2456	GGATGGCAACTCTGGGTGTGTCCTTTGGTGTGTGCCCTGCCCTGGTCTGTCTGA	2515
QY	2135	TGATCTGTCTGTGTACTCTCTGTGGTCTCTGTTCCTTAAGGCCCTGCAACGCTCTGCC	2194
Db	2516	GTTTCTG-----CTTTGCTACTGAGTCTCTGAGGTCTGTCCATCCGGAATA	2563
QY	2195	GCAGCATTTCCGCTCACGGGCACATAGCACCGCAGTTTGGCATCTTTTCGGTCTCTGCTTG	2254
Db	2564	CACCTCCAGGCCATCTCGGAGAGCGTGGAGACGACGACGCCCTGGTCTGAGCTTGTCTGGTTG	2623
QY	2255	TGTTTACTTCTGCCATTGCCARATGTTCACTCTTCACTGTAAACACACCCCATACGAGCTGTG	2314
Db	2624	TGCTGACTCTTGGCAGCCTACTGACTGTGCCATCATTAACATGCCACTGACCTTTAACC	2683
QY	2315	CAGCCCGGATGCTGAATTTAAACACTGCTGACATCACTGCTGCCACTGCCACAGCTCA	2374
Db	2684	CAGGCCACAGCAG-----CCTGGAGACAACAAGACAAGCCCACTGGCTGCACAGA	2734
QY	2375	ATTACTCTCGGCCCTGGATGCTCCCTGTGTAGGGCACCATTGCCACCTGCAGCTTTC	2434
Db	2735	ACAGAGTTGGGACCCCATGTGAGCTCCTCCGTACTACACTGAGCTGCACTCTTGGGCT	2794
QY	2435	CTGAGGTGCCATCGGGAACATGCTGCTAGTCTCTTGGCCAGCTGTCTTCTCTGCACA	2494
Db	2795	TCATTGCATGCTGTGTTTCTCGGATGAGCCTAGAGCTGAAGGCCACTGCTGTGACAG	2854
QY	2495	TCAGCAGATCGGGAAGTTGGCCATGATCTTTGTCTTTGGGGCTCATCTATTTGGTGTCTG	2554
Db	2855	TGGCCTTGGTGGCCTACCTGCTCTCTTCAACCTCTCCCATGCTGGCAGCT-CTCAGGC	2913
QY	2555	TTCTGCTGGTCCCCCAGCGCCATCTTTGACAACATATGACCTACTCTTGGGCTCCATG	2614
Db	2914	AACAGCACTGAGACCAACGGGACACAAGACACGGCTG--CTTCTGTCTGATGCACAAA	2971
QY	2615	GCTTGGCTTCTTCCAATGAGACCTTTTGATGGGCTGGAGTGTCCAGCTGCAGGAG-----	2669
Db	2972	GCATGCCACGACACACCTTGCTCCGGGGCTCGGAGACTGCCCCCTCTCCCAAGTTATT	3031
QY	2670	----GGTGGCCCTCAATATATGACCCCTGTGATTCTGTGGTGTTTTGGCCTGGCGCTGT	2725
Db	3032	TAGAGAGACCTTGAAGATCATGGTTAACTTCTACCTGATCTCTTGTATGCCACCCCTCA	3091
QY	2726	ATCTGATGCTCAGCAGGTGGAATCGACTGCCCGCCTAAACTCTCTCTGGAACATCAGG	2785
Db	3092	TCTTGTGTCTAGACAGATTGACTACTATGCGCCTTGGACTGTCTGTGGAAGAAGAAGT	3151
QY	2786	CACACGGGAAAAGAGGAGATGGAGAGCTACAGGCATACACCGGAGGCTCTGTGATTA	2845
Db	3152	TCAAAAGGAGCAGGAGAGTTTGAACAATGGAGATGTGAACCGCTCTCTCTGGAGA	3211

Qy 2846 ACATTCGCCAAGAGAGCTGGCGCCACATTCCTGGCCCGGAGCGCCGAATGATGAAC 2905
Db 3212 ATGTCGTCGGCGCACGTGGCTGCCACTTCATTG---GGCAAGGCACAGAGGATT 3268
Qy 2906 TCTACTATCAGTCTGTGAGTGTGGCTGTATGTTTGCTCCATTCGCAACTTCCTG 2965
Db 3269 GGTACCATCAATATGACTGTCTGTGTGTCATGTTTGCATCCGTTCCGGACTTCAAG 3328
Qy 2966 AGTTCTATGTGCTGGAGCAACAATGAGGTGGCGAGTGGCTGGCGTCTCAACG 3025
Db 3329 TGTTCACAGTGTGATGTCAACAAGAGAGACTGGAGTGGCTTCGACTGCTGATG 3398
Qy 3026 AGATCATGCTGACTTTGATGAGATTATACGAGGAGCGGTTCCGCGAGCTGGAAGA 3085
Db 3389 AGATAATGTCTGATTGACGAGTCTGTGTGTCATGTTTGCATCCGTTCCGGACTTCAAG 3448
Qy 3086 TCAAGACGATTGGTAGCACCTACATGCTGCTCAGGCGTGAAGCC----- 3132
Db 3449 TCAAGACATTGGCAGCACCTACATGGCGGAGGAGGCTCAGTGCCGCCCTCAGGACATG 3508
Qy 3133 --AGCACCTACGATCAGTGGCGGCTCCACATCACTGCTGCTGGCTGACTACGCTATGC 3190
Db 3509 AGAACAGGACCTGGAGCGGAGCACGTGCACATCGGAGTCTTGTAGAAATTAGCATGG 3568
Qy 3191 GGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCTCTCAACAATTTCCAGATGAAGA 3250
Db 3569 CCCTGATGAGCAAGCTGGATGGGATCAACAGGCACCTCTTCAACTGCTTCCGCCCTCGAG 3628
Qy 3251 TTGGGCTGAACATGGGCCAGTCTGGCAGGTGTCATGGGGCTCGGAAGCCACAGTATG 3310
Db 3629 TCGGCATAAACCCAGGGCTGTGATGCTGGAGTGATGGAGCAGCGAAGCTCAGTATG 3688
Qy 3311 ACATCTGGGGAACACAGTGAATCTCTAGTCTGTATGGAGAGAGCGGGTCCCGGACC 3370
Db 3689 ACATCTGGGGAACACAGTCAATGTCGACCGCATGGAGAGCACCGGAGCTTGGGA 3748
Qy 3371 GAATCCAGGTGACACGAGCCTGTACAGGTTCTAGCTGCGCAAGGGTACCAGCTGGAGT 3430
Db 3749 AAATCCAGGTTACCGAAGAGACATGCACTATCCTCCAGGGACTCGGATATTCGTGTAAT 3808
Qy 3431 GTCCAGGGGTGTCAAGGTGAAGGCAAGGGGAGAGATGACCACTACTTCTCAATGGG 3490
Db 3809 GCCGTGGCTGATCAAGCTCAAGGCAAGGGGAACTCGGAGCTTACTTTGTATGTACAG 3868
Qy 3491 GCCCCAGCTTAACAGGGCCCGCCACACAATTCAGCTGAAGG 3534
Db 3869 ACACCTGCCAAGTTTCAAGGGCTGGGCTAAACTGAGGTGGCTGG 3912

RESULT 10

US-10-338-044-2053
; Sequence 2053, Application US/10338044
; GENERAL INFORMATION:
; APPLICANT: MENDRICK, Donna
; APPLICANT: PORTER, Mark
; APPLICANT: JOHNSON, Kory
; APPLICANT: HIGGS, Brandon
; APPLICANT: CASTLE, Arthur
; APPLICANT: ELASHOFF, Michael
; TITLE OF INVENTION: Molecular Cardiototoxicology Modeling
; FILE REFERENCE: 44921-5090-01-US
; CURRENT APPLICATION NUMBER: US/10/338,044
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 60/303,819
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,623
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/369,351
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 2696
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2053
; LENGTH: 3357
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_019285
US-10-338-044-2053

Query Match 12.1%; Score 428; DB 6; Length 3357;
Best Local Similarity 50.0%; Pred. No. 7.4e-88;
Matches 1337; Conservative 0; Mismatches 1250; Indels 89; Gaps 7;

Qy 862 CAGCTCGGTGCAATGTCGTCTCTCTGTCACCAACGCTATTAGCATGTCACACAC 921
Db 626 CAGTTGGCAGCAATGCGGTGTTCTCTGTGTGGAACTGGTGGAGCATACACAA 685
Qy 922 TATCCAGCAGAGTGTCTCAGCGCCAGGCCCTTTTCAGGAGACCCCGAGTTACATCCAGGCC 981
Db 686 GCACTGATGGAGCGAGCATTCGCGGCCACGTTCCGGGAGGCTCTTAGTCCCTGCAATTC 745
Qy 982 CGGTCCACCTGTCAGCATGAGAATCGGCAGCAGGAGCGGCTGCTGCTGTGGTATTTGCC 1041
Db 746 GCCCGAGGTGGACACTGAGAAAAGCACCAGGAGCACTCCTCTTGTCTATCCTTCT 805
Qy 1042 CAGCACGTTGCGCATGGAGATGAAAGACATCAACA----- 1078
Db 806 GCCTACCTGGCCGAGAGATGAAGCGCAGAGATCATGGCTCGGCTGCAGGCTGGACAGAGC 865
Qy 1079 -----CAAAAAGAGAGACATGTTCCACAAGATCTACATACAGAAGCATGACATGTC 1131
Db 866 TCACGGCCAGAGAACACAACAACCTTTCACAGCCTGTATGTCAAGAGCAGCCCAAGAGATG 925
Qy 1132 AGCATCTGTTTGGCAGCATTTGAGGGCTTCACAGCCTGGCATCCACGTGCACTCGCGAG 1191
Db 926 AGTGTGCTGATGTCAGATCGTGGCTTCACAGGCTGGCCAGTGAAGTGTCCCTTAA 985
Qy 1192 GAGTGTGCTATGACCTGAAATGAGCTCTTTGCCCGGTTTGAAGCTGGCTGGCGAGAT 1251
Db 986 GAGTGTGCTCAATGCTCAATGAACTCTTCGGCAAAATTCGACCAAAATTCGAAAGAGCAC 1045
Qy 1252 CACTGCGCTGAGATCAGATCTGGGGACGTTTACTACTGTGTGTCAGGGCTGCGGAG 1311
Db 1046 GAATGCTATGCGGATCAAGATCCTGGGAGACTGTACTACTGTGTATCGGGCTGCCCTC 1105
Qy 1312 GCCCGGCGGACCATGCCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATC 1371
Db 1106 TCTCTGCTGACCAAGCATCAATTCGTCGCGATGGAGCTGGAGATGTCGCGGCGCATC 1165
Qy 1372 TCGTGTGCTGAGGTGACAGGTGTGAATGTGAACATGCGGTGGGCGATCCACAGCGG 1431
Db 1166 AGAAACTTCGGGTAGCCACCGGTGTGGATATCAACATGCGGTGTCGGTGTGCACCTCAGGC 1225
Qy 1432 CGCGTGCACCTGGGGCTCTTGGCTTGGGAATGGCAGTTTCGATGTCGTGGTCCCAATGAT 1491
Db 1226 AGCGTCTCTGTGGATCATCGGCTACAGAAGTGGCAGTATGATGTCTGGTCCCATGAT 1285
Qy 1492 GTGACCTTGGCCAAACCATATGGAAGCAGGAGCGGGCTGGCCGATCCACATCACTCGG 1551
Db 1286 GTCACATTGGCCAAACCATATGGAAGCAGGCGGCTTCAGGAGCAGTGCACATCACAGG 1345
Qy 1552 GCACACTGAGTACCTGAACGGGGACTACGAAGTGGAGCAGCGGCTGGTGGCAAGCGC 1611
Db 1346 GCCACGCTGGCCCTGCTGGCAGGAGCTTATGCTGTGTGGAGAGCAGACATGAGCATCGA 1405
Qy 1612 AACCGTACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCTCCCTGGGCGCCAGCAAAA 1671
Db 1406 GACCATACCTTCGGGAGCTAGGGGAACCCACATACCTTGGTCAATGATTCCTTGGGCTGAG 1465
Qy 1672 CGGAAAGAGGAAAGGCATGCTGGCCAAAGCTGACGCGGACTCGGGCCCAACTCCATCGAA 1731
Db 1466 GAGGAGACAGAGAGGCGCAGAGAGGATTTGCTGCTTCTCTAGAGGGGACACAGATG 1525
Qy 1732 GGGCTGATGCGCGATGGGTTCTTGATCGTGCCTTCTCCCGGACCAAGGACTCCCAAGGCC 1791

Db 1526 CGTCCGCTACACTGATGACTCGTATTC-TGGAGTCTTGGGGTGCAGCCAGCCTTTCCG 1584
Qy 1792 TTCCGCCAGATGGCAATGATTCAGCAAGACACACCGGGCACCAAGATGCCCTG 1851
Db 1585 CCACCTAAGCCAGCTGCACAGTCTCTGATCCACATCCACTCCCGGAGAAAGCCTT 1644
Qy 1852 AACCTGAGGATGAGTGGATGCTTCTGAGCCGTGCCATCGATGCCCGCAGCAITGAT 1911
Db 1645 CAGCCCCAGTGGAGCTGGACCGAGTGCACCCCCCGGGGTACACGATGAACCTGA 1704
Qy 1912 CAGCTCGGAGGACCATGTCGCCGGTTTGTG---CTACCTTCCAGAGAGAGGATTT 1967
Db 1705 CACTGAGATGCCCAAGTCTTCCAGGTTCATCGAACAACCTCAACTCTCAAAAACAGTGGAA 1764
Qy 1968 TGAGAAAGTACTCTCCGGAAGGTGGATCCCGCTTCGGAGCCCTACCTTGCCTGCGCCT 2027
Db 1765 ACAGTCAAGAGCTTCAACCTCCAGCGTCTACTTCAGAGAGAGGAGATGGAGAACA 1824
Qy 2028 GTTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCCCTGAT 2087
Db 1825 GTATCGGCTGTCTCGCTCCCGCCTTCAA-----ATACTACGACGCTGCACCTTCCT 1878
Qy 2088 GCTTGGATTTATGCCAGCATCTTCTGCTGCTGCTCTAATCACCGTGTGATCTGTGCTGT 2147
Db 1879 GGTTTTCTGTCCAACTTCAAAATCCAAATGCTGGTGACAACACGAGCCCGCAGCTCGGC 1938
Qy 2148 GTACTCTCTGTGTTCTCTGTTCCCTAAGGCCCTGCAACGCTCTGTCCCGCAGCACTGTGCCG 2207
Db 1939 CACCACCTACAGCATCACTTCT 1998
Qy 2208 CTCAGGGCACATAGCACCGAGTTGGCATCTTTTTCGCTCGCTCTGTTGTTTACTTCTGC 2267
Db 1999 GCACCTGACCAAGTGCCTCCAGAAAGCCCAAGATTTGCACTGTGGCTGCGCTGCTGTC 2058
Qy 2268 CATTGCCAAATGTTCACTGTACACACACCCCATACGAGGTGTACAGCCCGGATGCT 2327
Db 2059 TGTCTGTGGCCACAGCGCGGGATTTGGAGTAGCCCTGGGCACAGCCACCATCTCTCT 2118
Qy 2328 GAATTTAACACCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCAATTAATCTCTGCG 2387
Db 2119 GGTGTTTCACTATGCGCTGCTGAGCCTGCTCTTACCAGTGTCTGACACTGSCCCTTT 2178
Qy 2388 CTTGGATGCTCCCTGTGTGAGGACACCATGCCACCTGCAGCTTCTCTGAGGTGTCAT 2447
Db 2179 CTTGGCTCCCAATGTGCTGCTGAGTGGCTTTTAACTACTCTCTGGAGGTGCGCAGCATCCCT 2238
Qy 2448 CGGGAACATGCTGCTGAGTCTCTTGGCCAGCTCTGCTCTCTGACATCAGCAGCATCGG 2507
Db 2239 GCCTCTCATCAGATCCCATCTACTCCATGCAATTTGGTGTGGGTTTCTCTCTCTCTCT 2298
Qy 2508 GAAGTTGGCCATGATCTTTGCTTTGGGGCTCATCTAATTTGGTGTGCTTCTGCTGGTCC 2567
Db 2299 CTTTCTTCTGCATGAGCTTTCGAAGTGAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2358
Qy 2568 CCAGCCGCCATCTTTCAGCACTATGACCTACTGCTTGGGGTCCATGCTGGCTTCTTCT 2627
Db 2359 ATCTTGTGCTAATTTCTGCACTCCCAAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2418
Qy 2628 CAATGAGACCTTTGATGGCTGGAAGTCTCCAGCTGCAAGGAGGTGCGCTCAATATAT 2687
Db 2419 TTATCAAGGCTC-----ATTGGCTCCAGCGGGGGTACTGAAGAACCCGAACCTGAT 2472
Qy 2688 GACCCCTGTGATCTGCTGTTTGGCTGGCGCTGTATCTGCTGCTGCTGCTGCTGCTGCTGCT 2747
Db 2473 GGGAGCTATCTACTTCTCATCTCTTCTTTCACACTCTCTGCTGCTGCTGCTGCTGCTGCT 2532
Qy 2748 ATGACTGCGCGCCTAACTTCTCTGGAACACTACAGCAACAGGGGAAAGAGAGAT 2807
Db 2533 GTATTACTGTGCGCTGACTTCTCTATGGAAGAAAGAACTGAGGAGGAGGAGGAGAAAC 2592
Qy 2808 GGAGGACCTACAGCATACAAACCGAGGCTGCTGCATTAACATCTGCTCCCAAGGAGCTGGC 2867

Db 2593 TGAGACAA-----TGGGAATGTACTCCTCGACACGCTGGC 2628
Qy 2868 GGCCACTTCTGCTCCCGGAGCGCCCAATGATGAATGAACTTACTTATCAGTCTGCTGAGTG 2927
Db 2629 GCCCAGCTCATCGGCAGAACCGCGCACTTACCACATCAGTCTGACGAATG 2688
Qy 2928 TGTGGCTGTTATGTTTCCCTCCATTCGCAATCTCTGAGTCTTATGTGAGCTGGAGGC 2987
Db 2689 TGTGTTGTCTCTTTCATCCATCCAGACTTTAAGGAATCTTACTCGGAATCCAACAT 2748
Qy 2988 AACAATGAGGGTCCAGTGCCTGCGCTCAACGAGATCATCTGCTGACTTTGATGA 3047
Db 2749 CAACCTGAGGGGTAGAGTGTGCGCTGCTCAATGAGATCATTTGCCACTTTGATGA 2808
Qy 3048 GATTATCAGCGAGGAGCGGTTCGGCAGCTGGAAAGATCAAGACGATTTGTGACACCTA 3107
Db 2809 GCTGCTCTCCAGCCAAAGTTCACTGAGTAGAAGATCAAACTATCGGCACACCTA 2868
Qy 3108 CATGGCTGCTCAGGGGTGAACGCCAGC-----CTACGATCAGGT 3149
Db 2869 CATGGCGGCACAGCGCTAAATGCCACCTTGGGAGGACACACACAGGACGCTGAGAG 2928
Qy 3150 GGCGCGCTCCACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3209
Db 2929 AGCTGAGCAGCTGCTGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2988
Qy 3210 GCACATCAATGAGCAGCTCTTCAACAAATTTCCAGATGAAGATTTGGGCTGAACATGGGCC 3269
Db 2989 TGTATCAATAAGCAGCTCGTTCAACAACTTCCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 3048
Qy 3270 AGTCTGGGAGGTGCTATCGGGGCTCGGAGCCACATATGACATCTGCGGGGAAACAGT 3329
Db 3049 AGTCTGAGCAGGGTGTATTTGGGCACAGAACCAATATGACATCTGCGGGGAAATACAGT 3108
Qy 3330 GAATGCTCTAGTCTGATGGACAGCAGCGGGTCCCGACCGAATCCAGGTGACACCGGA 3389
Db 3109 GAACCTGCCAGCGCATGAGAGCAGCAGAGTCTCGGCAAGATCCAAAGTACCGCAGGA 3168
Qy 3390 CTTGTACAGGTTCTAGCTGCCAGGCTACCACTGAGTGTGAGGGGTGCTGCAAGGT 3449
Db 3169 GACAGCTAGGGGCTGCAATCTCGGTTACACATGCTACAGCGAGGTGTATCAAGGT 3228
Qy 3450 GAAGGCAAGGGGAGATGACCACTTCTCTCA 3485
Db 3229 CAAGGCAAGGGGAGCTGTACTCTCTCTGAA 3264

RESULT 11

US-10-144-771-16338
; Sequence 16338, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 16338
; LENGTH: 4633
; TYPE: DNA
; ORGANISM: HUMAN
; US-10-144-771-16338

Query Match 12.0%; Score 425.2; DB 6; Length 4633;
Best Local Similarity 50.7%; Pred. No. 3.7e-87;
Matches 1370; Conservative 0; Mismatches 1218; Indels 114; Gaps 10;
Qy 853 CTCTGGAAGCAGCTCGGTGCAATGTCTGTTCTCTGCAACACGCTCATAGATC 912
Db 664 CTGCTGAGGAGATCTCTGCGCAACGCTCTCTCTACCTGCTGCTATCATCTGGGATC 723
Qy 913 TGCACACTATCCAGCAGAGGTGCTCTCAGCGCAGGCTTTTACAGGAGACCGCAGTTAC 972

Db 724 ATGTCTACTATATGGCAGACCGCAAGCAGCGGCTTCTTGGAGGCCGCCAGTCA 783
Qy 973 ATCCAGGCCGGCTCCACCTGCAGCATGAGAAATCGGAGCAGGAGCGCTGCTGCTGCG 1032
Db 784 CTGAGGTGAGATGATCTGGAGGACGAGCCAGCAGGAAACCTTATGCTTTC 843
Qy 1033 GTATTGCCCCAGCAGCTTGC-----CATGGAGATGAAGAAGACATCAACACA 1080
Db 844 ATCTGCCCAAGCAGCTGGCTGAGGAGATGCTGAAGACATGAAGAAGCAGAGGCCAG 903
Qy 1081 AAAAAGAGACATGTTCCACAAGATCTACATACAGAGCATGACATGTCAGCATCCTG 1140
Db 904 AAGACAGCAGCAGTCAATATACCATGTATGATGATACCGGACGAGAAATGTCAGCATCCTG 963
Qy 1141 TTTTCAGACATTTGAGGCTTCAACAGCCTGGCATCCAGTCAGTGCACCTGGCAGGAGCTGTC 1200
Db 964 TTTTCAGATATTGTTGGCTTTACCCAGCTGTCCTCTGCTTGCACTGCCAGGAGCTCGTG 1023
Qy 1201 ATGACCTGAATGAGCTCTTTGCCGGTTTGACAAGCTGGCTGGGAGAAATCACTGCTG 1260
Db 1024 AAGTTACTCAACAGAGCTCTTCCCGCTTTGACAAGCTGGCAGGCAATACACACAGCTG 1083
Qy 1261 AGGATCAAGATCTTGGGGAGCTGTACTACTGTGTGTCAGGCTGCCGGAGGCCGGGCC 1320
Db 1084 AGGATCAAGATCTTAGGCGACTGTACTACTGTGCATCTGCGGCTTGCCTGACTACCGGAG 1143
Qy 1321 GACCATGCCACTGCTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCGCTGCTGA 1380
Db 1144 GACCATGCCGTGCTCCATCTTATGGGCTTCCCATGTGTAGAGCCATCTCGTACGTG 1203
Qy 1381 CGTAGGTGACAGTGTGAATGTGAACATGGCGCTGGCATCCACAGCGGCGGTGCAC 1440
Db 1204 CGGAGAGACCAAGACTGGAGTGGACATGCGTGTGGAGTGCACAGGCACTGTCTCA 1263
Qy 1441 TGGCGCTCTTGTGCGAAATGCAAGTTCGATGTGTGCTCCATGATGTGACCTG 1500
Db 1264 GCGCGTCTCTGGCCAGAGCGCTGGCAGTATGATGTATGTTGCTACTGATGTACCGTG 1323
Qy 1501 GCCAACCATGGAAGCAGGAGCGGGCTGGCGCATCCACATCACTCGGCGCAACACTG 1560
Db 1324 GCAACAAGATGGAGCTGGTGGCATCCAGGGCGGTGCACATTTCCACAGACCCATG 1383
Qy 1561 CAGTACCTGAACGGGACTAGCAAGTGGAGCGAGCGCTGTGTCAGCGCAACCGGTAC 1620
Db 1384 GACTGCCCTGAAGGGGAGTTGATGTGAGCGCTGTATGGGGCAGCTCGCTGCGACTAC 1443
Qy 1621 CTGAAGGAGCAGCATGAGACTTCTCATCTCTGCGGCC-AGCCAGAAACGGAAGA 1679
Db 1444 CTAGATGAAGAGGCATCGAAACCTACCTCATCATGCTCCAGCCAGAGGTGAAGAA 1503
Qy 1680 GGAGAAAGGCATGCTGCCAAAGCTGCAGCGGACTCGGGCCCACTCCATGGAAGGCTGAT 1739
Db 1504 ACAGCCCAAAATGGCTCAACGGCTCGGCCGTGCCAAAGCAGCGCGCATCTCCAAA 1563
Qy 1740 GCC-GCGATGGTTCTGATGCTGCTTCTCCCGGACCAAGGACTCCAAAGGCTTCCGCC 1798
Db 1564 CCCAGCTCCCTGCTCATCGAGACCAAGGAGCCCAATGAAGTGGCCCATGCCAGCGGC 1623
Qy 1799 AGATGGGATTTGATGATTCAGCAAAAGCAACCGGGGCAACCAAGATGCCCTGAAACCTG 1858
Db 1624 TCCACATCAGAGAGGCTGAAGACAGAGGCCCGCAGGCTGACACCCCTCGTCCCCAAC 1683
Qy 1859 AGGATGAGGTGGATGAG--TTCTGAGCCGTGGCCATCGATGCCCGCAGCATTTGATCAGCT 1916
Db 1684 CCCCGCCAGGCTCGCGCTCCAGGACCTGGCGGACCGCTGTGGTGGAGCGCTCTGAGGAT 1743
Qy 1917 CGGAGAGACCATGTGCCCGGTTTTCCTCACTTCCAGAGAGGATTTTGGAGAGAA 1976
Db 1744 GAGCACGAACCTGAACAGCTGCTTAATGAGCCCTGCTGGAGCGGGAGTCCGCCAGGTG 1803
Qy 1977 GTACTCCCGGAGGTGGATCCCGCTTCCGAGCCCTACCTGTTGCCCTGTGCTGCTGCT 2034
Db 1804 GTAAAGAGAGAAACACATCTCTCT---GACCATGAGGTTGATGGACCCAGAGATGGAA 1860

Qy 2035 TTCTGCTTCACTCTCTTATCCAGCTTCTAAATTTTCCACACTCCACCTGATGCTTGGG 2094
Db 1861 ACAGCTACTCTGGTGGAGAGAGAGAGCGGGCTGCTTCAGCTGCTCTGTGTG 1920
Qy 2095 ATTTATGCCAGCATCTTCTCTGCTGCTAATCAACCGTGTGATCTGTGTGTACTTCC 2154
Db 1921 GTCCTCTTCTGACGGCATGGTGGAGATCACTATGACC-----CTTGGCTGATG 1971
Qy 2155 TGTGTTCTCTGTTCCCTAAGGCCCTGCAAGCTGTGCCCGCAGCATGTCCTGTCACGG 2214
Db 1972 ACAACTATGTGACCTTGTGGTGGGAGGTTCTGCTCTGATCCTGACCATCTGTCTCG 2031
Qy 2215 GCACATAGCACCGCAGTGGCATCTTTTCCCTCTCTGCTGTGTGTGTACTTCTGCCATTGCC 2274
Db 2032 ATGCTGCCATCTTTCACAGTCAATTTCCCAAGAAGCTTGTGGCTTCTCATCTTGGATT 2091
Qy 2275 AACATGTTCACTGTAAACCAACCCCATACGGAGCTGTGAGCCCGGATGCTGAATTA 2334
Db 2092 GACCGGACCGCTGGCAAGAACACCTGGGCCATGTAGCCATCTTCAATCTGTTATG 2151
Qy 2335 ACACCTGCTGACATCACTGCTGCCACTGCAGCAGCTCAATTAATCTCTCTGGGCTGGAT 2394
Db 2152 GCCAATGTTGGACATGCTCAGCTGTCTCAGTACTACATGGGACCTTACAACATGACA 2211
Qy 2395 GCTCCCTGTGTGAGGACCATGCCACCTGCAGCTTTTCTGAGGTTCCTCGGGAAC 2454
Db 2212 GCTGGATGGAGCTGGAGCGGCTGCATGGAGAAC---CCCAAGTACTACAACCTACGTA 2268
Qy 2455 ATGCTGCTGAGTCTTGGGCCAGCTGTCTTCTTGCACATCAGCAGCATCGGAAGTTG 2514
Db 2269 GCTGTGTGCTGCATCGCCACCATCATGCTGTGTGAGGTGAGCCACATGGTGAAGCTG 2328
Qy 2515 GCCATGATCTTGTCTTGGGCTCATCTATTGTTGTGCTGCTTCTGCTGGTCCCCCAGCC 2574
Db 2329 ACGCTCATGCTGCTGCACAGGCGCGTGACTGCCCTCAACCTGTAGCCCTGTGTCTCT 2388
Qy 2575 GCCATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGCTTGGCTTCTTCCAATGAG 2634
Db 2389 GTCCTTGATGAATACGACCAAGCGCTTTCAGGAAAAGGACAGGCTGCC----- 2438
Qy 2635 ACCTTTGATGGGCTGGACTGCCAGCTGCAGGAGGTTGGGCTTCAATATATGACCCT 2694
Db 2439 -----CCTGGTGCCTTCCAAGTACTCCATGACT 2466
Qy 2695 GTGATCTGCTGTGTTTGGCTGCGCTGTATCTGCTCAGCTGAGCTGGAATGCGACT 2754
Db 2467 GTGATGATGTTGTCATGATGCTGAGCTTTTACTACTTCTCGGCCAGCTGGAAAACCTG 2526
Qy 2755 GCCCGCTTAACTTCTCTGGAACCTACAGGCAACAGGGGAAAAGAGAGATGGAGAG 2814
Db 2527 GCCGGAACACTGTCTTGTGGAAGATTGAGGTCCATGACCAAGAAAGACGTCTCTACGAG 2586
Qy 2815 CTACAGCATACACCGAGGCTGCTGCATAACTTCTGCCCAAGGAGCTGGCGCCAC 2874
Db 2587 ATGCGCGATGGAAGAGGCGCTTGTTCACCAACTGTTGCTGAGCATGTTGCGAGCCAT 2646
Qy 2875 TTTCTGGCGCGGAGCGCGCAATGATGAATCTACTATCAGTCTGTGAGTGTGTGCT 2934
Db 2647 TTTCTGGGTCGAAGAGAGATGAGGAGCTGTACAGCCAGTCTTATGACGAGATTGGA 2706
Qy 2935 GTTATGTTTGGCTCCATTTGCCAACTTCTCTGAGTCTTATGTTGGAGCTGGAGCAACAAT 2994
Db 2707 GTCATGTTTGGCTCTCTTGGCCAACTTGTGCTGACTTCTACACTGAGGAGCATCAACAAC 2766
Qy 2995 GAGGTGCCGAGTGTGCTGCGGCTGCTCAACGAGATCATCGCTGACTTGTGATGAGATTATC 3054
Db 2767 GCGGCGATCGAGTGTCTACGCTTCTCAATGAGATCATCTCTGATTTTGAATCTCTCTG 2826
Qy 3055 AGCAGGAGCGGTTCCGCGAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGCT 3114
Db 2827 GACAATCCCAATTTCCGGGTCATCACCAGATCAAACTATTGGCAGCACCTATATGCA 2886

QY 3115 GCCTCAGGGCT-----GAAGCCAGC 3135
Db 2887 GCTTCAGGAGTCACACAGATGTAACACCAATGGCTTTACAAAGCTCCAGCAAGGAGGAG 2946
QY 3136 ACCTACGATCAGGTGGCCGCTCCACATCAGTCCCTGCTGACTACGACGATGCGGCTC 3195
Db 2947 AAGTCAGACAAGAGGCGCTGGCAGCAGCTGCTGACCTGGCTGACTTTGGCATTAGCCATG 3006
QY 3196 ATGAGCAGATGAAGCAGATCAATAGCAGCTCTCTCAACAATTTCCAGATGAAGATTGGG 3255
Db 3007 AAGGACAGCTCACAACATCAACAACAGTCAATCAACAATTCATTTGGCATAGGC 3066
QY 3256 CTGAACATGGCCCGAGTCGTGGCAGTGTCTATCGGGCTCGGAAGCCACAGATATGACATC 3315
Db 3067 ATGAACAAGAGGGGTTCTGGCTGGCTCATTTGGAGCCCGAAACACACATATGACATC 3126
QY 3316 TGGGGACACAGTGAATGCTCTAGTCTGATGGACAGCAGGGGCTCCCGACCGGATC 3375
Db 3127 TGGGGCAATACGGTCAATGTGGCCAGCAGGATGGAATCCACAGGAGTCAATGGGCAACATC 3186
QY 3376 CAGGTGACCACGAGCTGTACCAGGTTCTAGCTGCCAAGGGCTACCAGCTGGAGTGTGCA 3435
Db 3187 CAGGTGTAGAAGAGCGCAGGTCACTCTCGAGAGTACGGCTTCCGCTTTGTGAGCGCA 3246
QY 3436 GGGGTGTCAAGGTGAAGGCAAGGGGAGATGACACACCTACTTTCCTCAATGGGGGGCC 3495
Db 3247 GGTCCCATCTTTGTGAAGGCAAGGGGAGCTTGTGACCTTTTCTTTGAAGGGGCGGGAC 3306
QY 3496 AG 3497
Db 3307 AG 3308

RESULT 12
US-10-144-771-3825
; Sequence 3825, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craly
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 3825
; LENGTH: 3458
; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-3825

Query Match 11.6%; Score 410.8; DB 6; Length 3458;
Best Local Similarity 50.4%; Pred. No. 6.5e-84;
Matches 1380; Conservative 0; Mismatches 1227; Indels 133; Gaps 10;

QY 862 CAGCTCGTCCCAATGCTGCTCTCTCCCTGCACCAACGCTATTAGCATCTCCACAC 921
Db 629 CAGTTGGCAGCAACGCGGTATTGTTCTCTGTGGGACGTTGGTGGGCGCTACCAAG 688
QY 922 TATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAGACCGCGAGTTACATCCAGGCC 981
Db 689 GCCTGTATGAGCGAGCATTTGCGGCCACGTTCCGGGAGCTCTTAGCTCTCTGCATCA 748
QY 982 CGGCTCCACCTGAGCATGAGATGCGCAGCAGAGCGGCTGCTGCTCGGTATTGCC 1041
Db 749 CGCCGGAGGTGAGACATGAGAAAAAGCAGGAGCACCCTCCTTGTCTATCTCTCT 808
QY 1042 CAGCAGCTTCCCATGGAGATGAAGAGACATCAAC----- 1077
Db 809 GCCTACTGCGCCGAGAGATGAAGAGAGATCATGGCCCGGCTGCGGCTGGACAGCGC 868
QY 1078 -----ACAAAAAAGAGACATGTTCCCAAGATCTACATACAGAGCATGACATGTC 1131
Db 869 TCACGGCCAGAGAACACAACTTTTCACAGCCTGTATGTCAGAGGAGCCACCAAGGAGTG 928

QY 1132 AGCATCTCTGTTTCAGACATTTAGGGGCTTACCAGCCTGGCATCCAGTGCATGCGCAG 1191
Db 929 AGTGTGCTGTATGCTGACATCGTGGGCTTTCACGCGGCTGCCAGCGAGTGTTCGCCGAAG 988
QY 1192 GAGCTGGTCAATGACCCCTGAATGAGCTCTTTGCCCGGTTTTCACAGAGCTGGCTGGCGAAT 1251
Db 989 GAGCTGGTGTCTGCTGAATGAGCTCTTTGGCAAGTTTCGACCAAAATTCGCAAGAGGAC 1048
QY 1252 CAGCTGTGAGGATCAAGATCTTGGGGAGCTGTTACTACTGTGTGTCAGGCTGCCGGAG 1311
Db 1049 GAATGATGCGGATCAAGATCTTGGGAGACTGTTACTACTGTGTCTCCGGCTGCCCTC 1108
QY 1312 GCCCGGCGCCAGCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGATTTAGAGCCATC 1371
Db 1109 TCCTGTGCTGACCCAGCTATCAATTTGTCGCATGGGCTGGACATGTCGCGGGCCATC 1168
QY 1372 TCCTGTGCTGAGGTGACAGGTGTGAATGTGAACATGCGGCTGGGCTCCACAGCGGG 1431
Db 1169 AGAAATCTTCGGGTAGCACCGGCTGTGGATATCAACATGCTGTGGCGTGCATCTCGGGC 1228
QY 1432 CGCTGTGACTCGCGGCTTGGCTTGCAGAAATGGCAGTTTCGATGTGTGTCCTCAATGAT 1491
Db 1229 AGCTTCTCTGTGGCTTACAGAGTGGCAGTATGATGTCTGTGTCCTCCATGAT 1288
QY 1492 GTGACCTTGCCCAACACATGGAAGAGAGAGCGGGCTGGCCGATPCCACATCACTCGG 1551
Db 1289 GTCACATTTGGCCCAACATATGGAAGCAGCGGCTGTACCAGGAGAGTGCACATCACAGG 1348
QY 1552 GCAACACTGCAGTACCTGAACGGGAGTACGAAGTGGAGCAGCGCTGTGTGGCAAGCGC 1611
Db 1349 GCCACGCTGGCCCTGTAGCAGGAGCTTATGCTGTGGAGAGGCGACACAGCGAACCAG 1408
QY 1612 AAGCGCTTACCTCAAGGAGCAGCACATTTGAGACTTTCCTCATCTCTGGCGCCAGCAGAAA 1671
Db 1409 GACCCATACCTTCGGGAGCTAGGAGAACCTACATACCTGGTCACTGCTCGGGCTGAG 1468
QY 1672 CGAAAGAGGAGAGAGCATGCTGGCCCAAGCTGCAGCGGAGCTGGGCCAACTCATGAGAA 1731
Db 1469 GAGGAAGACAGAGAGGAGCGCCGCAAAAGAGTGTCTCTCTGGAGGGGCGACAGATG 1528
QY 1732 GGCTGTATGCGCGGATGGGTTCTGATGCTGCTTCCCGGAC---CAAGGACTCCAAAG 1788
Db 1529 CTTCGCTCACTACTGATGACTCGCTATCTGAGTCTTGGGCTGCAGCCAGCCCTTCGCC 1588
QY 1789 GCCTTCGCGCAGATGGGCTATTGATTTCC----- 1818
Db 1589 CACCTAAGCCACCTTGACAGCTCGCTGCCACTCCACTCCACTCCCGGAGAAAGCCTTC 1648
QY 1819 -----AGCAAGACAAACCGGGGCAACCAAGATGCCCTGAACCTGTA---GGAT 1863
Db 1649 AGCCCCCAGTGGAGCCTTGGACCGGAGTGCACACCCCGGGGAGCTAGATGATGAACCTGC 1708
QY 1864 GAGTGTGATCAGTCTCTGACCGTGCATCGATGCCCGCAGCATTTGATGAGTGCAGGAG 1923
Db 1709 ACTGTGTATGCTAAGTCTTCCAGGTCTCAACAACCTCACTCTCAGAAGATGAAGC 1768
QY 1924 GACCATGTGCGCGGCTTTTGTCTCACCTTCCAGAGAGAGGATTTTGAGAAAGATGATCC 1983
Db 1769 CAGAGGCTGGAAGCCCAATGGTGTGTGGAGAGGTGGAAGCAGTGCAGAGGACTTC 1828
QY 1984 CGAAAGTGGATCCCGCTTCGGAGCCTAGTTCCTGTCCTGTCCTGTCCTCTCTGCTTC 2043
Db 1829 AACCTCTGACGCTGATTTTCAGAGAGAGGAGATGAGAAACAGTATCGGCTCTCTGCA 1888
QY 2044 ATCTGCTTACAGCTTCTAATTTTCCACACTCCACCTGATGCTGGGATTTATGCC 2103
Db 1889 CTCCCGCTTCAA-----ATACTAGCAGCCTGCACCTTCTCTGTTTCTGTCTCAAC 1942
QY 2104 AGCATCTTCTGCTGCTTAATCAGCGTGTCTGATCTGTCTGTGTACTCTCTCTG--- 2159
Db 1943 TTCATCTCAAAATGCTGTGTGACAAACCGAGCCCGCAGCTCTGATCATCACTACAGCATC 2002
QY 2160 -----TTCCTCTGTTCCCTAAGCCCTGCAACGTCTGTCTCCCGCAGCATTTGTCCGCTAC 2212

Qy	3365	CGACCGAATCAGAGGTACACGAGGACCTGTACCAAGGTTCTAGCTGCCAAGGGCTACCA	GC	3424
Db	2987	TGGACAAAATACAGAGTGACTGAGGAGACAAGCCTCATCTGCAGACGCTTGGCTACACGT		3046
Qy	3425	TGGAGTGTCTGAGGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACCACTACTTTCCTCA		3484
Db	3047	GTACATGTGAGGTATCATCAACGTGAAGGGGAAAGGGACCTGAAGACGTA	CTTTGTAA	3106
Qy	3485	A 3485		
Db	3107	A 3107		

RESULT 14

US-09-724-676-11592

; Sequence 11592, Application US/09724676

; GENERAL INFORMATION:

; APPLICANT: CompuGen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 CompuGen

; CURRENT APPLICATION NUMBER: US/09/724,676

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 11592

; LENGTH: 3756

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-724-676-11592

Query Match	10.2%;	Score 362.8;	DB 5;	Length 3756;	...
Best Local Similarity	50.6%;	Pred. No. 6.3e-73;			
Matches 1172;	Conservative	0;	Mismatches 1082;	Indels	60; Gaps
Qy	861	GCAGCTCGGTGCCAATGTGCTGCTTCCTCTGCACCAACGATTCATTAGCATCTGCACACA	920		
Db	819	GGAGATCCTGGCCCAACGCTTCTCTACCTGTGGCCCATCGCTGTGGCATCATGTCTCTA	878		
Qy	921	CTATCCACGAGAGGTGTCTACGGCCGACGCCCTTTTCAGGACGCCAGCTTACATCCAGGC	980		
Db	879	CTACATGGCTGACCGCAAGCAGCCGAAGGCCCTTCGTGGAGGCCGCCACAGTCGCTGGAGGT	938		
Qy	981	CCGCTCCACCTCCAGCATGAGAATCGGCAGACGAGCGGCTGCTGCTCGGTATTGCC	1040		
Db	939	GAAGATGAACCTGGASAGACGAGCCAGCCAGCGACGAGAACCTTCATCTTTTCATCCTGCC	998		
Qy	1041	CCAGCACGTTGCCATGGAGATGAAGAGACATCAACACA	1088		
Db	999	CAAGCACGTGGCTGACGAGATGCTGAAGACATGAAGAAAGACGAGAGCCAGMAAGACCA	1058		
Qy	1089	AGACATGTTCCACAAGATCTACATACAGAAGCATGACATGTACAGATCCTGTTTGCAGA	1148		
Db	1059	GCAGCAGTTTCAACACCATGTACATGTACCGTCAAGAGAACGTCAGCATCCTCTTTGCCGA	1118		
Qy	1149	CATTGAGGGCTTCACCAGCTGGCATCCAGTGCACCTGCGCAGGAGCTGGTCATGACCT	1208		
Db	1119	CATCGTGGGCTTTACCCAGCTGCTTCTGCCCTGCAGTGCCAGGAGCTGTGCAAGCTGCT	1178		
Qy	1209	GAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGATACACTGCTGAGGATCAA	1268		
Db	1179	CAACGAGCTCTTTGCCCGCTTTTGACAAGCTGGCAGCTAAATACCAACAGCTCGGATTA	1238		
Qy	1269	GATCTGGGGAGCTGTACTACTGTCTGTCAAGGCTGCCGAGGCCGCCGCCGACCATGCC	1328		
Db	1239	GATCCTGGGGAGCTGTACTACTGTGCATCTGCGGCTTGCCYGACTACCGGGAGGACCCAGC	1298		
Qy	1329	CCACTGTGTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCGCTGTTACGTGAGGT	1388		
Db	1299	CGTCTGCTCCATCCTCATGGGCTGGCCATGGTGGAGGCCATCTCGTATGTGCGGGAGAA	1358		
Qy	1389	GACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGGTGCATCTGCGGGCT	1448		
Db	1359	GACCAAGACTGGGGTGACATGCTGTGGGGGTGCACACGGGCACGCTGCTGGGGGGCT	1418		

Qy	1449	CTTTGGCTTGGGAAATGGCAGTTGCATGTGTGGTCTCAATGATGTGACCCCTGGGCAACCA	1508
Db	1419	CCTGGGCGAAGCGCTGGCAGTAGCACGTGTGGTFCGACTGATGTCTACTGTGTGACCAAA	1478
Qy	1509	CATGGAAGCAGGAAGCGGCTGGCGGATCCACATCACTCGGCAACACTGCAGTAGCTT	1568
Db	1479	GATGGAGCGCGGGCATCCCTGGGGCGTGCATCTCCAGAGCACCATGTGACTGCCT	1538
Qy	1569	GAACGGGACTACGAAGTGGAGCCAGGCGGTGGTGGCAAGCGCAACGCGTACTCTCAAGGA	1628
Db	1539	GAAGGGGAGTTTGTGTGGAGCAGCGATGGGGCAGCGCTGTGATTACCTTAGAAGA	1598
Qy	1629	GCAGCACATTGACACTTTCCTCATCTGGGCGCC--AGCCAGAAACGGAAGAGAGAAG	1687
Db	1599	GAAGGTGTTGAACCTACTCATATTGCCFCCAAGCAGAGGTGAAGAAACAGCCAC	1658
Qy	1688	GCATGCTGGCCAAAGCTGCAGCGGACTCGGGCCCACTCCATGGAAGGCGTGTATGCCGGAT	1747
Db	1659	CCAGAATGGCTCAAT-----GGCTCGGCCCTGCCCCAATGGAGCACCACTTCTCTAAA	1712
Qy	1748	GGGTTCTGTATCTGCTTCTCCGGACCAAGGACTCCAAAGCCTTCGCGCAGATGGCA	1807
Db	1713	GTCCAGCT--CCCCGTGCCCTCATTTGAGCAAGAGGCCCAACGGGAGTGGCCA-----CA	1765
Qy	1808	TTGATGATTTCCAGCAAAAGACAACCGGGGCACCAAGATGCCCTGAACCTCAGGATGAGG	1867
Db	1766	GCAGTGGGTCCACGTGCGAGAAGCCGAGGACAGGATGCCAGCGCAACCCCTCAT	1825
Qy	1868	TGATGATGTTCTGAGCGGTGCATCGATGCCCGCAGACATTTGATCAGCTGCGGAAGACC	1927
Db	1826	TCGCCAACCCACCGCGAGGCTGCGCCTGCAGAGACTGGCTGACCGAGTGTGTGATGCCT	1885
Qy	1928	ATGTGCGCCGGTTTTTGTCTCAC----TTCCAGAGAGAGGATTTTGAAGAAGTACTCCC	1984
Db	1886	CTGAGATGAGCAGAGCTCAACCAGTCTCTCAACGAGGCCCTGCTTGAGCGAGAGTCGG	1945
Qy	1985	GGAAAGTGGATCCCGCTTCGGAGCCTAGCTTGGCTGTGCCCTGTTGGTCTTTCTGCTTCA	2044
Db	1946	CCCAAGTAGTAAAGAGAGAAACACCTTCTCTTTGTCCATGCGGTTCATGGACCCCGAGA	2005
Qy	2045	TCTGCTTCATCCAGCTCTTAATTTTCCCACACTCCACCTGATGCTTGGGATTTATGCCA	2104
Db	2006	TGGAACCCCGTACTCGGTGGAGAAGAGAAGAGTGGGGCTGCCCTCAGCTGCTCCT	2065
Qy	2105	GCATCTTCCTGCT-----GCTGCTAATCACCGCTGCTGATCTGTGCTGTACTCCTGTG	2158
Db	2066	CGGTGCTTCTGCTGTGCACGGCCCTGGTGAGATACTATCAGCCCTTGGCTAATGACAA	2125
Qy	2159	GTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCGGCAGATTTGCCGCTCACGGCAC	2218
Db	2126	ACTATGTGACTTCATGTGTGGGGGAGTTCTGCTCCTCATCTCTGACCATCTGCTCCCTGG	2185
Qy	2219	ATAGCACCGCAGTTGGGCATCTTTTTCGCTCCTGCTTGTGTTTACTTCTGCCATTTGCCAACA	2278
Db	2186	CTGCCATCTTCCCGGGCCCTTTCTCTAAGAAGCTGTGGCCCTCTCAACTTGGATTGACC	2245
Qy	2279	TGTTTCACTGTAAACACACCCCCATACGGAGCTGTGCAGCCCGGATGCTGTAATTTAAACAC	2338
Db	2246	GGACCCGCTGGGCAGGAACACCTCGGGCCATGCTCGCCATCTTCATCTCTGTTGATGGCAA	2305
Qy	2339	CTGCTGACATCACTGCTCGCCACTCGACAGCTCAATTTACTCTCTGGGCTGGATGCTC	2398
Db	2306	ATGTCGTGGACATGCTCAGCTGTCTCCAGTACTACAGGGACCACGAATGCAACGGCAG	2365
Qy	2399	CCCTGTGTGAGGGCACCATGCCACCTGACGCTTTTCTGAGGTGTCCATCGGGAACTATGC	2458
Db	2366	GGATGGAGACGGGGCAGCTGCTGGAGAAC----CCCCAAGTATTACAACATGTGTGGCG	2422
Qy	2459	TGCTGAGTCTTGTGGCCAGCTGTCTTCTCTGCACATCAGCAGCATCGGGAGTTGGCCA	2518
Db	2423	TGCTGTCCCTCATCTGCCACCATCATGCTGGTGCAGTCAAGCACAATGTTGAAGTCAAGC	2482

